



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 174325**

**TO: Patricia Duffy**  
**Location: REM-3B05/3C18**  
**Art Unit: 1645**  
**Thursday, December 22, 2005**

**Case Serial Number: 10/077137**

**From: Paul Schulwitz**  
**Location: Biotech-Chem Library**  
**REM-1A65**  
**Phone: 571-272-2527**

**Paul.schulwitz@uspto.gov**

### **Search Notes**

Examiner Duffy,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
REM-1A65  
571-272-2527



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From: Duffy, Patricia  
Sent: Thursday, December 15, 2005 9:06 AM  
To: STIC-Biotech/ChemLib  
Subject: SEQUENCE SEARCH 10/077,137

IN RE: 10/077,137

PLEASE SEARCH RESIDUES 1-51 OF SEQ ID NO:1.  
PLEASE SEARCH RESIDUES 8-41 OF SEQ ID NO:1

PLEASE SEARCH BOTH COMMERCIAL AND INTERFERENCE DATABASES.  
PLEASE PRINT OUT TOP 75 HITS IN EACH CATEGORY.

THANKS MUCHO.

Patricia A. Duffy, Ph.D.  
Art Unit 1645  
Remsen 3B05; Mailbox 3C18  
571-272-0855

RECEIVED  
DEC 15 2005  
STIC

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_



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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 15:43:09 ; Search time 159.6 Seconds  
(without alignments)  
140.403 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_1\_51

Perfect score: 283

Sequence: 1 MLOAGQCSQNEFYFDSLLHA.....TPPLTCQRCYNASVTNSVKG 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : A Geneseq 21.\*

1: geneseqp1980s.\*

2: geneseqp1990s.\*

3: geneseqp2000s.\*

4: geneseqp2001s.\*

5: geneseqp2002s.\*

6: geneseqp2003as.\*

7: geneseqp2003bs.\*

8: geneseqp2004s.\*

9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	283	100.0	52	9	AEC02032 Amino aci
2	283	100.0	184	3	AB08843 Amino aci
3	283	100.0	184	3	AY94001 A human B
4	283	100.0	184	4	AE09241 Human BCM
5	283	100.0	184	4	AY71979 Human B C
6	283	100.0	184	4	AB60698 Human BAF
7	283	100.0	184	4	AB06056 Human B C
8	283	100.0	184	5	AB81487 Human BCM
9	283	100.0	184	5	ABP54694 Metastati
10	283	100.0	184	5	ABP28961 Human B-C
11	283	100.0	184	6	AE35216 Human BCM
12	283	100.0	184	6	ADA49361 Human BCM
13	283	100.0	184	6	ABP60552 Human tum
14	283	100.0	184	6	ABP97717 Amino aci
15	283	100.0	184	7	ADD67527 Human B-C
16	283	100.0	184	7	ADG43715 Native hu
17	283	100.0	184	8	ADK00756 Neutrokin
18	283	100.0	184	8	ADQ94442 Human PRO
19	283	100.0	184	8	ADP56014 Human BCM
20	283	100.0	184	9	ADW03432 Human tum
21	283	100.0	184	9	ADZ67760 Tumor ant
22	283	100.0	184	9	AEA23348 Amino aci
23	283	100.0	184	9	AEC02031 Amino aci
24	283	100.0	302	4	AB60699 Mouse Igg

25	283	100.0	302	4	AAE00507 Human BCM
26	283	100.0	302	7	ADG43717 Human B-C
27	277	97.9	184	6	ABR40082 Human Gen
28	274	96.8	288	5	ABG95060 Human tra
29	269	95.1	51	5	AAE15485 Human B-C
30	269	95.1	181	5	AAE15484 Human B-C
31	269	95.1	283	5	AAE15488 Human BCM
32	257	90.8	296	9	AEC02042 Amino aci
33	249	88.0	58	5	AAE15501 Human B C
34	230	81.3	40	9	ADZ67761 Human tum
35	215	76.0	38	9	AEC02033 Amino aci
36	206	72.8	157	4	AB60700 Human BAF
37	201	71.0	34	5	AAE15486 Human B-C
38	197	69.6	34	6	ADA49366 Human BCM
39	197	69.6	34	9	AEC02026 Formula I
40	196	69.3	34	9	AEC02027 Formula I
41	194	68.6	34	9	AEC02028 Formula I
42	194	68.6	34	9	AEC02017 Formula I
43	192	67.8	34	9	AEC02025 Formula I
44	192	67.8	34	9	AEC02024 Formula I
45	191	67.5	34	9	AEC02020 Formula I
46	189	66.8	34	9	AEC02029 Formula I
47	189	66.8	34	9	AEC02019 Formula I
48	182	64.3	185	3	AB08844 Amino aci
49	181	64.0	185	3	AAE15491 Human BCM
50	181	64.0	185	5	AAE15490 Mouse B C
51	181	64.0	185	5	AAE15490 Mouse B C
52	181	64.0	185	5	ADZ67762 Mouse tum
53	181	64.0	281	5	AAE15489 Mouse BCM
54	158	55.8	42	6	ABJ38417 TALL-1 re
55	151	53.4	26	7	AD153060 Human BCM
56	104	36.7	117	5	AAE15491 Human-mur
57	90.5	32.0	24	3	AY94006 A murine
58	71.5	25.3	249	3	AAE15492 Mouse pro
59	71.5	25.3	249	7	ABM85744 Mouse tum
60	71.5	25.3	249	9	ADZ67773 Mouse nec
61	71.5	25.3	249	9	AEAS5078 Tumor nec
62	70.5	24.9	1548	7	ADC71568 Murine su
63	70.5	24.9	1877	7	ABB80243 Murine su
64	68.5	24.2	332	6	AAE35228 Human TAC
65	68.5	24.2	1569	8	AD18921 Human muc
66	68.5	24.2	2240	8	AD18914 Mature Hu
67	68.5	24.2	2258	8	AD18913 Human muc
68	68.5	24.2	2264	8	AD18915 H1e-tagge
69	67.5	23.9	37	5	AAU10951 Human AGP
70	67.5	23.9	48	9	ADZ67772 Human tum
71	67.5	23.9	59	5	AAE15500 Human TAC
72	67.5	23.9	166	2	AAW75785 Human TAC
73	67.5	23.9	166	5	AAE15494 Human TAC
74	67.5	23.9	171	8	ADN03188 Human TAC
75	67.5	23.9	265	4	AE09244 Human TAC
76	67.5	23.9	266	6	ABP97723 Amino aci
77	67.5	23.9	266	9	ADW03442 Human TAC
78	67.5	23.9	291	5	AAU10949 Human AGP
79	67.5	23.9	292	9	ADZ67771 Human tum
80	67.5	23.9	293	2	AAW75783 Human neu
81	67.5	23.9	293	3	AAE36312 Human neu
82	67.5	23.9	293	3	AAE36312 Human neu
83	67.5	23.9	293	4	AAE36312 Human neu
84	67.5	23.9	293	4	AAE36312 Human neu
85	67.5	23.9	293	5	AB881488 Human tra
86	67.5	23.9	293	5	AAU99512 Human TAC
87	67.5	23.9	293	5	AAU99512 Human TAC
88	67.5	23.9	293	5	AAU99512 Human TAC
89	67.5	23.9	293	5	AAU99512 Human TAC
90	67.5	23.9	293	5	AAU99512 Human TAC
91	67.5	23.9	293	5	AAU99512 Human TAC
92	67.5	23.9	293	5	AAU99512 Human TAC
93	67.5	23.9	293	5	AAU99512 Human TAC
94	67.5	23.9	293	6	ABE35211 Human tra
95	67.5	23.9	293	6	ABP60551 Human TAC
96	67.5	23.9	293	6	ABP97716 Human tum
97	67.5	23.9	293	6	AAO29592 Amino aci
98	67.5	23.9	293	7	ADZ67762 Human tum



98	67.5	23.9	293	7	ADF77379	Adf77379 Human tum	171	63	22.3	175	9	AEA01659	Aea01659 B-cell ac
99	67.5	23.9	293	7	ABM85745	Abm85745 Human pro	172	63	22.3	314	9	ADW03396	Adw03396 Mouse BR3
100	67.5	23.9	293	8	ADK00754	Adk00754 Native hu	173	63	22.3	316	9	AEA01660	Aea01660 Murine BA
101	67.5	23.9	293	8	ADJ92514	Adj92514 Human TAC	174	63	22.3	1887	6	ABU12113	Abu12113 Human pro
102	67.5	23.9	293	8	ADN03174	Adn03174 Human TAC	175	63	22.3	1887	7	ABB80242	Abb80242 Human sub
103	67.5	23.9	293	8	ADQ76815	Adq76815 Human TAC	176	63	22.3	1887	7	ADM29324	Adm29324 Human nov
104	67.5	23.9	293	8	ADQ94440	Adq94440 Neutrokin	177	62.5	22.1	138	5	ABP69063	Abp69063 Human pol
105	67.5	23.9	293	9	ADW03430	Adw03430 Human TAC	178	62.5	22.1	558	8	AQD82379	Aqd82379 Novel hum
106	67.5	23.9	294	8	ADK00765	Adk00765 hTACI epl	179	62.5	22.1	775	8	AQD82382	Aqd82382 Fibulin-1
107	67.5	23.9	294	9	ADW03443	Adw03443 Human TAC	180	62.5	22.1	818	8	ADQ82380	Aqd82380 Fibulin-1
108	67.5	23.9	312	5	AAO14135	Aao14135 Protein o	181	62.5	22.1	818	8	AQD82377	Aqd82377 Novel hum
109	67.5	23.9	334	5	AAO14133	Aao14133 Protein o	182	62.5	22.1	818	8	AQD82383	Aqd82383 Fibulin-1
110	67.5	23.9	344	6	AAE35224	Aae35224 Human TAC	183	62.5	22.1	985	7	ADM04189	Adm04189 Human pro
111	67.5	23.9	348	6	AAE35225	Aae35225 Human TAC	184	62.5	22.1	992	7	AAE35809	Aae35809 Human POL
112	67.5	23.9	357	6	AAE35226	Aae35226 Human TAC	185	62.5	22.1	999	8	ADN23019	Adn23019 Bacterial
113	67.5	23.9	366	5	AAO14132	Aao14132 Protein o	186	62.5	22.1	999	8	ADN23018	Adn23018 Bacterial
114	67.5	23.9	392	6	AAE35223	Aae35223 Human TAC	187	61.5	21.7	99	5	AAO21327	Aao21327 Arabidops
115	67.5	23.9	397	5	AAE15498	Aae15498 Human TAC	188	61.5	21.7	99	8	ADG74883	Adg74883 Plant dev
116	67.5	23.9	404	5	AAO14136	Aao14136 Protein o	189	61.5	21.7	99	8	ADJ63800	Adj63800 Plant lip
117	67.5	23.9	1994	8	ADR18912	Adr18912 Human muc	190	61.5	21.7	353	4	ABW71555	Abw71555 Drosophil
118	66.5	23.5	33	5	AAE15495	Aae15495 Human TAC	191	61.5	21.7	798	4	ABB6495	Abb6495 Drosophil
119	66.5	23.5	33	6	ADMA9368	Adma9368 Human TAC	192	61	21.6	246	6	ABP97720	Abp97720 Amino aci
120	65	23.0	1895	8	ADM90835	Adm90835 Human pha	193	61	21.6	246	8	ADK00762	Adk00762 Native hu
121	65	23.0	2417	8	ADH71332	Adh71332 Human pro	194	61	21.6	246	9	ADW03438	Adw03438 Human TAC
122	65	23.0	2420	5	ABJ10587	Abj10587 Human nov	195	61	21.6	247	3	AAV93998	Aav93998 Human BR4
123	65	23.0	2420	8	ADO09838	Ado09838 Human NOV	196	61	21.6	247	7	ABR61797	AbR61797 Human RYZ
124	65	23.0	2551	8	ADH71360	Adh71360 Human pro	197	60.5	21.4	40	9	AEC02013	Aec02013 Formula I
125	65	23.0	2675	5	ABJ10586	Abj10586 Human nov	198	60.5	21.4	1417	7	ADG39820	Adg39820 Protein s
126	65	23.0	2675	8	ADO09971	Ado09971 Human NOV	199	60.5	21.4	3034	7	ADG42709	Adg42709 Mouse cel
127	65	23.0	2675	8	ADO09836	Ado09836 Human NOV	200	60.5	21.4	3034	7	ADJ55778	Adj55778 Peptide h
128	64.5	22.8	418	5	ABR08238	Abbr08238 Human 567	201	60.5	21.4	3034	8	ADM76616	Adm76616 Human NOV
129	64.5	22.8	418	9	ADY54276	Ady54276 Human 567	202	60.5	21.4	3034	8	ADM49429	Adm49429 Mouse sev
130	64.5	22.8	581	7	ADB64650	Adb64650 Human pro	203	60.5	21.4	3034	8	ADN49434	Adn49434 Mouse sev
131	64.5	22.8	735	5	AAE68258	Aae68258 Human POL	204	60.5	21.4	3034	8	ADP29244	Adp29244 Mouse GPC
132	64.5	22.8	735	6	ABU12091	Abu12091 Novel hum	205	60	21.2	426	6	ABP55405	Abp55405 Human MDD
133	64.5	22.8	845	5	AAE68259	Aae68259 Human POL	206	60	21.2	672	8	ADQ82385	Adq82385 Fibulin-1
134	64.5	22.8	845	6	ABU12092	Abu12092 Novel hum	207	60	21.2	934	8	ADH72262	Adh72262 Human pro
135	64.5	22.8	845	7	AAE38807	Aae38807 Human POL	208	60	21.2	955	6	ADA55084	Ada55084 Human pro
136	64.5	22.8	880	7	ADB64680	Adb64680 Human pro	209	60	21.2	955	6	ADQ82381	Adq82381 Fibulin-1
137	64.5	22.8	897	4	AAE65887	Aae65887 Amino aci	210	60	21.2	955	8	AQD82384	Aqd82384 Fibulin-1
138	64.5	22.8	897	4	ABG06309	Abg06309 Novel hum	211	59	20.8	34	5	AAE15496	Aae15496 Human TAC
139	64.5	22.8	897	5	ABG91402	Abg91402 Primate L	212	59	20.8	34	6	ADA49369	Ada49369 Human TAC
140	64.5	22.8	897	7	ADR07852	Adr07852 Novel pro	213	59	20.8	38	5	AAU10952	Aau10952 Human AGP
141	64.5	22.8	897	7	ADR08940	Adr08940 Novel pro	214	59	20.8	73	5	AAE22250	Aae22250 Human AGP
142	64.5	22.8	914	8	AD127628	Ad127628 Human SCU	215	59	20.8	73	5	AAE22251	Aae22251 Human BAF
143	64.5	22.8	939	6	AAE29932	Aae29932 Human LP2	216	59	20.8	87	4	AAU41056	Aau41056 Propionib
144	64.5	22.8	973	5	AAE68260	Aae68260 Human LP2	217	59	20.8	87	6	ABM37575	Abm37575 Propionib
145	64.5	22.8	974	6	ABU12093	Abu12093 Novel hum	218	59	20.8	266	7	ADO69971	Ado69971 Plasmodi
146	64.5	22.8	974	7	AAE38808	Aae38808 Human POL	219	59	20.8	266	8	ADO69969	Ado69969 Plasmodi
147	64.5	22.8	989	6	AAE30306	Aae30306 Human LP2	220	59	20.8	2459	8	ADO69969	Ado69969 Plasmodi
148	64.5	22.8	991	6	AAO16645	Aao16645 Human ext	221	58.5	20.7	682	7	ADB70224	Adb70224 C. neofor
149	64.5	22.8	993	4	AAE65888	Aae65888 Amino aci	222	58.5	20.7	796	4	ABB63128	Abb63128 Drosophil
150	64.5	22.8	993	6	AAE29931	Aae29931 Human LP2	223	58	20.5	124	2	AAW56732	Aaw56732 Nucellu
151	64.5	22.8	993	8	AD127630	Ad127630 Human SCU	224	58	20.5	271	7	ADJ92151	Adj92151 Human hai
152	64.5	22.8	993	8	AD127637	Ad127637 SCUBE3-2	225	58	20.5	940	8	ADS24125	Ads24125 Bacterial
153	64.5	22.8	1006	5	AAU79172	Aau79172 Human MEG	226	58	20.5	1792	3	AAE48443	Aae48443 Human lam
154	64.5	22.8	1009	5	AAE68261	Aae68261 Human POL	227	58	20.5	1800	3	AAE48445	Aae48445 Human lam
155	64.5	22.8	1009	6	AAE29930	Aae29930 Human LP2	228	58	20.5	1816	3	AAE48444	Aae48444 Human lam
156	64.5	22.8	1009	6	ABU12094	Abu12094 Novel hum	229	58	20.5	1816	7	ADC01877	Adc01877 Human lam
157	64	22.6	175	9	ADW03418	Adw03418 Rat BR3 p	230	58	20.5	1816	7	ADC01879	Adc01879 Human lam
158	64	22.6	175	9	ADM21317	Adm21317 Rat Blys	231	58	20.5	1816	8	ADP08401	Adp08401 Human lam
159	63.5	22.4	428	8	ADQ97204	Adq97204 Mouse can	232	58	20.5	1816	8	ADP87600	Adp87600 Human lam
160	63	22.3	65	5	AAE22247	Aae22247 Mouse BAF	233	58	20.5	1823	5	ABP63020	Abp63020 Human pol
161	63	22.3	67	8	ADT94167	Adt94167 Murine BA	234	58	20.5	1824	3	AAE48444	Aae48444 Human lam
162	63	22.3	128	9	ADZ12994	Adz12994 Murine ca	235	57.5	20.3	76	8	ABO58265	Abos58265 Human gen
163	63	22.3	175	5	ABB78398	Abb78398 Amino aci	236	57.5	20.3	142	8	ADJ92512	Adj92512 Human tk2
164	63	22.3	175	5	AAE22244	Aae22244 Murine BA	237	57.5	20.3	142	8	ADJ92512	Adj92512 Human tk2
165	63	22.3	175	5	ABE81489	Abbe81489 Mouse Ztn	238	57.5	20.3	154	5	AAE29295	Aae29295 Human gen
166	63	22.3	175	6	ABP97722	Abp97722 Amino aci	239	57.5	20.3	499	9	ADW17813	Adw17813 Pinus rad
167	63	22.3	175	9	ADW03417	Adw03417 Murine BR	240	57.5	20.3	499	9	ADW18484	Adw18484 Pinus rad
168	63	22.3	175	9	ADW03444	Adw03444 Murine BR	241	57.5	20.3	508	9	ADW17814	Adw17814 Pinus rad
169	63	22.3	175	9	ADW21300	Adw21300 Mouse Bly	242	57.5	20.3	798	6	ABU58243	Abu58243 Soybean s
170	63	22.3	175	9	ADZ67759	Adz67759 Mouse tum	243	57.5	20.3	1679	4	ABB60498	Abb60498 Drosophil



244	57.5	20.3	1679	4	ABB60502	AbB60502 Drosophil
245	57.5	20.3	1680	8	ADS96568	AdS96568 Drosophil
246	57.5	20.3	1997	5	AU84802	Au84802 KCV HepC
247	57.5	20.3	2957	5	ABG22214	Abg22214 Novel hum
248	57.5	20.3	5985	5	AAU84799	Aau84799 HCV HepC1
249	57	20.1	281	7	AD807963	Ad807963 Novel pro
250	57	20.1	292	7	ADJ92159	Adj92159 Human hai
251	57	20.1	477	7	ADC32665	Adc32665 Human nov
252	57	20.1	477	9	Aea21141	Aea21141 Novel hum
253	57	20.1	658	5	Aam49759	Aam49759 TNF-selac
254	57	20.1	739	9	AEA20333	Aea20333 Novel hum
255	57	20.1	751	7	ADC31546	Adc31546 Human nov
256	57	20.1	770	5	AAE23388	Aae23388 Human int
257	57	20.1	770	7	ADC30933	Adc30933 Human nov
258	57	20.1	824	6	ADA55005	Ada55005 Human pro
259	57	20.1	838	6	ADN23792	Adn23792 Bacterial
260	57	20.1	858	8	ABM80296	Abm80296 Tumour-as
261	57	20.1	955	4	ABG22836	Abg22836 Novel hum
262	57	20.1	1511	4	ABB61693	Abb61693 Drosophil
263	56.5	20.0	2820	4	ABB63296	Abb63296 Drosophil
264	56.5	20.0	2820	8	ADO01056	Ado01056 Fruit fly
265	56	19.8	74	5	AB96689	Ab96689 Omega-con
266	56	19.8	126	4	ABG01557	Abg01557 Novel hum
267	56	19.8	268	8	ADT60022	Adt60022 Plant pol
268	56	19.8	337	4	ABB63629	Abb63629 Drosophil
269	56	19.8	337	4	AAU38954	Aau38954 Drosophil
270	56	19.8	337	7	ADC35844	Adc35844 Drosophil
271	56	19.8	760	4	AB862427	Ab862427 Drosophil
272	56	19.8	2476	2	AAW67738	Aaw67738 Pig p105
273	56	19.8	2824	8	ADN22513	Adn22513 Bacterial
274	56	19.8	3597	5	AB809503	Ab809503 Human lam
275	56	19.8	3597	8	AD010047	Ad010047 Novel hum
276	56	19.8	3600	5	ABB09501	Abb09501 Human lam
277	56	19.8	3600	8	ADO10043	Ado10043 Novel hum
278	55.5	19.6	225	4	ABB71511	Abb71511 Drosophil
279	55.5	19.6	339	7	ADB79814	Adb79814 Rat cathe
280	55.5	19.6	350	4	ABB68635	Abb68635 Drosophil
281	55.5	19.6	419	2	AAW11478	Aaw11478 Human vas
282	55.5	19.6	508	4	ABG22213	Abg22213 Novel hum
283	55.5	19.6	815	5	ABB93120	Abb93120 Herbicida
284	55.5	19.6	976	4	ABB11195	Abb11195 Human tra
285	55.5	19.6	1149	8	ADL33455	Adl33455 Festuca a
286	55.5	19.6	3650	8	ADM87254	Adm87254 Human pro
287	55.5	19.6	3655	8	ADN04478	Adn04478 Antipsori
288	55.5	19.6	3695	9	ADY25780	Ady25780 MRAC LAMA
289	55.5	19.6	3696	5	AAE17310	Aae17310 Human lam
290	55.5	19.6	3705	5	AAE17309	Aae17309 Human lam
291	55.5	19.6	5405	6	AAW14749	Aaw14749 IGG-Fe bi
292	55.5	19.6	5405	6	ABP55383	Abp55383 Human col
293	55.5	19.6	5405	7	ADL15023	Adl15023 Human Igg
294	55.5	19.6	5405	8	ADQ18828	Adq18828 Human sof
295	55.5	19.6	5405	9	ADV70227	Adv70227 Tumour-ass
296	55.5	19.6	7337	4	ABG22216	Abg22216 Novel hum
297	55	19.4	109	5	ABP09548	Abp09548 Human ORF
298	55	19.4	117	4	ABB63166	Abb63166 Drosophil
299	55	19.4	161	9	ADV69654	Adv69654 Human sol
300	55	19.4	328	2	AAR67628	Aar67628 Non-A Non

ALIGNMENTS

RESULT 1	
AEC02032	
ID	AEC02032 standard; peptide; 52 AA.
XX	
AC	AEC02032;
XX	
DT	20-OCT-2005 (first entry)
XX	
DE	Amino acid sequence of an extracellular domain of BCMA.
XX	
KW	APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;

Query Match	100.0%; Score 283; DB 9; Length 52;
Best Local Similarity	100.0%; Pred. No. 3.7e-26;
Matches	51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLQMGQCSQNEYFDSLHACIPCLRCSSNTPPLTCQRYCNASVTNSVKG	51
Db	1	MLQMGQCSQNEYFDSLHACIPCLRCSSNTPPLTCQRYCNASVTNSVKG	51

RESULT 2	
AAB08843	
ID	AAB08843 standard; peptide; 184 AA.
XX	
AC	AAB08843;
XX	
DT	02-JAN-2001 (first entry)
XX	
DE	Amino acid sequence of human.
XX	
KW	BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;
KW	anti-cell death gene; apoptosis; viral infection; inflammatory response;
KW	rheumatoid arthritis; inflammatory bowel disease; septic shock.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Domain 57..77
FT	/note= "putative transmembrane domain"
XX	
XX	
PN	WO200050633-A1.
XX	
PD	31-AUG-2000.
XX	
XX	
PF	24-FEB-2000; 2000WO-US0004925.
XX	

cytostatic; neoplasm; immunosuppressive; therapeutic;  
B-cell maturation antigen; BCMA.

Synthetic.

WO20005075511-A1.

18-AUG-2005.

04-AUG-2004; 2004WO-US025247.

29-JAN-2004; 2004US-0540271P.

(GETH ) GENENTECH INC.

Kelley RF, Patel D;

WPI; 2005-555932/56.

New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation.

Disclosure; SEQ ID NO 21; 140pp; English.

The specification describes polypeptides that bind April or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple sclerosis; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents an extracellular domain of BCMA.

Sequence 52 AA;



```

PR 24-FEB-1999; 99US-0121485P.
XX (GEO) GEN HOSPITAL CORP.
XX Seed B, Ting A;
XX WPI; 2000-558405/51.
DR Identifying a modulator of gene expression for drug designing, by
XX contacting a compound library with a cell expressing an anti-cell death
PT gene and reporter gene, and determining alteration in reporter gene
PT expression.
XX Claim 32; Fig 7A; 53pp; English.
XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is
CC a necrosis factor (NF)-kB activator. The method of the invention is used
CC to identify compounds which modulate BCMA activity (and thus NF-kB
CC activity). The specification describes a method of identifying a
CC polypeptide which increases gene expression from a promoter. The method
CC involves contacting a library of with a cell which expresses a
CC recombinant anti-cell death gene and a reporter gene operably linked to
CC the promoter, and then determining whether the expression of the reporter
CC gene is altered as a result of contact with library. The method is useful
CC for identifying polypeptides which increase or decrease gene expression
CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
CC preparing a pharmaceutical composition for treating cancer, apoptosis,
CC viral infections, inflammatory response, such as rheumatoid arthritis,
CC inflammatory bowel disease or septic shock. BCMA is useful for
CC identifying compounds that modulate NF-kB expression and thus for drug
XX designing
XX Sequence 184 AA;
SQ
Query Match 100.0%; Score 283; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKG 51
DB 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKG 51
RESULT 3
AA94001
ID AA94001 standard; protein; 184 AA.
XX AA94001;
XX AC
XX 20-OCT-2000 (first entry)
XX DE A human BCMA protein, a B cell protein related to TACI.
XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
KW znf4 activity; antibody production; autoimmune disease; amyloidosis;
KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
KW immune response; immunosuppression; graft rejection; joint pain;
KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
KW renal artery stenosis; occlusion; cholesterol; renal emboli.
XX Homo sapiens.
XX OS
XX WO200040716-A2.
XX PN
XX 13-JUL-2000.
XX PD
XX 07-JAN-2000; 2000WO-US000396.
XX ,XX

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PR 07-JAN-1999; 99US-00226533.
XX (ZYMO) ZYMOGENETICS INC.
XX Gross JA, Xu W, Madden K, Yee DP;
XX WPI; 2000-452538/39.
DR N-PSDB; AA58559.
XX Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,
PT renal disease, graft versus host disease, and inflammation, comprises
PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
XX Disclosure; Page 152; 175pp; English.
XX The present sequence represents a human BCMA protein, a B cell protein
CC related to transmembrane activator and CAML-interactor (TACI) receptor.
CC TACI is a tumour necrosis factor (TNF) receptor. The extracellular
CC domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell
CC protein) receptor contain a cysteine rich domain, and are used for
CC inhibiting znf4 activity. Znf4 is a TNF ligand. They may also be used
CC for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
CC with activated or resting B lymphocytes, effector T-cells, or with
CC antibody production. The antibody production is associated with an
CC autoimmune disease selected from systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis and rheumatoid arthritis. The znf4 activity
CC and BR43x2, TACI or BCMA receptor-ligand engagement is associated with
CC asthma, bronchitis, emphysema, end stage renal failure,
CC glomerulonephritis, vasculitis, nephritis, light chain neuropathy,
CC neoplasms, multiple myelomas, lymphomas, immunosuppression, graft
CC rejection, graft versus host disease, inflammation, insulin dependent
CC diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or
CC septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies,
CC agonists or antagonists can be used to treat hypertension, renal artery
CC stenosis, or occlusion, and cholesterol or renal emboli
XX Sequence 184 AA;
SQ
Query Match 100.0%; Score 283; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKG 51
DB 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCQRYCNASVTNSVKG 51
RESULT 4
AAE09241
ID AAE09241 standard; protein; 184 AA.
XX AAE09241;
XX AC
XX 19-NOV-2001 (first entry)
XX DT Human BCMA protein.
XX DE Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
XX Homo sapiens.
XX OS
XX WO200160397-A1.
XX PN
XX 23-AUG-2001.
XX PD
XX 28-NOV-2000; 2000WO-US032378.
XX PF
XX 16-FEB-2000; 2000US-0182938P.
XX PR
XX 22-AUG-2000; 2000US-0226986P.
XX ,XX

```



PA (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM,  
 PI Yan M;  
 XX WPI: 2001-541628/60.  
 DR N-PSDB; AAD15902.  
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological  
 PT activity, for treating autoimmune disorders and cancer, comprises  
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or  
 PT antagonists:  
 XX Example 2; Fig 2; 160pp; English.  
 XX The invention relates to methods of using one or more agonists or  
 CC antagonists to modulate the activity of the members of TNF (tumour  
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.  
 CC TACI or BCMA. The method is useful for treating pathological conditions  
 CC or diseases associated with increased TALL-1 and APRIL expression or  
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction  
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating  
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,  
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid  
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The  
 CC present sequence is human BCMA protein  
 XX Sequence 184 AA;  
 SQ  
 Query Match 100.0%; Score 283; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51  
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51  
 RESULT 5  
 AAY71979  
 ID AAY71979 standard; protein; 184 AA.  
 XX AAY71979;  
 XX 28-MAR-2001 (first entry)  
 DT Human B cell maturation factor (BCMA) protein.  
 DE Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;  
 XX Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;  
 KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;  
 KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;  
 KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;  
 KW haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16;  
 KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;  
 KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Domain 1..62  
 FT /label= Extracellular\_domain  
 FT  
 XX WO200068378-A1.  
 PN  
 XX 16-NOV-2000.  
 PD  
 XX 05-MAY-2000; 2000WO-US012266.  
 PF  
 XX 06-MAY-1999; 98US-0132892P.  
 PR  
 XX 01-MAY-2000; 2000US-0201012P.  
 XX  
 PA . (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Shu HS;  
 PI WPI: 2001-016094/02.  
 DR N-PSDB; AAD02125.  
 XX Isolated TALL-1 protein is used to identify compounds that regulate B  
 PT lymphocyte proliferation, used to treat B lymphocyte associated  
 PT autoimmune disorders.  
 XX Claim 37; Page 104-105; 112pp; English.  
 PS  
 XX The present invention relates to Tumour necrosis factor (TNF) and Apol-  
 CC related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,  
 CC proteins (including homologues), and their antibodies. The invention in  
 CC particular relates to methods for regulating the interaction between TALL  
 CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to  
 CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.  
 CC TALL-1 protein is useful for identifying compounds that regulate B  
 CC lymphocyte proliferation. It is also useful for treating B lymphocyte  
 CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus  
 CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple  
 CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,  
 CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal  
 CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its  
 CC corresponding nucleic acid sequence are also useful in diagnostic assays.  
 CC The present sequence is a human B cell maturation factor (BCMA) protein.  
 CC It is the receptor for TALL-1 protein. BCMA gene is located on chromosome  
 CC 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not  
 CC by brain, muscle, heart, lung, kidney, pancreas, testis and placenta.  
 CC BCMA mRNA is absent in the pro-B lymphocyte stage but its expression  
 CC increases with B lymphocyte maturation  
 XX Sequence 184 AA;  
 SQ  
 Query Match 100.0%; Score 283; DB 4; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51  
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51  
 RESULT 6  
 AAB60698  
 ID AAB60698 standard; protein; 184 AA.  
 XX AAB60698;  
 AC 22-MAY-2001 (first entry)  
 DT Human BAFF receptor (BAFF-R).  
 DE Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
 KW immune-related disorder; B-cell growth inhibitor; BCMA;  
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;  
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;  
 KW renal disorder; immunosuppressive disorder; HIV infection;  
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;  
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
 KW lymphoma; gene therapy; cancer; tumour.  
 XX Homo sapiens.  
 OS  
 XX WO200112812-A2.  
 PN  
 XX 22-FEB-2001.  
 PD  
 XX 16-AUG-2000; 2000WO-US022507.  
 PF  
 XX







KW light chain neuropathy; hypertension; large vessel disease;  
KW graft-versus host disease; graft rejection; Crohn's disease.  
XX

OS Homo sapiens.  
XX

XX WO200238766-A2.  
XX

XX 16-MAY-2002.  
XX

XX 05-NOV-2001; 2001WO-US047018.  
XX

XX 07-NOV-2000; 2000US-0246449P.  
XX

XX 20-DEC-2000; 2000US-0257131P.  
XX

XX 28-JUN-2001; 2001US-0301715P.  
XX

XX 29-AUG-2001; 2001US-0315565P.  
XX

XX (ZYMO ) ZYMOGENETICS INC.  
XX

XX Gross JA, Xu W, Henne RM, Grant FJ;  
XX

XX WPI; 2002-508212/54.  
XX

XX Novel isolated human tumor necrosis factor receptor polypeptide, termed  
XX

XX Znf12, useful for treating autoimmune disorders, emphysema, end stage  
XX

XX renal failure or renal disease and lymphoma.  
XX

XX Disclosure; Page 135-136; 154pp; English.  
XX

XX The present invention describes a human tumour necrosis factor receptor  
XX

XX designated Znf12 (I). (I) has cytostatic, immunosuppressive,  
XX

XX dermatological, antiinflammatory, neuroprotective, antidiabetic,  
XX

XX antirheumatic, antiarthritic, antiaesthetic, nephrotropic and hypotensive  
XX

XX activities, and can be used in gene therapy. (I) can be used for  
XX

XX inhibiting, in a mammal, the activity of a ligand that binds Znf12  
XX

XX (e.g. ZTNF4), for treating disorders and diseases associated with B  
XX

XX lymphocytes, activated B lymphocytes or resting B lymphocytes, and for  
XX

XX inhibiting the proliferation of tumour cells. (I) is useful for treating  
XX

XX autoimmune disorders such as systemic lupus erythematosus, myasthenia  
XX

XX gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,  
XX

XX rheumatoid arthritis, bronchitis, emphysema and end stage renal failure  
XX

XX or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid  
XX

XX leukaemia, nephritis, and pyelonephritis, and for treating renal  
XX

XX neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or  
XX

XX amyloidosis, hypertension, large vessel diseases, graft-versus host  
XX

XX disease, graft rejection and Crohn's disease. (I) is useful for  
XX

XX modulating the immune system, for regulating B cell responses and  
XX

XX development, for modulating development of other cells, antibody  
XX

XX production and cytokine production, and for modulating T and B cell  
XX

XX communication. The present sequence represents a protein which is given  
XX

XX in the exemplification of the present invention  
XX

XX Sequence 184 AA;  
XX

Query Match 100.0%; Score 283; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51

Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51

RESULT 9

ABP54694

ID ABP54694 standard; protein; 184 AA.

XX

XX ABP54694;

XX 30-DEC-2002 (first entry)

XX Metastatic colorectal cancer-associated polypeptide.

XX Colorectal cancer; metastasis; differential expression; cytostatic;

KW diagnosis; gene therapy; vaccine.

XX Homo sapiens.

XX WO200268677-A2.

XX 06-SEP-2002.

XX 27-FEB-2002; 2002WO-US006001.

XX 27-FEB-2001; 2001US-0272206P.

XX 02-APR-2001; 2001US-0281149P.

XX 17-APR-2001; 2001US-0284555P.

XX (BOSB-) EOS BIOTECHNOLOGY INC.

XX (UYCA-) UNIV CASE WESTERN RESERVE.

XX Mack DH, Markowitz SD;

XX WPI; 2002-698677/75.

XX N-PSDB; ABQ81560.

XX New genes that are up- or down-regulated in colorectal cancer, useful for

XX diagnosing colorectal cancer in a subject, or for identifying modulators

XX of colorectal cancer-associated proteins and genes for treating

XX colorectal cancer.

XX Claim 8; Page 255; 260pp; English.

XX The present sequence is the protein sequence of a human polypeptide

XX encoded by a gene that exhibits decreased expression in colon cancer-

XX derived metastases compared to normal colon tissue. It is an example of

XX claimed polypeptides that are encoded by genes which are differentially

XX expressed in metastatic colorectal cancer cells. Such polypeptides are

XX useful in diagnostic and prognostic assays, for raising antibodies useful

XX e.g. in immunotherapy, and in screening for modulator compounds of

XX therapeutic value

XX Sequence 184 AA;

XX Query Match 100.0%; Score 283; DB 5; Length 184;

XX Best Local Similarity 100.0%; Pred. No. 1.4e-25;

XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51

Db 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51

RESULT 10

AAE28961

ID AAE28961 standard; protein; 184 AA.

XX

XX AAE28961;

XX 27-JAN-2003 (first entry)

XX Human B-cell maturation antigen (BCMA).

XX Human; tumour; B-cell maturation antigen; transmembrane activator;

XX calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;

XX neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;

XX non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;

XX BCMA; multiple myeloma.

XX Homo sapiens.

XX Location/Qualifiers

XX Key 1.54

XX Region /note= "Antigenic epitope"

XX FT 1.48

XX Domain /note= "Extracellular domain"

XX FT 8.41

XX Region



```

FT /note= "Cysteine rich region"
PN WO200266516-A2.
XX
XX 29-AUG-2002.
XX
XX 06-FEB-2002; 2002WO-US003500.
XX
XX 20-FEB-2001; 2001US-0270274P.
XX 12-APR-2001; 2001US-0283447P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Kindevogel W;
XX
XX WPI; 2002-723183/78.
XX N-PSDB; AAD46410.
XX
XX B-cell maturation antigen and transmembrane activator and calcium-
PT modulator and cyclophilin ligand-interactor, useful for treating
PT disorders e.g. inflammation or lymphoma.
XX
XX Disclosure; Page 63; 67pp; English.
XX
XX The invention relates to the manufacture of a composition for inhibiting
CC the proliferation of tumour cells. The method involves using an antibody
CC component that binds both the B-cell maturation antigen (BCMA) and the
CC transmembrane activator and calcium-modulator and cyclophilin ligand-
CC interactor (TACI). BCMA and TACI binding antibody compositions are useful
CC for inhibiting proliferation of tumour cells, particularly inhibiting
CC ZTNF4 activity in a mammal associated with increased endogenous antibody
CC production or a disorder consisting of neoplasm, chronic lymphocytic
CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
CC lymphoproliferative disease or light chain gammopathy or inflammation
CC e.g. asthma. The invention is also useful in gene therapy. The present is
CC human BCMA protein
XX
XX Sequence 184 AA;
XX
XX Query Match 100.0%; Score 283; DB 5; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-25;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCQSQNEYFDSLLHACIPCOLRCSSTPPLTTCORYCNASVTNSVKG 51
DB 1 MLQAGQCQSQNEYFDSLLHACIPCOLRCSSTPPLTTCORYCNASVTNSVKG 51

RESULT 11
AAE35216
ID AAE35216 standard; protein; 184 AA.
XX
XX AAE35216;
XX
XX 28-MAY-2003 (first entry)
XX
XX Human B-cell maturation receptor (BCMA) protein.
XX
XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;
XX TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
XX anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;
XX glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;
XX dermatological; neuroprotective; cyclophilin ligand-interactor; human;
XX autoimmune disease; systemic lupus erythematosus; multiple sclerosis;
XX diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
XX B-cell maturation receptor; BCMA; receptor.
XX
XX Homo sapiens.
XX
XX WO200294852-A2.
XX
XX 28-NOV-2002.
XX

/note= "Cysteine rich region"
PN WO200266516-A2.
XX
XX 29-AUG-2002.
XX
XX 06-FEB-2002; 2002WO-US003500.
XX
XX 20-FEB-2001; 2001US-0270274P.
XX 12-APR-2001; 2001US-0283447P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Kindevogel W;
XX
XX WPI; 2002-723183/78.
XX N-PSDB; AAD46410.
XX
XX B-cell maturation antigen and transmembrane activator and calcium-
PT modulator and cyclophilin ligand-interactor, useful for treating
PT disorders e.g. inflammation or lymphoma.
XX
XX Disclosure; Page 63; 67pp; English.
XX
XX The invention relates to the manufacture of a composition for inhibiting
CC the proliferation of tumour cells. The method involves using an antibody
CC component that binds both the B-cell maturation antigen (BCMA) and the
CC transmembrane activator and calcium-modulator and cyclophilin ligand-
CC interactor (TACI). BCMA and TACI binding antibody compositions are useful
CC for inhibiting proliferation of tumour cells, particularly inhibiting
CC ZTNF4 activity in a mammal associated with increased endogenous antibody
CC production or a disorder consisting of neoplasm, chronic lymphocytic
CC leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation
CC lymphoproliferative disease or light chain gammopathy or inflammation
CC e.g. asthma. The invention is also useful in gene therapy. The present is
CC human BCMA protein
XX
XX Sequence 184 AA;
XX
XX Query Match 100.0%; Score 283; DB 5; Length 184;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-25;
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCQSQNEYFDSLLHACIPCOLRCSSTPPLTTCORYCNASVTNSVKG 51
DB 1 MLQAGQCQSQNEYFDSLLHACIPCOLRCSSTPPLTTCORYCNASVTNSVKG 51

RESULT 12
ADA49361
ID ADA49361 standard; protein; 184 AA.
XX
XX ADA49361;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human BCMA protein.
XX
XX human; TALL-1; antagonist; immunosuppressive; antirheumatic;
XX antiinflammatory; antiarthritis; dermatological; antidiabetic;
XX neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic;
XX vaccine; autoimmune disease; rheumatoid arthritis;
XX systemic lupus erythematosus; insulin dependent diabetes mellitus;
XX multiple sclerosis; myasthenia gravis; Grave's disease;
XX autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;
XX Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;
XX post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.
XX
XX Homo sapiens.
XX
XX WO2003035846-A2.
XX
XX 01-MAY-2003.
XX
XX 24-OCT-2002; 2002WO-US034376.
XX
XX 24-OCT-2001; 2001US-0345106P.
XX 14-JAN-2002; 2002US-0348962P.
XX 07-FEB-2002; 2002US-0354966P.
XX

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PR 13-AUG-2002; 2002US-0403364P.
XX
XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
XX Zhang G, Shu H, Liu Y, Xu L;
XX
XX WPI; 2003-403345/38.
XX
XX N-PSDB; ADA49360.
XX
XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
XX
XX activity in mammal, has a modification in the region connecting beta
XX
XX strands D and E that reduces the biological activity of TALL-1
XX
XX antagonist.
XX
XX Claim 62; Page 613; 618pp; English.
XX
XX The invention relates to a novel TALL-1 antagonist protein, comprising a
XX
XX sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
XX
XX NO:2, by at least one modification in the region connecting  $\delta$ gr; strands
XX
XX D and E that reduces the biological activity of the TALL-1 antagonist as
XX
XX compared to wild-type TALL-1. A protein of the invention has
XX
XX immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
XX
XX dermatological, antidiabetic, neuroprotective, antithyroid, antipruritic,
XX
XX nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
XX
XX a vaccine. A protein of the invention is useful for inhibiting TALL-1
XX
XX biological activity in a mammal. TC is useful for treating autoimmune
XX
XX diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
XX
XX dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
XX
XX Grave's disease, autoimmune hemolytic anaemia, autoimmune
XX
XX thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
XX
XX acute rheumatic fever, post-streptococcal glomerulonephritis and
XX
XX polyarteritis nodosa. The present sequence represents human BCMA.
XX
XX
XX Sequence 184 AA;
XX
XX Query Match 100.0%; Score 283; DB 6; Length 184;
XX
XX Best Local Similarity 100.0%; Pred. No. 1.4e-25;
XX
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 MLQWAGQCQSQNEYFDSLHACIPQLRCSSNTPTPLTCQRYCNASVTNSVKG 51
XX
XX 1 MLQWAGQCQSQNEYFDSLHACIPQLRCSSNTPTPLTCQRYCNASVTNSVKG 51
XX
XX
XX RESULT 13
XX
XX ABP60552
XX
XX ID ABP60552 standard; protein; 184 AA.
XX
XX AC ABP60552;
XX
XX
XX 28-MAR-2003 (first entry)
XX
XX DE Human tumour necrosis factor BCMA.
XX
XX APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
XX
XX dermatological; immunosuppressive; antiinflammatory; antirheumatic;
XX
XX antiarthritic; cytostatic; antianaemic; antiallergic; antiasthmatic;
XX
XX neuroprotective; ophthalmological; tuberculostatic; antidiabetic;
XX
XX antipruritic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
XX
XX haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
XX
XX inflammatory disorder; proliferative disorder; single chain antibody;
XX
XX antibody; human; BCMA; tumour necrosis factor.
XX
XX Homo sapiens.
XX
XX OS
XX
XX WO200294192-A2.
XX
XX PN
XX
XX 28-NOV-2002.
XX
XX PD
XX
XX 22-MAY-2002; 2002WO-US016106.
XX
XX PF
XX
XX 24-MAY-2001; 2001US-0293100P.
XX
XX PR
XX
XX

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PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM;
XX
XX WPI; 2003-156740/15.
XX
XX Novel isolated antibody that immunospecifically binds tumor necrosis
XX
XX factor delta, useful for treating, preventing or ameliorating Non-
XX
XX Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
XX
XX syndrome.
XX
XX Disclosure; Page 222; 225pp; English.
XX
XX The invention relates to a novel antibody or its fragment, which
XX
XX immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).
XX
XX The antibody of the invention has dermatological, immunosuppressive,
XX
XX antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,
XX
XX antiallergic, antidiabetic, neuroprotective, ophthalmological,
XX
XX tuberculostatic, antipruritic, antipapular, anti-HIV,
XX
XX antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
XX
XX The antibody or its fragment are useful for treating, preventing or
XX
XX ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
XX
XX human, disease or disorder such as autoimmune disease, and graft versus
XX
XX host disease (GVHD). The autoimmune disease is systemic lupus
XX
XX erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
XX
XX is useful for detecting, diagnosing, prognosing, treating, preventing or
XX
XX ameliorating a disease or disorder associated with aberrant APRIL or
XX
XX APRIL receptor expression or aberrant function of APRIL or APRIL
XX
XX receptor. The disease or disorders includes autoimmune and inflammatory
XX
XX disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
XX
XX asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
XX
XX uveitis, tuberculostatic, diabetes mellitus, psoriasis, cancer of the immune
XX
XX system, particularly B cell cancers, immune disorders such as myasthenia
XX
XX gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
XX
XX infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
XX
XX proliferative disorders (e.g. leukemia). The present sequence represents
XX
XX the tumour necrosis factor BCMA
XX
XX
XX Sequence 184 AA;
XX
XX Query Match 100.0%; Score 283; DB 6; Length 184;
XX
XX Best Local Similarity 100.0%; Pred. No. 1.4e-25;
XX
XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 1 MLQWAGQCQSQNEYFDSLHACIPQLRCSSNTPTPLTCQRYCNASVTNSVKG 51
XX
XX 1 MLQWAGQCQSQNEYFDSLHACIPQLRCSSNTPTPLTCQRYCNASVTNSVKG 51
XX
XX
XX RESULT 14
XX
XX ABP97717
XX
XX ID ABP97717 standard; protein; 184 AA.
XX
XX AC ABP97717;
XX
XX
XX 28-MAY-2003 (first entry)
XX
XX DE Amino acid sequence of human BCMA receptor.
XX
XX Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
XX
XX TALL-1; April; systemic lupus erythematosus; BCMA.
XX
XX Homo sapiens.
XX
XX OS
XX
XX WO2003014294-A2.
XX
XX PN
XX
XX 20-FEB-2003.
XX
XX PD
XX
XX 24-JUL-2002; 2002WO-US023487.
XX
XX PF
XX
XX 03-AUG-2001; 2001US-0310114P.
XX
XX PR
XX
XX 30-APR-2002; 2002US-0377171P.
XX
XX

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PA (GETH ) GENENTECH INC.  
XX  
PI Dixit V, Grewal I, Ridgway J, Yan M;  
XX  
DR WPI; 2003-256560/25.  
DR N-PSDB; AB268871.  
XX  
XX  
PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for  
PT preparing a composition for treating systemic lupus erythematosus.  
XX  
PS Disclosure; Fig 2; 153pp; English.  
XX  
XX The present sequence represents a human BCMA polypeptide. The  
CC specification also describes TACI and BR3 polypeptides. TACI and BR3 are  
CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April  
CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to  
CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for  
CC preparing a composition for treating systemic lupus erythematosus  
XX  
XX Sequence 184 AA;  
SQ

Query Match 100.0%; Score 283; DB 6; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGQCQSQNEYFDSLHACIPCOLRCSSNTPLTCQRYCNASVTNSVKG 51  
DB 1 MLQMGQCQSQNEYFDSLHACIPCOLRCSSNTPLTCQRYCNASVTNSVKG 51

RESULT 15  
ADD67527  
ID ADD67527 standard; protein; 184 AA.  
XX  
AC ADD67527;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human Ly1732P protein SEQ ID NO:4.  
XX  
XX haematological malignancy; immunoconjugate; cytostatic; immunoostimulant;  
KW vaccine; immunotherapy; cancer; multiple myeloma cell;  
KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;  
KW human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003062401-A2.  
XX  
PD 31-JUL-2003.  
XX  
PF 22-JAN-2003; 2003WO-US002353.  
XX  
PR 22-JAN-2002; 2002US-00057475.  
XX  
XX (CORI-) CORIXA CORP.  
PA  
XX Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;  
PI Carter L, Mcneill PD;  
XX  
XX WPI; 2003-598749/56.  
DR N-PSDB; ADD67526.  
XX  
XX New hematological malignancy-related genes and polypeptides, useful for  
PT screening anti-cancer agents, and generating antibodies or  
PT immunoconjugates for treating e.g. multiple myeloma cell or chronic  
PT lymphocytic leukemia.  
XX  
XX Claim 9; SEQ ID NO 4; 307pp; English.  
PS  
XX The present invention describes an isolated polynucleotide (I), which is  
CC overexpressed in haematological malignancies, and which encodes a  
CC polypeptide or an immunogenic fragment of the polypeptide. Also

CC described: (1) an isolated polypeptide; (2) an expression vector  
CC comprising (I) operably linked to an expression control sequence; (3) a  
CC host cell comprising an expression vector; (4) an isolated antibody that  
CC specifically binds to the polypeptide or its immunogenic fragment; and  
CC (5) immunoconjugates comprising the antibody above, or an antibody that  
CC specifically binds to a polypeptide, or its immunogenic fragment, encoded  
CC by (I). (I) has cytostatic and immunoostimulant activities, and can be  
CC used in vaccines and immunotherapy. The immunoconjugates are useful in  
CC the manufacture of a medicament, particularly as active ingredients in a  
CC composition for treating cancer, e.g. multiple myeloma cell, chronic  
CC lymphocytic leukaemia, B cell leukaemia, or lymphomas in humans, sheep,  
CC primates, goats, bovines, equines, porcines, lupines, canines or felines.  
CC The polynucleotide (I) or polypeptide can be used for screening anti-  
CC cancer agents, and generating antibodies or immunoconjugates for treating  
CC or preventing the above-mentioned diseases. The polynucleotide,  
CC polypeptide or antibody can be used for detecting, diagnosing or  
CC prognosticating the haematological malignancies described above. The  
CC present sequence is used in the exemplification of the present invention.  
XX  
XX Sequence 184 AA;  
SQ

Query Match 100.0%; Score 283; DB 7; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQMGQCQSQNEYFDSLHACIPCOLRCSSNTPLTCQRYCNASVTNSVKG 51  
DB 1 MLQMGQCQSQNEYFDSLHACIPCOLRCSSNTPLTCQRYCNASVTNSVKG 51

RESULT 16  
ADG43715  
ID ADG43715 standard; protein; 184 AA.  
XX  
AC ADG43715;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human B-cell maturation antigen SEQ ID NO:1.  
XX  
XX human; neurodegenerative immunological disorder; demyelination;  
KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;  
KW BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;  
KW gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX WO2003072713-A2.  
PN  
XX 04-SEP-2003.  
PD  
XX 21-FEB-2003; 2003WO-US005147.  
PF  
XX 21-FEB-2002; 2002US-0358427P.  
PR  
XX (BIOJ ) BIOGEN INC.  
PA  
XX Kalled SL, Reid H;  
PI  
XX WPI; 2003-721758/68.  
DR N-PSDB; ADG43716.  
DR  
XX  
XX Treating a neurodegenerative immunological disorder, e.g. demyelination  
PT or inflammation in a mammal comprises administering a B-cell maturation  
PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.  
XX  
PS Claim 8; Page 68-69; 72pp; English.  
XX  
XX The invention relates to a novel method for treating a neurodegenerative  
CC immunological disorder, demyelination or Central Nervous System (CNS)  
CC inflammation in a mammal. The method comprises administering B-cell  
CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand  
CC (the mammal has or is at risk of developing multiple sclerosis). The



CC method of the invention has neuroprotective, neurotropic, and  
 CC antiinflammatory activity, and may have a use in gene therapy. The  
 CC methods, BCMA, and antibodies are useful for treating a neurodegenerative  
 CC immunological disorder such as multiple sclerosis, demyelination or CNS  
 CC inflammation. The present sequence represents human BCMA.

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 7; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51  
 |||||  
 DB 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51  
 |||||

RESULT 17

ADK00756  
 ID ADK00756 standard; protein; 184 AA.

XX AC ADK00756;

DT 06-MAY-2004 (first entry)

XX DE Native human BCMA.

XX KW CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;  
 KW Dermatological; Immunosuppressive; Antiirheumatic; Antiarthritic;  
 KW Antidiabetic; Neuroprotective; Antialasthmatic; Antiallergic; Anti-HIV;  
 KW Antibacterial; antiparasitic; systemic lupus erythematosus;  
 KW diabetes mellitus; AIDS; BCMA.

XX OS Homo sapiens.

XX PN WO2004011611-A2.

XX PD 05-FEB-2004.

XX PF 25-JUL-2003; 2003WO-US023421.

XX PR 25-JUL-2002; 2002US-0398530P.

XX PA (GETH ) GENENTECH INC.

XX PI Chuntharapai A, Grewal I, Kim KJ, Yan M;

XX DR WPI; 2004-143841/14.

XX DR N-PSDB; ADK00755.

XX PT New anti-TACI receptor monoclonal antibody, useful for diagnosing and  
 PT treating pathological conditions associated with tumor necrosis factor,  
 PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or  
 PT psoriasis.

XX PS Disclosure; SEQ ID NO 6; 110pp; English.

XX CC The present invention relates to an isolated monoclonal antibody which  
 CC binds to a transmembrane activator of and CAML interactor (TACI)  
 CC receptor. The TACI antibodies are useful for modulating TALL-1 or TACI  
 CC polypeptide biological activity in mammalian cells, or for diagnosing and  
 CC treating pathological conditions associated with TNF and TNF receptor-  
 CC related molecules, e.g. cancer or immune-related disease, such as  
 CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,  
 CC systemic vasculitis, diabetes mellitus, Crohn's disease,  
 CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or  
 CC infectious diseases including AIDS, hepatitis infection, bacterial  
 CC infection, fungal infection, protozoal infection and parasitic infection.

XX CC The present sequence represents native human BCMA.

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 8; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51  
 |||||  
 DB 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSTPPLTCQRYCNASVTNSVKG 51  
 |||||

RESULT 18

ADQ94442  
 ID ADQ94442 standard; protein; 184 AA.

XX AC ADQ94442;

DT 07-OCT-2004 (first entry)

XX DE Neurokine-alpha, BCMA.

XX KW neurokine-alpha; chelator; B-lymphocyte stimulator; BlyS; TALL-1; THANK;  
 KW BAFF; neurokine-alpha receptor; complex; metal ion; radiotherapy;  
 KW B-cell mediated disease; non-Hodgkin's lymphoma;  
 KW chronic lymphocytic leukaemia; multiple myeloma;  
 KW systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis;  
 KW Crohn's disease; diabetes; Wegener's granulomatosis; myasthenia gravis;  
 KW asthma; cancer; Sjogren's syndrome; diagnostic imaging; lymphocyte;  
 KW B cell; cancerous cell; metastasis; lymphatic system.

XX OS Homo sapiens.

XX PN WO2004058309-A1.

XX PD 15-JUL-2004.

XX PF 22-DEC-2003; 2003WO-US040979.

XX PR 23-DEC-2002; 2002US-0435262P.

XX PR 02-MAY-2003; 2003US-0467198P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Parmelee D, Yeh R, Galperina O, Hilbert D, Rosen CA;

XX DR WPI; 2004-553134/53.

XX DR N-PSDB; ADQ94441.

XX DR GENBANK; NM\_001192.

XX PT Neurokine-alpha conjugate useful for targeting complexed metal ion to  
 PT cells expressing receptor (predominantly lymphoid) for radiotherapy  
 PT treatment of, for example, non-Hodgkin's lymphoma comprises neurokine-  
 PT alpha protein and chelator.

XX PS Disclosure; SEQ ID NO 9; 228pp; English.

XX CC This sequence represents neurokine-alpha, BCMA, which may be used in the  
 CC protein conjugate of the invention. The neurokine-alpha protein  
 CC conjugate comprises neurokine-alpha protein and chelator, where the  
 CC neurokine-alpha protein (also known as B-lymphocyte stimulator (BLyS),  
 CC TALL-1, THANK and BAFF) is capable of binding neurokine-alpha receptor.  
 CC and is selected from full length or mature neurokine-alpha protein. The  
 CC protein conjugate of the invention is useful in a complex with a metal  
 CC ion associated with the chelator which is useful for administering  
 CC radiotherapy to a subject such as human who is in need of radiotherapy,  
 CC which involves administering the complex to the subject, where it is  
 CC administered as an injectable solution, and the subject has a B-cell  
 CC mediated disease. The subject has a condition chosen from non-Hodgkin's  
 CC lymphoma, chronic lymphocytic leukaemia, multiple myeloma, systemic lupus  
 CC erythematosus, rheumatoid arthritis, multiple sclerosis, Crohn's disease,  
 CC diabetes, Wegener's granulomatosis, myasthenia gravis and asthma,  
 CC preferably non-Hodgkin's lymphoma. The complex is useful for treating  
 CC cancer, which involves administering it to a subject having cancer, where  
 CC a cell of the cancer expresses a neurokine-alpha receptor on its  
 CC surface. The cancer is a B cell cancer, which is chosen from non-  
 CC Hodgkin's lymphoma, multiple myeloma and chronic lymphocytic leukaemia.



CC The complex is also useful for treating an autoimmune disease or  
 CC disorder, chosen from systemic lupus erythematosus, rheumatoid arthritis  
 CC and Sjogren's syndrome. The complex may also be used for diagnostic  
 CC imaging. A composition comprising the protein conjugate or the complex is  
 CC useful for killing a cell chosen from a cell bearing a neurokinine-alpha  
 CC receptor, and a cell in close proximity to a cell bearing neurokinine-  
 CC alpha receptor, which involves contacting the cell with the composition  
 CC to kill the cell. The cell is lymphocyte, B cell or cancerous cell that  
 CC has metastasised into the lymphatic system.

XX  
 SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 8; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51  
 |||||  
 DB 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51  
 |||||

RESULT 19  
 ADP56014  
 ID ADP56014 standard; protein; 184 AA.

XX  
 AC ADP56014;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human PRO protein sequence SEQ ID NO:1990.

XX  
 KW human; PRO; immune related disease; inflammatory immune response;  
 KW immune response stimulation; antiallergic; antianaemic; antiarthritic;  
 KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;  
 KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;  
 KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;  
 KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;  
 KW virucide; gene therapy.

XX  
 OS Homo sapiens.

XX  
 PN WO2004039956-A2.  
 XX  
 PD 13-MAY-2004.

XX  
 PF 28-OCT-2003; 2003WO-US034381.  
 XX  
 PR 29-OCT-2002; 2002US-0422472P.

XX  
 PA (GETH ) GENENTECH INC.

XX  
 PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;  
 PI Wood WI, Wu TD;  
 XX  
 DR WPI: 2004-376182/35.  
 DR N-PSDB; ADP56013.

XX  
 PT New PRO polynucleotides and polypeptides, useful in useful in diagnosing  
 PT and treating an immune related disease, e.g. systemic lupus  
 PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in  
 PT stimulating an immune response.

XX  
 PS Claim 1; SEQ ID NO 1990; 3009pp; English.

XX  
 CC The present invention describes an isolated PRO nucleic acid (I). Also  
 CC described: (1) a vector comprising (I); (2) a host cell comprising the  
 CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an  
 CC isolated PRO polypeptide; (5) a chimeric molecule comprising the  
 CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
 CC antibody which specifically binds to a polypeptide of (4); (7) a  
 CC composition of matter comprising a polypeptide of (4), an agonist or  
 CC antagonist of the polypeptide or an antibody that binds to the  
 CC polypeptide in combination with a carrier; (8) an article of manufacture

CC comprising a container, a label on the container and a composition of  
 CC matter of (7); (9) a method of treating an immune related disease in a  
 CC mammal; (10) a method for determining the presence of a PRO polypeptide  
 CC in a sample suspected of having the polypeptide; (11) a method of  
 CC diagnosing an immune related disease or an inflammatory immune response  
 CC in mammal; (12) a method of identifying a compound that inhibits or  
 CC mimics the activity of or expression of a gene encoding a PRO polypeptide  
 CC ; and (13) a method of stimulating the immune response in a mammal. The  
 CC PRO sequences have anti-allergic, antianaemic, antiarthritic,  
 CC antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic,  
 CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,  
 CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,  
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and  
 CC virucide activities, and can be used in gene therapy. The nucleic acid  
 CC (i) and the encoded polypeptides, compositions, kits and methods are  
 CC useful in diagnosing and treating an immune related disease and in  
 CC stimulating an immune response. The present sequence represents a human  
 CC PRO protein from the present invention.

XX  
 SQ Sequence 184 AA;

Query Match 100.0%; Score 283; DB 8; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-25;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51  
 |||||  
 DB 1 MLQAGQCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTNSVKG 51  
 |||||

RESULT 20  
 ADW03432  
 ID ADW03432 standard; protein; 184 AA.

XX  
 AC ADW03432;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Human BCMA protein amino acid sequence.

XX  
 KW B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive;  
 KW non-hodgkin lymphoma; hodgkins disease; cytostatic;  
 KW chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis;  
 KW antiarthritic; antirheumatic; systemic lupus erythematosus;  
 KW Wegener granulomatosis; antiallergic; antiinflammatory; vasotropic;  
 KW inflammatory bowel disease; gastrointestinal-gen.;  
 KW idiopathic thrombocytopenic purpura; hemostatic; multiple sclerosis;  
 KW asthma; antiasthmatic; psoriasis; antipsoriatic; myasthenia gravis;  
 KW muscular-gen.; neuroprotective; vasculitis; diabetes; antidiabetic;  
 KW glomerulonephritis; nephrotropic; BCMA.

XX  
 OS Homo sapiens.

XX  
 PN WO2005000351-A2.  
 XX  
 PD 06-JAN-2005.

XX  
 PF 04-JUN-2004; 2004WO-US017693.  
 XX  
 PR 05-JUN-2003; 2003US-0476414P.  
 PR 05-JUN-2003; 2003US-0476481P.  
 PR 06-JUN-2003; 2003US-0476531P.

XX  
 PA (GETH ) GENENTECH INC.

XX  
 PI Chan A, Gong Q, Martin F;  
 XX  
 DR WPI: 2005-058069/06.  
 DR N-PSDB; ADW03431.

XX  
 PT Depleting B cells from a mixed population of cells by contacting the  
 PT cells with a Blys antagonist and a CD20 binding antibody, useful for  
 PT treating B cell malignancies and autoimmune disorders.







CC cell proliferative disorder. Also disclosed are anti-tumor antigens of  
CC hematopoietic origin (TAHO) polypeptides, encoding nucleic acids, methods of  
CC oligopeptides, vectors, host cells and antibodies used in the methods of  
CC the invention. The methods and compositions of the present invention are  
CC useful for treating hematopoietic and malignant tumors in mammals. This  
CC is the amino acid sequence of tumor antigen of hematopoietic origin  
CC TAHO23.  
XX  
SQ Sequence 184 AA;  
  
Query Match 100.0%; Score 283; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. NO. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSVKG 51  
DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSVKG 51  
  
RESULT 23  
ABC02031  
ID AEC02031 standard; protein; 184 AA.  
XX AC AEC02031;  
XX DT 20-OCT-2005 (first entry)  
XX DE Amino acid sequence of a BCMA protein.  
XX KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
XX KW cytostatic; neoplasm; immunosuppressive; therapeutic; BCMA;  
XX KW B-cell maturation antigen.  
XX OS Homo sapiens.  
XX PN WO2005075511-A1.  
XX PD 18-AUG-2005.  
XX PF 04-AUG-2004; 2004WO-US025247.  
XX PR 29-JAN-2004; 2004US-0540271P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Kelley RF, Patel D;  
XX DR WPI; 2005-555932/56.  
XX PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
XX PT for treating immune-related disease, cancer or T-cell mediated disease  
XX PT such as graft rejection, graft versus host disease (GVHD) and  
XX PT inflammation.  
XX PS Disclosure; SEQ ID NO 20, 140pp; English.  
XX CC The specification describes polypeptides that bind April or BAFF. The  
XX CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
XX CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
XX CC polypeptides of the invention are useful for treating immune-related  
XX CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
XX CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
XX CC scleroma; or T-cell mediated disease such as graft rejection, graft  
XX CC versus host disease (GVHD) and inflammation. The present sequence  
XX CC represents a BCMA protein.  
SQ Sequence 184 AA;  
  
Query Match 100.0%; Score 283; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. NO. 1.4e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSVKG 51

DB 1 MLQAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTSVKG 51  
  
RESULT 24  
AAB60699  
ID AAB60699 standard; protein; 302 AA.  
XX AC AAB60699;  
XX DT 11-SEP-2003 (revised)  
XX DT 22-MAY-2001 (first entry)  
XX DE Mouse IgG signal/human BAFF-R/human IGG Fc fusion protein, BAFF-R-Fc.  
XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
XX KW immune-related disorder; B-cell growth inhibitor;  
XX KW B-cell maturation inhibitor; immunoglobulin production inhibitor;  
XX KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;  
XX KW renal disorder; immunosuppressive disorder; HIV infection;  
XX KW organ transplantation; antiinflammatory; systemic lupus erythematosus;  
XX KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
XX KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
XX KW lymphoma; gene therapy; cancer; tumour; IGG Fc; fusion construct.  
XX OS Homo sapiens.  
XX OS Mus sp.  
XX OS Chimeric.  
XX PN WO200112812-A2.  
XX PD 22-FEB-2001.  
XX PF 16-AUG-2000; 2000WO-US022507.  
XX PR 17-AUG-1999; 99US-0149378P.  
XX PR 11-FEB-2000; 2000US-0181684P.  
XX PR 18-FEB-2000; 2000US-0183536P.  
XX PA (BIOJ ) BIOGEN INC.  
XX PA (APOT-) APOTEC R & D SA.  
XX PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;  
XX PI Thompson J;  
XX DR WPI; 2001-202866/20.  
XX DR N-PSDB; AAF59999.  
XX PT Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell  
XX PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,  
XX PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.  
XX PS Example 4; Fig 2; 59pp; English.  
XX CC The invention relates to the use of a BAFF receptor (BAFF-R, also known  
XX CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the  
XX CC treatment of a variety of immune-related disorders. BAFF-R is a member of  
XX CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory  
XX CC agent, and also plays a role in the development of hypertension and  
XX CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-  
XX CC specific antibodies can be used for inhibiting B-cell growth, dendritic  
XX CC cell-induced B-cell growth and maturation, and immunoglobulin production,  
XX CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative,  
XX CC disorders, hypertension and renal disorders. The BAFF-R proteins may also  
XX CC be used in the treatment of immunosuppressive disorders and HIV  
XX CC infection, and in patients undergoing organ transplantation. The BAFF-R  
XX CC proteins or BAFF-R specific antibodies may be used for treating,  
XX CC suppressing or altering an immune response involving a signalling pathway  
XX CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R  
XX CC inhibits B-cell growth and maturation it is useful for treating diseases  
XX CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,  
XX CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly  
XX CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding



CC human BAPF-R may be used in gene therapy to treat tumours, lymphomas,  
 CC autoimmune disorders and inherited B-cell-associated disorders. The  
 CC present sequence represents the BAPF-R fusion protein BAPF-R-Fc.  
 CC comprising a mouse IgG-kappa signal sequence, residues 1-153 of human  
 CC BAPF-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to  
 CC standardise OS field)  
 XX  
 XX Sequence 302 AA;  
 XX  
 Query Match 100.0%; Score 283; DB 4; Length 302;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-25;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLQAGQCSQNEFYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASTNSVKG 51  
 DB 24 MLQAGQCSQNEFYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASTNSVKG 74

RESULT 25  
 AAE00507  
 ID AAE00507 standard; protein; 302 AA.  
 AC AAE00507;  
 DT 11-SEP-2003 (revised)  
 DT 31-JUL-2001 (first entry)  
 DE Human BCMA-Immunoglobulin G Fc region fusion construct.  
 XX  
 XX Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;  
 KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;  
 KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;  
 KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;  
 KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;  
 KW organ transplantation; HIV; human immunodeficiency virus; TNF; murine;  
 KW tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;  
 KW immunoglobulin G; IgG; Fc region.  
 XX  
 OS Homo sapiens.  
 OS Mus sp.  
 OS Chimeric.

XX  
 FH Key Location/Qualifiers  
 FT Protein 1..22  
 FT /label= Signal\_peptide  
 FT /note= "Derived from murine Ig kappa sequence"  
 FT Protein 23..302  
 FT /label= Mature\_human\_BCMA\_IgG\_Fc\_fusion\_protein  
 FT Region 23..75  
 FT /note= "Derived from human BCMA protein"  
 FT Domain 24..302  
 FT /label= Cysteine\_rich\_domain  
 FT /note= "Derived from human BCMA"  
 FT Region 76..302  
 FT /note= "Derived from human IgG Fc region"  
 XX  
 PN WO200124811-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US027579.  
 XX  
 PR 06-OCT-1999; 99US-0157933P.  
 PR 11-FEB-2000; 2000US-0181807P.  
 PR 30-JUN-2000; 2000US-0215688P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 PA (APOT-) APOTEC R & D SA.  
 XX  
 PI Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;  
 XX WPI; 2001-266242/27.  
 DR N-PSDB; AAD03847.  
 XX

XX  
 PT Treating a mammal for a condition associated with undesired cell  
 PT proliferation such as cancer or carcinoma, comprises administering a  
 PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)  
 PT antagonist.  
 XX  
 PS Example 1; Fig 3B; 85pp; English.  
 XX  
 CC The invention relates to a method of treating a mammal for a condition  
 CC associated with undesired cell proliferation such as cancer or carcinoma.  
 CC The method involves administering a composition comprising A  
 CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell  
 CC maturation protein (BCM or BCMA) antagonist that antagonises the  
 CC interaction between APRIL and its cognate receptor(s). This method is  
 CC useful for treating undesired cell proliferation such as cancer or  
 CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,  
 CC prostate carcinoma, and other carcinomas whose proliferation is modulated  
 CC by APRIL. It is also useful for treating autoimmune diseases (Grave's  
 CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular  
 CC diseases, renal disorders, B-cell lympho-proliferative disorders,  
 CC immunosuppressive diseases, organ transplantation, inflammation and human  
 CC immunodeficiency virus (HIV), and for treating, suppressing or altering  
 CC an immune response involving a signalling pathway between APRIL-R and its  
 CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence  
 CC is a fusion construct containing human APRIL-R also referred as BCMA or  
 CC BCM protein, Fc region of human immunoglobulin G (IgG) and a signal  
 CC sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to  
 CC standardise OS field)  
 XX  
 XX Sequence 302 AA;  
 XX  
 Query Match 100.0%; Score 283; DB 4; Length 302;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-25;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLQAGQCSQNEFYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASTNSVKG 51  
 DB 24 MLQAGQCSQNEFYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASTNSVKG 74

RESULT 26  
 ADG43717  
 ID ADG43717 standard; protein; 302 AA.  
 AC ADG43717;  
 DT 26-FEB-2004 (first entry)  
 DE Human B-cell maturation antigen-Fc SEQ ID NO:3.  
 XX  
 XX human; neurodegenerative immunological disorder; demyelination;  
 KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;  
 KW BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;  
 KW gene therapy; mouse.  
 XX  
 OS Chimeric.  
 OS Homo sapiens.  
 OS Mus sp.

XX  
 FH Key Location/Qualifiers  
 FT Region 1..23  
 FT /note= "Murine IgGkappa signal sequence"  
 FT Region 24..74  
 FT /note= "Human BCMA extracellular domain"  
 FT Region 75..302  
 FT /note= "Human Ig heavy chain Fc region"  
 XX  
 PN WO2003072713-A2.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 21-FEB-2003; 2003WO-US005147.  
 XX



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PR 21-FEB-2002; 2002US-0358427P.
XX (BIOJ ) BIOGEN INC.
PA Kalled SL, Reid H;
XX WPI; 2003-721758/68.
DR N-PSDB; ADG43718.
XX Treating a neurodegenerative immunological disorder, e.g. demyelination
PT or inflammation in a mammal comprises administering a B-cell maturation
PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.
XX Claim 12; Page 70-71; 72pp; English.
XX The invention relates to a novel method for treating a neurodegenerative
CC immunological disorder, demyelination or Central Nervous System (CNS)
CC inflammation in a mammal. The method comprises administering B-cell
CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand
CC (the mammal has or is at risk of developing multiple sclerosis). The
CC method of the invention has neuroprotective, nootropic, and
CC antiinflammatory activity, and may have a use in gene therapy. The
CC methods, BCMA, and antibodies are useful for treating a neurodegenerative
CC immunological disorder such as multiple sclerosis, demyelination or CNS
CC inflammation. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 302 AA;
Query Match 100.0%; Score 283; DB 7; Length 302;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51
DB 24 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 74
RESULT 27
ABR40082
ID ABR40082 standard; protein; 184 AA.
XX
AC ABR40082;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human Genoxit.
XX
KW Human; Genoxit; anorectic; antilipaemic; antiarteriosclerotic; cardiant;
KW antidiabetic; hypotensive; ophthalmological; neuroprotective;
KW nephrotropic; obesity; Tumour Necrosis Factor Receptor Super Family;
KW Type III transmembrane protein; insulin resistance; atherosclerosis;
KW atheronatus disease; heart disease; hypertension; stroke; syndrome X;
KW diabetes mellitus; hyperlipidaemia; hyperuricaemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..54
FT /label= Extracellular_domain
FT Misc-difference 3
FT /label= Gln, Lys
FT Domain 55..77
FT /label= Transmembrane_domain
FT Domain 78..184
FT /label= Intracellular_domain
XX
PN WO2003013582-A1.
XX
PD 20-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-IB003498.
XX
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```
PR 06-AUG-2001; 2001US-0310754P.
XX (GEST ) GENSET SA.
XX Lucas J, Dialynas D, Briggs K;
XX WPI; 2003-268160/26.
DR N-PSDB; ACC00340.
XX New use of agonist or antagonist of Genoxit activity for preventing or
PT treating obesity-related diseases or disorders, e.g. hyperlipidemia and
PT atherosclerosis.
XX
PS Disclosure; Page 32; 35pp; English.
XX The present invention relates to the use of an agonist or antagonist of
CC Genoxit activity for preventing or treating obesity. Genoxit is a member
CC of the Tumour Necrosis Factor Receptor Super Family and is a Type III
CC transmembrane protein. The agonists or antagonists of the invention are
CC useful for treating or preventing obesity-related diseases or disorders,
CC e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,
CC heart disease (e.g. cardiac insufficiency, coronary insufficiency, high
CC blood pressure), hypertension, stroke, syndrome X, diabetes mellitus
CC (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic
CC complications, e.g. microangiopathic lesions, ocular lesions,
CC retinopathy, neuropathy and renal lesions
XX
SQ Sequence 184 AA;
Query Match 97.9%; Score 277; DB 6; Length 184;
Best Local Similarity 98.0%; Pred. No. 7.3e-25;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51
DB 1 MLXWAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51
RESULT 28
ABG95060
ID ABG95060 standard; protein; 288 AA.
XX
AC ABG95060;
XX
DT 04-DEC-2002 (first entry)
XX
DE Human translocation (4; 16)(q26; p13) protein.
XX
KW Chromosome aberration; oncogenic fusion protein; cancer;
KW proliferative disease; cellular protein isoform; heat shock protein 90;
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KW rhabdomyosarcoma; synovial sarcoma; viral infection.
XX
OS Homo sapiens.
XX
PN WO200269900-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WO-US006518.
XX
PR 01-MAR-2001; 2001US-0272751P.
XX (CONF-) CONFORMA THERAPEUTICS CORP.
XX
PI Fritz LC, Burrows FJ;
XX
DR WPI; 2002-698710/75.
DR N-PSDB; ABS73235.
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XX Treating genetically-defined disease associated with chromosomal  
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
PT diseases, involves administering an inhibitor of heat shock protein 90.  
XX  
XX Disclosure; Page 189-190; 389pp; English.  
XX  
CC The invention describes a method of treating genetically-defined disease  
CC associated with chromosomal aberrations yielding oncogenic fusion  
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
CC cell population, treating proliferative diseases associated with mutant  
CC protein or cellular protein isoforms (II) dependent on heat shock protein  
CC (HSP)-90, or selectively treating cells expressing (II) involving  
CC administering HSP90-inhibitor. The method is useful for treating  
CC genetically-defined disease with chromosomal aberration yielding  
CC oncogenic fusion protein, treating cancerous cells containing fusion  
CC protein in heterogeneous cell population, treating proliferative disease  
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
CC p53), or selectively treating cells expressing mutant protein or cellular  
CC protein isoform in a patient heterozygous for (II). The method is useful  
CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,  
CC or a disease characterised by a solid tumour such as papillary thyroid  
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and  
CC synovial sarcoma. The method is also useful for treating viral  
CC infections. This represents a protein encoded by the DNA sequence of a  
CC chromosome aberration  
XX  
SQ Sequence 288 AA;  
  
Query Match 96.8%; Score 274; DB 5; Length 288;  
Best Local Similarity 98.0%; Pred. No. 2.7e-24;  
Matches 49; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 LQWAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTSVKG 51  
|:|||||  
Db 106 LKMGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTSVKG 155  
|:|||||  
  
RESULT 29  
AAE15485  
ID AAE15485 standard; peptide; 51 AA.  
XX AC AAE15485;  
XX XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human B-cell maturation (BCMA) protein extracellular domain.  
XX  
KW Human; transmembrane activator and intracellular CAML interactor; TACI;  
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis.  
XX  
XX Homo sapiens.  
XX  
XX WO200187979-A2.  
XX  
XX PD 22-NOV-2001.  
XX  
XX PF 14-MAY-2001; 2001WO-US015567.  
XX  
XX PR 12-MAY-2000; 2000US-0204039P.  
XX 27-JUN-2000; 2000US-0214591P.  
XX PR 14-MAY-2001; 2001US-00214591.  
XX  
XX PA (AMGE-) AMGEN INC.  
XX

PI Theill LE, Yu G;  
XX WPI; 2002-066686/09.  
XX  
DR Inhibiting activity of B cell maturation protein and/or transmembrane  
XX activator and intracellular cyclophilin ligand interactor, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX  
XX Claim 1; Fig 10A; 94pp; English.  
PS  
XX  
CC The invention relates to a method for inhibiting TACI (transmembrane  
CC activator and intracellular CAML interactor) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is human BCMA protein extracellular domain  
XX  
SQ Sequence 51 AA;  
  
Query Match 95.1%; Score 269; DB 5; Length 51;  
Best Local Similarity 100.0%; Pred. No. 1.7e-24;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTSVKG 51  
|||||  
Db 1 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTSVKG 48  
|||||  
  
RESULT 30  
AAE15484  
ID AAE15484 standard; protein; 181 AA.  
XX AC AAE15484;  
XX XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human B-cell maturation (BCMA) protein.  
XX  
KW Human; transmembrane activator and intracellular CAML interactor; TACI;  
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis.  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX Key Location/Qualifiers  
XX Region 5..38  
XX /note= "Cysteine-rich consensus region; This is region is  
XX specifically claimed as SEQ ID NO: 7 in claim 1 of the  
XX specification"  
XX Domain 52..72  
XX /label= Transmembrane\_domain  
XX  
XX WO200187979-A2.  
XX



PD 22-NOV-2001.  
XX  
PF 14-MAY-2001; 2001WO-US015567.  
XX  
PR 12-MAY-2000; 2000US-0204039P.  
PR 27-JUN-2000; 2000US-0214591P.  
PR 14-MAY-2001; 2001US-00214591.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Theill LE, Yu G;  
XX  
XX WPI; 2002-066686/09.  
XX  
XX Inhibiting activity of B cell maturation protein and/or transmembrane  
PT activator and intracellular cyclophilin ligand interact, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX  
PS Disclosure; Fig 10A; 94pp; English.  
XX  
CC The invention relates to a method for inhibiting TACI (transmembrane  
CC activator and intracellular CAML interact) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is human BCMA protein  
XX  
SQ Sequence 181 AA;  
Query Match 95.1%; Score 269; DB 5; Length 181;  
Best Local Similarity 100.0%; Pred. No. 6.5e-24;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 MAGQCSQNEYFDSLHACIPQLRCSSTNPPLTCQRYCNASVTNSVKG 51  
|||||  
DB 1 MAGQCSQNEYFDSLHACIPQLRCSSTNPPLTCQRYCNASVTNSVKG 48  
|||||  
RESULT 31  
AAE15488  
ID AAE15488 standard; protein; 283 AA.  
XX  
AC AAE15488;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
XX Human BCMA-immunoglobulin Fc region fusion protein.  
XX  
XX Human; transmembrane activator and intracellular CAML interact; TACI;  
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis; fusion protein.  
XX  
OS Homo sapiens.  
XX  
XX

PN WO200187979-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 14-MAY-2001; 2001WO-US015567.  
XX  
PR 12-MAY-2000; 2000US-0204039P.  
PR 27-JUN-2000; 2000US-0214591P.  
PR 14-MAY-2001; 2001US-00214591.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Theill LE, Yu G;  
XX  
XX WPI; 2002-066686/09.  
XX  
XX Inhibiting activity of B cell maturation protein and/or transmembrane  
PT activator and intracellular cyclophilin ligand interact, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX  
PS Disclosure; Fig 10B; 94pp; English.  
XX  
CC The invention relates to a method for inhibiting TACI (transmembrane  
CC activator and intracellular CAML interact) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is human BCMA protein-immunoglobulin Fc region fusion protein  
XX  
SQ Sequence 283 AA;  
Query Match 95.1%; Score 269; DB 5; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1e-23;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 MAGQCSQNEYFDSLHACIPQLRCSSTNPPLTCQRYCNASVTNSVKG 51  
|||||  
DB 1 MAGQCSQNEYFDSLHACIPQLRCSSTNPPLTCQRYCNASVTNSVKG 48  
|||||  
RESULT 32  
AEC02042  
ID AEC02042 standard; protein; 296 AA.  
XX  
AC AEC02042;  
XX  
DT 20-OCT-2005 (first entry)  
XX  
XX Amino acid sequence of a BCMA-Fc fusion protein.  
XX  
XX APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic; BCMA;  
KW B-cell maturation antigen; Fc.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
XX  
XX WO2005075511-A1.  
XX  
XX



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PD 18-AUG-2005.
XX
XX 04-AUG-2004; 2004WO-US025247.
XX
XX 29-JAN-2004; 2004US-0540271P.
XX (GETH ) GENENTECH INC.
XX
XX Kelley RF, Patel D;
XX
XX WPI; 2005-555932/56.
XX
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
XX for treating immune-related disease, cancer or T-cell mediated disease
XX such as graft rejection, graft versus host disease (GVHD) and
XX inflammation.
XX
XX Example 6; SEQ ID NO 31; 140pp; English.
XX
XX The specification describes polypeptides that bind APRIL or BAFF. The
XX polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
XX (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
XX polypeptides of the invention are useful for treating immune-related
XX diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
XX lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
XX sclerosis; or T-cell mediated disease such as graft rejection, graft
XX versus host disease (GVHD) and inflammation. The present sequence
XX represents a BCMA-Fc fusion protein, where 122 of BCMA is changed to Lys.
XX
XX Sequence 296 AA;
XX
Query Match 90.8%; Score 257; DB 9; Length 296;
Best Local Similarity 97.9%; Pred. No. 2.9e-22;
Matches 46; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 AGCQSQNEYFDSLHACIPQLRCSNTPLTTCORYCNASVTNSVKG 51
DB 18 AGCQSQNEYFDSLHACKPQLRCSNTPLTTCORYCNASVTNSVKG 64
RESULT 33
AAE15501
ID AAE15501 standard; peptide; 58 AA.
XX
XX AAE15501;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human B cell maturation protein cysteine rich extracellular region.
XX
XX Human; transmembrane activator and intracellular CAML interactor; TACI;
XX cytosolic; B cell maturation protein; BCMA; tumor necrosis factor; TNF;
XX lymphoproliferative disorder; tumor; lung; gastrointestinal; pancreatic;
XX prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX rheumatoid arthritis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX WO200187979-A2.
XX
XX 22-NOV-2001.
XX
XX 14-MAY-2001; 2001WO-US015567.
XX
XX 12-MAY-2000; 2000US-0204039P.
XX 27-JUN-2000; 2000US-0214591P.
XX 14-MAY-2001; 2001US-00214591.
XX
XX (ANGE-) AMGEN INC.
XX
PI Theill LE, Yu G;
XX
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor family
XX ligand.
XX
XX Disclosure; Fig 13; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering a
XX specific binding partner for APRIL (G70, a tumor necrosis factor-TNF
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/
XX BCMA extracellular consensus sequence, but not the extracellular region
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX lymphoproliferative disorders, one or more solid tumors such as lung,
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
XX antagonists are useful for treating inflammation and immune function
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX disease), drug and insect sting allergy, inflammatory bowel disease
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX with leucocyte infiltration of the skin or organs. The present sequence
XX is human BCMA cysteine-rich extracellular region
XX
XX Sequence 58 AA;
XX
Query Match 88.0%; Score 249; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CSQNEYFDSLHACIPQLRCSNTPLTTCORYCNASVTNSVKG 51
DB 1 CSQNEYFDSLHACIPQLRCSNTPLTTCORYCNASVTNSVKG 44
RESULT 34
ADZ67761
ID ADZ67761 standard; protein; 40 AA.
XX
XX ADZ67761;
XX
XX 14-JUL-2005 (first entry)
XX
XX Human tumor necrosis factor receptor BCMA Cys-rich domain.
XX
XX Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;
XX cytostatic.
XX
XX Homo sapiens.
XX
XX WO2005037865-A2.
XX
XX 28-APR-2005.
XX
XX 18-OCT-2004; 2004WO-US034375.
XX
XX 16-OCT-2003; 2003US-0511698P.
XX 18-OCT-2004; 2004US-0619552P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Fox BA, Holloway JL, Sheppard PO, Dillon SR;
XX
XX WPI; 2005-315682/32.
XX
XX New tumor necrosis factor receptor (TNFR) polypeptides, useful as

```



PT detecting ligands, and for modulating tumor growth, metastasis and  
PT immunity, such as separating resting from stimulated immune cells.  
XX  
XX Disclosure; SEQ ID NO 9; 132pp; English.

XX The invention provides novel tumor necrosis factor receptor ztnfr14  
CC polynucleotides ADZ67753 and polypeptides ADZ67754, expression vectors  
CC and antibodies. Ztnfr14 polynucleotides are used in claimed methods for  
CC detecting a genetic abnormality in a patient and for detecting a cancer  
CC in a patient. Recombinant ztnfr14 polypeptide, optionally conjugated to a  
CC toxin, is used in a claimed method of killing cancer cells. ztnfr14  
CC polypeptides can be used to detect ligands, agonists and antagonists. The  
CC polypeptides, polynucleotides and antibodies may also be used in methods  
CC that modulate tumor growth, metastasis, and immunity such as separating  
CC resting from stimulated immune cells. The present sequence is that of the  
CC Cys-rich domain of human TNFR BCMA ADZ67760. This sequence was compared  
CC with that of ztnfr14 in the identification of ztnfr14 as a member of the  
CC TNFR family.

XX  
XX Sequence 40 AA;  
SQ

Query Match 81.3%; Score 230; DB 9; Length 40;  
Best Local Similarity 100.0%; Pred. No. 5.9e-20;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASV 45  
DB 1 GQCSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNASV 40  
|||||

RESULT 35  
AEC02033  
ID AEC02033 standard; peptide; 38 AA.  
XX  
XX AEC02033;  
AC  
DT 20-OCT-2005 (first entry)  
XX  
DE Amino acid sequence of an extracellular domain of BCMA.

XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic;  
KW B-cell maturation antigen; BCMA.  
XX  
XX Synthetic.  
OS  
XX WO2005075511-A1.  
PN  
XX 18-AUG-2005.  
PD  
XX 04-AUG-2004; 2004WO-US025247.  
PF  
XX 29-JAN-2004; 2004US-0540271P.  
PR  
XX (GETH ) GENENTECH INC.  
PA  
XX Kelley RF, Patel D;  
PI  
XX WPI; 2005-555932/56.  
DR  
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.

XX Disclosure; SEQ ID NO 22; 140pp; English.

XX The specification describes polypeptides that bind April or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple

CC scleroma; or T-cell mediated disease such as graft rejection, graft  
CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents an extracellular domain of BCMA.

XX  
XX Sequence 38 AA;  
SQ

Query Match 76.0%; Score 215; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 3.4e-18;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 SONEYFDSLHACIPQLRCSSNTPPLTCORYCNASVT 46  
DB 1 SONEYFDSLHACIPQLRCSSNTPPLTCORYCNASVT 38  
|||||

RESULT 36  
AAB60700  
ID AAB60700 standard; protein; 157 AA.  
XX  
XX AAB60700;  
AC  
XX  
DT 22-MAY-2001 (first entry)  
XX  
DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pUST535.

XX Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
KW immune-related disorder; B-cell growth inhibitor; BCMA; inhibitor;  
KW B-cell maturation inhibitor; immunoglobulin production inhibitor;  
KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;  
KW renal disorder; immunosuppressive disorder; HIV infection;  
KW organ transplantation; antiinflammatory; systemic lupus erythematosus;  
KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
KW lymphoma; gene therapy; cancer; tumour; plasmid pUST535.

XX Homo sapiens.  
OS  
XX WO200112812-A2.  
PN  
XX 22-FEB-2001.  
PD  
XX 16-AUG-2000; 2000WO-US022507.  
PF  
XX 17-AUG-1999; 99US-0149378P.  
PR  
XX 11-FEB-2000; 2000US-0181684P.  
PR  
XX 18-FEB-2000; 2000US-0183536P.  
PR  
XX (BIOJ ) BIOGEN INC.  
PA  
XX (APOT-) APOTEC R & D SA.  
PA  
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;  
PI Thompson J;  
PI  
XX WPI; 2001-202866/20.  
DR  
XX N-PSDB; AAF60000.  
DR  
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell  
PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,  
PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.

XX Example 1; Fig 3; 59pp; English.

XX The invention relates to the use of a BAFF receptor (BAFF-R, also known  
CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the  
CC treatment of a variety of immune-related disorders. BAFF-R is a member of  
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory  
CC agent, and also plays a role in the development of hypertension and  
CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-  
CC specific antibodies can be used for inhibiting B-cell growth, dendritic  
CC cell-induced B-cell growth and maturation, and immunoglobulin production,  
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative  
CC disorders, hypertension and renal disorders. The BAFF-R proteins may also  
CC be used in the treatment of immunosuppressive disorders and HIV



XX CC The invention relates to a method for inhibiting TNF $\alpha$  (transmembrane  
CC CC activator and intracellular CAML interactor) and/or B cell maturation  
CC CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC CC specific binding partner for APRIL (G70), a tumour necrosis factor-TNF







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RESULT 41
AEC02028
ID AEC02028 standard; peptide; 34 AA.
XX
AC AEC02028;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula II derived polypeptide G that binds BAFF.
XX
KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
DR WPI; 2005-555932/56.
XX
PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
for treating immune-related disease, cancer or T-cell mediated disease
such as graft rejection, graft versus host disease (GVHD) and
inflammation.
XX
PS Claim 7; SEQ ID NO 6; 140pp; English.
XX
CC The specification describes polypeptides that bind APRIL or BAFF. The
polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
(BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
polypeptides of the invention are useful for treating immune-related
diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
sclerosis; or T-cell mediated disease such as graft rejection, graft
versus host disease (GVHD) and inflammation. The present sequence
represents a polypeptide of the invention that binds APRIL, derived from
AEC02012.
XX
SQ Sequence 34 AA;
XX
Query Match 68.6%; Score 194; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 9.7e-16;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

RESULT 42
AEC02025
ID AEC02025 standard; peptide; 34 AA.
XX
AC AEC02025;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula II derived polypeptide D that binds BAFF.
XX
KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
PN WO2005075511-A1.
XX
PD 18-AUG-2005.
XX
PF 04-AUG-2004; 2004WO-US025247.
XX
PR 29-JAN-2004; 2004US-0540271P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Kelley RF, Patel D;
XX
DR WPI; 2005-555932/56.
XX
PT New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
for treating immune-related disease, cancer or T-cell mediated disease
such as graft rejection, graft versus host disease (GVHD) and
inflammation.
XX
PS Claim 13; SEQ ID NO 17; 140pp; English.
XX
CC The specification describes polypeptides that bind April or BAFF. The
polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
(BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
polypeptides of the invention are useful for treating immune-related
diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
sclerosis; or T-cell mediated disease such as graft rejection, graft
versus host disease (GVHD) and inflammation. The present sequence
represents a polypeptide of the invention, derived from formula II (see
AEC02021), that that bind BAFF.
XX
SQ Sequence 34 AA;
XX
Query Match 68.6%; Score 194; DB 9; Length 34;
Best Local Similarity 97.1%; Pred. No. 9.7e-16;
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41
Db 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

RESULT 42
AEC02017
ID AEC02017 standard; peptide; 34 AA.
XX
AC AEC02017;
XX
DT 20-OCT-2005 (first entry)
XX
DE Formula I derived polypeptide F that binds APRIL.
XX
KW APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
XX cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX

```



PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
XX Claim 13; SEQ ID NO 14; 140pp; English.  
XX  
XX The specification describes polypeptides that bind April or BAFF. The  
XX polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
XX (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
XX polypeptides of the invention are useful for treating immune-related  
XX diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
XX lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
XX scleroma; or T-cell mediated disease such as graft rejection, graft  
XX versus host disease (GVHD) and inflammation. The present sequence  
XX represents a polypeptide of the invention, derived from formula II (see  
XX AEC02021), that that bind BAFF.  
XX  
XX Sequence 34 AA;  
SQ  
  
Query Match 67.8%; Score 192; DB 9; Length 34;  
Best Local Similarity 97.1%; Pred. No. 1.7e-15;  
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CSQNEVFDLSLLHACIPCOLRCSSNTPLTCQRYC 41  
DB 1 CSQNEVFDLSLLHACIPCOLRCSSNTPLTCQRYC 34  
  
RESULT 44  
AEC02024  
ID AEC02024 standard; peptide; 34 AA.  
XX  
AC AEC02024;  
XX  
DT 20-OCT-2005 (first entry)  
XX  
DE Formula II derived polypeptide C that binds BAFF.  
XX  
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
XX  
XX Synthetic.  
XX  
XX WO2005075511-A1.  
XX  
XX 19-AUG-2005.  
XX  
XX 04-AUG-2004; 2004WO-US025247.  
XX  
XX 29-JAN-2004; 2004US-0540271P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Kelley RF, Patel D;  
XX  
XX WPI; 2005-555932/56.  
XX  
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
XX Claim 13; SEQ ID NO 13; 140pp; English.  
XX  
XX The specification describes polypeptides that bind April or BAFF. The  
XX polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
XX (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
XX polypeptides of the invention are useful for treating immune-related  
XX diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
XX lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
XX scleroma; or T-cell mediated disease such as graft rejection, graft  
XX versus host disease (GVHD) and inflammation. The present sequence  
XX represents a polypeptide of the invention, derived from formula II (see

CC AEC02021), that that bind BAFF.  
XX  
XX Sequence 34 AA;  
SQ  
  
Query Match 67.8%; Score 192; DB 9; Length 34;  
Best Local Similarity 97.1%; Pred. No. 1.7e-15;  
Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CSQNEVFDLSLLHACIPCOLRCSSNTPLTCQRYC 41  
DB 1 CSQNEVFDLSLLHACIPCOLRCSSNTPLTCQRYC 34  
  
RESULT 45  
AEC02020  
ID AEC02020 standard; peptide; 34 AA.  
XX  
AC AEC02020;  
XX  
DT 20-OCT-2005 (first entry)  
XX  
DE Formula I derived polypeptide I that binds APRIL.  
XX  
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
XX  
XX Synthetic.  
XX  
XX WO2005075511-A1.  
XX  
XX 18-AUG-2005.  
XX  
XX 04-AUG-2004; 2004WO-US025247.  
XX  
XX 29-JAN-2004; 2004US-0540271P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Kelley RF, Patel D;  
XX  
XX WPI; 2005-555932/56.  
XX  
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
XX Claim 7; SEQ ID NO 9; 140pp; English.  
XX  
XX The specification describes polypeptides that bind APRIL or BAFF. The  
XX polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
XX (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
XX polypeptides of the invention are useful for treating immune-related  
XX diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
XX lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
XX scleroma; or T-cell mediated disease such as graft rejection, graft  
XX versus host disease (GVHD) and inflammation. The present sequence  
XX represents polypeptide of the invention that binds APRIL, derived from  
XX AEC02012.  
XX  
XX Sequence 34 AA;  
SQ  
  
Query Match 67.5%; Score 191; DB 9; Length 34;  
Best Local Similarity 94.1%; Pred. No. 2.2e-15;  
Matches 32; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 8 CSQNEVFDLSLLHACIPCOLRCSSNTPLTCQRYC 41  
DB 1 CSQNEVFDLSLVHACIPCOLRCSSNTPLTCQRYC 34  
  
RESULT 46  
AEC02018



```

ID AEC02018 standard; peptide; 34 AA.
XX
AC AEC02018;
XX
DT 20-OCT-2005 (first entry)
DE
DE Formula I derived polypeptide G that binds APRIL.
XX
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
XX WO2005075511-A1.
PN
XX
XX 18-AUG-2005.
PD
XX
XX 04-AUG-2004; 2004WO-US025247.
PF
XX
XX 29-JAN-2004; 2004US-0540271P.
PR
XX
XX (GETH ) GENENTECH INC.
PA
XX
XX Kelley RF, Patel D;
PI
XX
XX WPI; 2005-555932/56.
DR
XX
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
XX Claim 13; SEQ ID NO 18; 140pp; English.
PS
XX
XX The specification describes polypeptides that bind APRIL or BAFF. The
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention, derived from formula II (see
CC AEC02012), that that bind BAFF.
XX
XX Sequence 34 AA;
SQ
Query Match 66.8%; Score 189; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 3.8e-15;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
| | | | | | | | | | | | | | | | | | | |
DB 1 CSQNEYFDSLHACIPCDLYCSSNTPLTCQRYC 34
| | | | | | | | | | | | | | | | | | | |

RESULT 48
AEC02019
ID AEC02019 standard; peptide; 34 AA.
XX
AC AEC02019;
XX
XX
DT 20-OCT-2005 (first entry)
DE
DE Formula I derived polypeptide H that binds APRIL.
XX
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
XX WO2005075511-A1.
PN
XX
XX 18-AUG-2005.
PD
XX
XX 04-AUG-2004; 2004WO-US025247.
PF
XX
XX 29-JAN-2004; 2004US-0540271P.
PR
XX
XX (GETH ) GENENTECH INC.
PA
XX
XX Kelley RF, Patel D;
PI
XX
XX WPI; 2005-555932/56.
DR
XX
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful
PT for treating immune-related disease, cancer or T-cell mediated disease
PT such as graft rejection, graft versus host disease (GVHD) and
PT inflammation.
XX
XX Claim 7; SEQ ID NO 7; 140pp; English.
PS
XX
XX The specification describes polypeptides that bind APRIL or BAFF. The
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The
CC polypeptides of the invention are useful for treating immune-related
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple
CC scleroma; or T-cell mediated disease such as graft rejection, graft
CC versus host disease (GVHD) and inflammation. The present sequence
CC represents a polypeptide of the invention that binds APRIL, derived from
CC AEC02012.
XX
XX Sequence 34 AA;
SQ
Query Match 66.8%; Score 189; DB 9; Length 34;
Best Local Similarity 94.1%; Pred. No. 3.8e-15;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY 8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
| | | | | | | | | | | | | | | | | | | |
DB 1 CSQNEYFDSLHACIPCDLYCSSNTPLTCQRYC 34
| | | | | | | | | | | | | | | | | | | |

RESULT 47
AEC02029
ID AEC02029 standard; peptide; 34 AA.
XX
AC AEC02029;
XX
XX
DT 20-OCT-2005 (first entry)
DE
DE Formula II derived polypeptide H that binds BAFF.
XX
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;
KW cytostatic; neoplasm; immunosuppressive; therapeutic.
XX
OS Synthetic.
XX
XX WO2005075511-A1.
PN
XX

```



PT inflammation.

XX Claim 7; SEQ ID NO 8; 140pp; English.

XX The specification describes polypeptides that bind APRIL or BAFF. The polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen (BCMA) APRIL and BAFF are tumor necrosis factor (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple sclerosis; or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents polypeptide of the invention that binds APRIL, derived from AEC02012.

XX SQ Sequence 34 AA;

Query Match 64.3%; Score 182; DB 9; Length 34;  
Best Local Similarity 91.2%; Pred. No. 2.6e-14;  
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPCOLRCSSNTPLTCQRYC 41  
|||||  
Db 1 CSQNEYFDSLHACKPCDLYCSTNPPLTCQRYC 34  
|||||

RESULT 49  
AAB08844

ID AAB08844 standard; peptide; 185 AA.

AC AAB08844;

XX 02-JAN-2001 (first entry)

XX Amino acid sequence of murine BCMA polypeptide.

XX BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;  
KW anti-cell death gene; apoptosis; viral infection; inflammatory response;  
KW rheumatoid arthritis; inflammatory bowel disease; septic shock.

XX Mus musculus.

XX Key Location/Qualifiers  
FT Domain 47..72  
FT /note= "putative transmembrane domain"

XX WO200005633-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-US004925.

XX 24-FEB-1999; 99US-0121485P.

XX (GEO ) GEN HOSPITAL CORP.

XX Seed B, Ting A;

XX WPI; 2000-558405/51.

XX Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene expression.

XX Claim 32; Fig 7B; 53pp; English.

XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a

CC recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug designing

XX SQ Sequence 185 AA;

Query Match 64.0%; Score 181; DB 3; Length 185;  
Best Local Similarity 70.8%; Pred. No. 2e-13;  
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY 4 MAGQSQNEYFDSLHACIPCOLRCSSNTPLTCQRYCNASVTNSVKG 51  
||||| :|||||  
Db 1 MAQCQFHSEYFDSLHACKPCHLRCN--PPATCQPCDPSVTSSVKG 46  
||||| :|||||

RESULT 50  
AAAY71980

ID AAY71980 standard; protein; 185 AA.

AC AAY71980;

XX 28-MAR-2001 (first entry)

XX Murine B cell maturation factor (BCMA) protein.

XX Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;  
KW Tumour necrosis factor and Apol-related leucocyte expressed Ligand 1;  
KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;  
KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;  
KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;  
KW haenolytic anemia; Grave's disease; myasthenia gravis; BCMA;  
KW B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation;  
KW post-streptococcal glomerulonephritis; polyarteritis nodosa.

XX Mus musculus.

XX WO2000068378-A1.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US012266.

XX 06-MAY-1999; 99US-0132892P.

XX 01-MAY-2000; 2000US-0201012P.

XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.

XX Shu HS;

XX WPI; 2001-016094/02.

XX N-PSDB; AAD02130.

XX Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.

XX Claim 37; Page 107-108; 112pp; English.

XX The present invention relates to Tumour necrosis factor (TNF) and Apol-related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte



CC	associated autoimmune disorders like rheumatoid arthritis, systemic lupus
CC	erythematosus (SLE), insulin dependent diabetes mellitus, multiple
CC	sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
CC	anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
CC	pemphigus vulgaris, acute rheumatic fever, post-streptococcal
CC	glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
CC	corresponding nucleic acid sequence are also useful in diagnostic assays.
CC	The present sequence is a murine B cell maturation factor (BCMA). BCMA is
CC	the receptor for TALL-1 protein
XX	
SQ	Sequence 185 AA;
Query Match 64.0%; Score 181; DB 4; Length 185;	
Best Local Similarity 70.8%; Pred. No. 2e-13;	
Matches 34; Conservative 4; Mismatches 2; Indels 8; Gaps 1;	
QY	4 MAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51
DB	1 MAQCQPHSEYFDSLHACKPCHLRCNS--PPATCQPCYCDPSVTSSVKG 46
RESULT 51	
AAE15490	
ID	AAE15490 standard; protein; 185 AA.
XX	
AC	AAE15490;
DT	
DT	12-MAR-2002 (first entry)
XX	
DE	Mouse B cell maturation (BCMA) protein.
XX	
KW	Mouse; transmembrane activator and intracellular CAML interactor; TACI;
KW	cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW	lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW	prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW	drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW	Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW	human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW	rheumatoid arthritis; atherosclerosis.
XX	
OS	Mus sp.
XX	
PN	W0200187979-A2.
XX	
PD	22-NOV-2001.
XX	
PF	14-MAY-2001; 2001WO-US015567.
XX	
PR	12-MAY-2000; 2000US-0204039P.
PR	27-JUN-2000; 2000US-0214591P.
PR	14-MAY-2001; 2001US-00214591.
XX	
PA	(AMGE-) AMGEN INC.
XX	
PI	Theill LE, Yu G;
XX	
DR	WPI; 2002-066686/09.
XX	
PT	Inhibiting activity of B cell maturation protein and/or transmembrane
PT	activator and intracellular cyclophilin ligand interactor, by
PT	administering a binding partner for APRIL, a tumor necrosis factor family
PT	ligand.
XX	
PS	Disclosure; Fig 11; 94pp; English.
XX	
CC	The invention relates to a method for inhibiting TACI (transmembrane
CC	activator and intracellular CAML interactor) and/or B cell maturation
CC	protein (BCMA) activity in a mammal. The method comprises administering a
CC	specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC	family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC	BCMA extracellular consensus sequence, but not the extracellular region
CC	of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC	and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC	
CC	lymphoproliferative disorders, one or more solid tumours such as lung,
CC	gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC	antagonists are useful for treating inflammation and immune function
CC	diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC	dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC	disease), drug and insect sting allergy, inflammatory bowel disease
CC	(Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC	sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC	bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC	with leucocyte infiltration of the skin or organs. The present sequence
CC	is mouse BCMA protein
XX	
SQ	Sequence 185 AA;
Query Match 64.0%; Score 181; DB 5; Length 185;	
Best Local Similarity 70.8%; Pred. No. 2e-13;	
Matches 34; Conservative 4; Mismatches 2; Indels 8; Gaps 1;	
QY	4 MAGQCSQNEYFDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVKG 51
DB	1 MAQCQPHSEYFDSLHACKPCHLRCNS--PPATCQPCYCDPSVTSSVKG 46
RESULT 52	
ADZ67762	
ID	ADZ67762 standard; protein; 185 AA.
XX	
AC	ADZ67762;
DT	
DT	14-JUL-2005 (first entry)
XX	
DE	Mouse tumor necrosis factor receptor BCMA.
XX	
KW	Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;
KW	cytostatic.
XX	
OS	Mus musculus.
XX	
PN	W02005037865-A2.
XX	
PD	28-APR-2005.
XX	
PF	18-OCT-2004; 2004WO-US034375.
XX	
PR	16-OCT-2003; 2003US-0511698P.
PR	18-OCT-2004; 2004US-0619552P.
XX	
PA	(ZYMO ) ZYMOGENETICS INC.
XX	
PI	Fox BA, Holloway JL, Sheppard PO, Dillon SR;
XX	
DR	WPI; 2005-315682/32.
XX	
PT	New tumor necrosis factor receptor (TNFR) polypeptides, useful as
PT	detecting ligands, and for modulating tumor growth, metastasis and
PT	immunity, such as separating resting from stimulated immune cells.
XX	
PS	Disclosure; SEQ ID NO 10; 132pp; English.
XX	
CC	The invention provides novel tumor necrosis factor receptor ztnfr14
CC	polynucleotides ADZ67753 and polypeptides ADZ67754, expression vectors
CC	and antibodies. Human ztnfr14 polynucleotides are used in claimed methods
CC	for detecting a genetic abnormality in a patient and for detecting a
CC	cancer in a patient. Recombinant ztnfr14 polypeptide, optionally
CC	conjugated to a toxin, is used in a claimed method of killing cancer
CC	cells. Ztnfr14 polypeptides can be used to detect ligands, agonists and
CC	antagonists. The polypeptides, polynucleotides and antibodies may also be
CC	used in methods that modulate tumor growth, metastasis, and immunity such
CC	as separating resting from stimulated immune cells. The present sequence
CC	is that of murine TNFR BCMA. This sequence was compared with that of
CC	murine ztnfr14 ADZ67756 in the identification of ztnfr14 as a member of
CC	the TNFR family.
XX	







```
Query Match      55.8%; Score 158; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MLQWAGCQSQNEYFDSLHACIPQLRC 28
Db      15 MLQWAGCQSQNEYFDSLHACIPQLRC 42
        |||||
RESULT 55
ADIS3060
ID      ADIS3060 standard; peptide; 26 AA.
XX
AC      ADIS3060;
XX
DT      22-APR-2004 (first entry)
XX
DE      Human BCMA receptor binding site.
XX
KW      protein co-ordinate data; cytostatic; anti-allergic; immunosuppressive;
KW      antirheumatic; antiarthritic; neuroprotective; anti-inflammatory;
KW      antidiabetic; dermatological; antiasthmatic; neurokinine-alpha;
KW      crystallography; cancer; allergic disorder; autoimmune disease;
KW      rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;
KW      systemic lupus erythematosus; asthma; receptor.
XX
OS      Homo sapiens.
XX
PN      WO2003050134-A2.
XX
PD      19-JUN-2003.
XX
PF      07-NOV-2002; 2002WO-US035661.
XX
PR      07-NOV-2001; 2001US-0331049P.
XX
PA      (HUMA-) HUMAN GENOME SCI INC.
XX
PI      Li Y, Oren DE, Arnold E, Volovik Y;
XX
WPI; 2003-532895/50.
XX
New crystalline Neurokinine-alpha protein, useful for designing compounds
PT that bind, inhibit or mimic a Neurokinine-alpha protein or enhance the
PT activity of a Neurokinine-alpha protein for treating e.g. cancer or
PT allergic disorders.
XX
PS      Disclosure; Fig 4; 362pp; English.
XX
CC      The invention relates to a neurokinine-alpha protein in crystalline form.
CC      The crystalline neurokinine-alpha protein is useful for designing
CC      molecules that have biological activity or compounds that bind, inhibit
CC      or mimic a neurokinine-alpha protein and/or enhance the activity of a
CC      neurokinine-alpha protein. The three-dimensional structure of a neurokinine
CC      -alpha protein is useful in determining the three-dimensional of other
CC      neurokinine-alpha proteins and their homologs. The compounds that mimic,
CC      prevent or inhibit the activity of the protein are useful for treating
CC      cancer, allergic disorders, or autoimmune diseases such as rheumatoid
CC      arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus
CC      erythematosus or asthma. This sequence represents the residues in the
CC      receptor for binding a cytokine ligand.
XX
SQ      Sequence 26 AA;
Query Match      53.4%; Score 151; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 9.7e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 EYFDSLHACIPQLRCSSNTPPLTC 37
Db      1 EYFDSLHACIPQLRCSSNTPPLTC 26
        |||||
```

## RESULT 56

```
AAE15491
ID      AAE15491 standard; protein; 117 AA.
XX
AC      AAE15491;
XX
DT      29-AUG-2003 (revised)
DT      12-MAR-2002 (first entry)
XX
DE      Human-murine B cell maturation protein (BCMA) consensus sequence.
XX
KW      Human; transmembrane activator and intracellular CAML interactor; TACI;
KW      cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW      lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW      prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW      drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW      Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW      human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW      rheumatoid arthritis; atherosclerosis; mouse.
XX
OS      Homo sapiens.
OS      Mus sp.
OS      Chimeric.
XX
PN      WO200187979-A2.
XX
PD      22-NOV-2001.
XX
PF      14-MAY-2001; 2001WO-US015567.
XX
PR      12-MAY-2000; 2000US-0204039P.
PR      27-JUN-2000; 2000US-0214591P.
PR      14-MAY-2001; 2001US-00214591.
XX
PA      (AMGE-) AMGEN INC.
XX
PI      Theill LE, Yu G;
XX
WPI; 2002-066686/09.
XX
Inhibiting activity of B cell maturation protein and/or transmembrane
PT activator and intracellular cyclophilin ligand interactor, by
PT administering a binding partner for APRIL, a tumor necrosis factor family
PT ligand.
XX
PS      Disclosure; Fig 11; 94pp; English.
XX
CC      The invention relates to a method for inhibiting TACI (transmembrane
CC      activator and intracellular CAML interactor) and/or B cell maturation
CC      protein (BCMA) activity in a mammal. The method comprises administering a
CC      specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC      family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC      BCMA extracellular consensus sequence, but not the extracellular region
CC      of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC      and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC      lymphoproliferative disorders, one or more solid tumours such as lung,
CC      gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC      antagonists are useful for treating inflammation and immune function
CC      diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC      dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC      disease), drug and insect sting allergy, inflammatory bowel disease
CC      (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC      sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC      bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC      with leucocyte infiltration of the skin or organs. The present sequence
CC      is human-murine B cell maturation protein (BCMA) consensus sequence.
CC      (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ      Sequence 117 AA;
Query Match      36.7%; Score 104; DB 5; Length 117;
Best Local Similarity 69.8%; Pred. No. 0.00019;
Matches 30; Conservative 1; Mismatches 2; Indels 10; Gaps 6;
```











KW Plasma membrane; diagnosis; therapeutic; cancer; cytostatic; neoplasm;  
 KW tumor necrosis factor receptor.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2005052182-A2.  
 XX  
 XX  
 PD 09-JUN-2005.  
 XX  
 PF 25-NOV-2004; 2004WO-IL001085.  
 XX  
 XX  
 PR 26-NOV-2003; 2003US-0524885P.  
 XX  
 PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX  
 PI Linial M, Inberg A, Bledi Y;  
 XX  
 DR WPI; 2005-418017/42.  
 DR REFSEQ; NP\_067324.  
 XX  
 XX Characterizing proteins present in a plasma membrane of a cell, useful in  
 PT identifying diagnostic markers and potential drugs, comprises subjecting  
 PT a cell to a protease treatment.  
 XX  
 XX Claim 25; SEQ ID NO 54; 196pp; English.  
 PS  
 XX The present invention relates to a method of characterizing proteins  
 CC present in the plasma membrane (PM) of live cells. The proteins of the  
 CC invention are useful in identifying diagnostic markers and potential  
 CC drugs. The invention is useful for identifying drugs for diagnosing and  
 CC treating disorders such as cancer which are associated with abnormal  
 CC representation of cell surface proteins. The present sequence is mouse  
 CC tumor necrosis factor receptor superfamily member 13b protein.  
 XX  
 SQ Sequence 249 AA;

Query Match 25.3%; Score 71.5; DB 9; Length 249;  
 Best Local Similarity 35.3%; Pred. No. 3.1;  
 Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;  
 QY 8 CSQNEYFDSLHLHACIPCOLRCSSNTPLTQRYC 41  
 DB 6 CPKQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38

RESULT 62  
 ADC71568  
 ID ADC71568 standard; protein; 1548 AA.  
 AC ADC71568;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 XX Mouse subtilisin-like protein convertase 6 (SPC6).  
 DE  
 XX neuroleptic; subtilisin-like protein convertase 6 agonist;  
 KW subtilisin-like protein convertase 6 antagonist; transgenic;  
 KW subtilisin-like protein convertase 6; SPC6; schizophrania.  
 XX  
 OS Mus sp.  
 XX  
 PN US2003093824-A1.  
 XX  
 PD 15-MAY-2003.  
 XX  
 XX 25-JUN-2002; 2002US-00180903.  
 XX  
 PR 26-JUN-2001; 2001US-0300978P.  
 PR 24-SEP-2001; 2001US-0324820P.  
 XX  
 XX (ALLE/) ALLEN K D.  
 PA Allen KD;  
 XX  
 PI

XX  
 DR WPI; 2003-777261/73.  
 DR N-PSDB; ADC71567.  
 XX  
 XX New transgenic mouse useful in methods for identifying potential  
 PT therapeutic agents for treating a variety of diseases, including  
 PT schizophrania, comprises a disruption in a subtilisin-like protein  
 PT convertase 6 (SPC6) gene.  
 XX  
 XX Disclosure; SEQ ID NO 2; 34pp; English.  
 XX  
 CC The invention describes a transgenic mouse (I) comprising a disruption in  
 CC an subtilisin-like protein convertase (SPC6) gene, where there is no  
 CC native expression of an endogenous SPC6 gene. The therapeutic agent is  
 CC administered by inhalation or insufflation or oral, buccal, parenteral,  
 CC topical, subcutaneous, intraperitoneal, intravenous, intrapleural,  
 CC intraocular, intraarterial, or rectal route. The transgenic mouse and  
 CC associated methods are useful for identifying potential therapeutic  
 CC agents (e.g. SPC6 agonists and antagonists) for treating conditions  
 CC associated with SPC6. The identified agents are potentially useful for  
 CC treating diseases such as schizophrania. The mouse is useful for  
 CC investigating the biological roles of SPC6. This is the amino acid  
 CC sequence of mouse SPC6.  
 XX  
 SQ Sequence 1548 AA;

Query Match 24.9%; Score 70.5; DB 7; Length 1548;  
 Best Local Similarity 34.7%; Pred. No. 28;  
 Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;  
 QY 7 QCSQNEYFDSLHLHACIPCOLRCSSNTPP-----LTCQRYCNASVTNSVK 50  
 DB 1151 ECAAVEYWDGSHRCQPCHKKCRCSGSDQCYTCPRFTLLNTTCVK 1199

RESULT 63  
 ABB80243  
 ID ABB80243 standard; protein; 1877 AA.  
 XX  
 AC ABB80243;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Murine subtilase.

XX Subtilase; chromosome 9q21.13; EST; expressed sequence tag; kidney;  
 KW renal cell; head; neck; heart; multiple sclerosis; lesion; cervix;  
 KW pooled germ cell; tumour; uterus; adenocarcinoma; retina II; stomach;  
 KW proprotein convertase subtilisin; furin-like repeat; Alzheimer's disease;  
 KW Parkinson's disease; pain; colon; pelvic pain; pre-oesophageal dysphagia;  
 KW gastritis; ulcers; urinary incontinence; lupus nephritis;  
 KW renal transplant rejection; myocardial infarction; erectile dysfunction;  
 KW ovary; lung; thyroid; carcinoma; lymphoma; Kaposi's sarcoma;  
 KW congestive heart failure; ischaemia; hypertensive vascular disease.  
 XX  
 OS Mus musculus.

XX WO2003060109-A2.  
 PN  
 XX  
 PD 24-JUL-2003.  
 XX  
 XX 14-JAN-2003; 2003WO-EP0000253.  
 PF  
 XX 15-JAN-2002; 2002US-0347876P.  
 PR 29-JUL-2002; 2002US-0398734P.  
 PR  
 XX (FARB ) BAYER AG.  
 PA  
 XX Koehler RH;  
 PI  
 XX WPI; 2003-608065/57.  
 DR  
 XX New subtilase-encoding polynucleotide and its encoded protein, useful for  
 PT



PT identifying modulators of subtilase activity, and in gene therapy for  
PT treating e.g. Alzheimer's disease, cancers, congestive heart failure or  
PT ischemia.  
XX Disclosure; Page 122-26; 135pp; English.  
XX This sequence shows a murine subtilase. The homologous human subtilase  
CC coding sequence is located on chromosome 9q21.13. Related EST's are  
CC expressed in kidney (renal cell adenocarcinoma), head and neck tissue,  
CC heart, multiple sclerosis lesions, cervix, pooled germ cell tumours,  
CC uterus tumour, adenocarcinoma, retina II and stomach. The subtilisin  
CC protein is a long membrane bound protein which shows 96% identity to  
CC human proprotein convertase subtilisin. There are two blocks of 11 furin-  
CC like repeats in the C-terminal portion of the protein. It has one  
CC transmembrane domain, also in the C-terminal portion, suggesting that the  
CC protein is localised on the outside of the membrane. The subtilase  
CC polynucleotide and polypeptide are useful for identifying test compounds,  
CC which may act as agonists or antagonists at the receptor site and which  
CC can be regulated to provide therapeutic effects. Vectors comprising the  
CC polynucleotide are useful for modulating the activity of subtilase in a  
CC disease, e.g. a central nervous system disorder, a gastrointestinal  
CC disorder, cancer, a cardiovascular disorder, a genitourinary disorder, or  
CC diabetes. In particular, these diseases are Alzheimer's disease,  
CC Parkinson's disease, pain, colon tumour, pre-oesophageal dysphagia,  
CC gastritis, ulcers, urinary incontinence, lupus nephritis, renal  
CC transplant rejection, pelvic pain, erectile dysfunction, ovary tumour,  
CC lung tumour, thyroid tumour, carcinoma, lymphoma, Kaposi's sarcoma,  
CC congestive heart failure, myocardial infarction, ischaemia, hypertensive  
CC vascular diseases, etc. These are also useful for preventing or  
CC ameliorating the diseases cited above  
XX Sequence 1877 AA;

Query Match 24.9%; Score 70.5; DB 7; Length 1877;  
Best Local Similarity 34.7%; Pred. No. 35;  
Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;

OY 7 QCSQNEYFDSLLHACIPQCLRCSSNTPT-----LTCQRYCNAVSTNSVK 50  
DB 1480 ECAAVEYWDGSHRCQPKCKRCGSPGSDQCYTCPTFTLLNTTCVK 1528

RESULT 64  
AAE35228  
ID AAE35228 standard; protein; 332 AA.

AC AAE35228;  
XX 23-OCT-2003 (revised)  
DT 28-MAY-2003 (first entry)  
XX Human TACI-Fc5 fusion protein comprising murine 26-10 VH signal peptide.  
XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;  
KW TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;  
KW anaemia; gene therapy; cytostatic; antinflammatory; immunosuppressive;  
KW glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;  
KW dermatological; neuroprotective; cyclophilin ligand-interactor; human;  
KW autoimmune disease; systemic lupus erythematosus; multiple sclerosis;  
KW diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;  
KW mouse; Fc5 protein; chimeric.  
XX Homo sapiens.  
OS Mus sp.  
OS Chimeric.  
XX WO200294852-A2.  
FN 28-NOV-2002.  
XX 20-MAY-2002; 2002WO-US015910.  
XX 24-MAY-2001; 2001US-0293343P.  
XX

XX (ZYMO ) ZYMOGENETICS INC.  
PA Rixon MW, Gross JA;  
XX WPI; 2003-148455/14.  
XX

XX Transmembrane activator and calcium modulator and cyclophilin ligand-  
PT interactor (TACI)-immunoglobulin fusion protein, for treating cancer or  
PT diabetes, comprises a TACI receptor group and an immunoglobulin group.  
XX Disclosure; Col 137-138; 71pp; English.

XX The invention relates to fusion proteins comprising transmembrane  
CC activator and calcium modulator and cyclophilin ligand-interactor (TACI)  
CC receptor group that binds tumour necrosis factor-like protein (ZTNF2) or  
CC ZTNF4; and an immunoglobulin group comprising a constant region of an  
CC immunoglobulin. The invention is used to manufacture a medicament for  
CC inhibiting the proliferation of tumour cells in a mammalian subject. The  
CC composition comprising the fusion protein may also be used in treating  
CC autoimmune diseases (e.g. systemic lupus erythematosus, multiple  
CC sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal  
CC diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft  
CC rejection, anaemia and septic shock. The fusion proteins are also used in  
CC gene therapy. The present sequence is human TACI-Fc5 fusion protein  
CC comprising murine 26-10 VH signal peptide. This sequence is used in the  
CC invention. (Updated on 23-OCT-2003 to standardise OS field)

XX Sequence 332 AA;

Query Match 24.2%; Score 68.5; DB 6; Length 332;  
Best Local Similarity 27.9%; Pred. No. 9.7;  
Matches 12; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

OY 1 MLOMACQCSQNEYFDSLLHACIPQCLRCSSNTPTLTCQRYCNA 43  
DB 17 VLSMRSCPEQYWDPLLTCTMCKTICNHQS-QRTCAAFCRS 59

RESULT 65  
ADRI8921  
ID ADRI8921 standard; protein; 1569 AA.

XX ADRI8921;  
XX 04-NOV-2004 (first entry)  
XX Human mucin glycoprotein, MUC6.  
XX Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antinflammatory;  
KW Ophthalmological; Auditory; Vulnery; Gastrointestinal; Cytostatic;  
KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;  
KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;  
KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;  
KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;  
KW gastric intestinal metaplasia; chronic cholecystitis; skin cancer;  
KW mucin glycoprotein.  
XX Homo sapiens.  
XX WO2004069136-A2.  
XX 19-AUG-2004.  
XX 04-FEB-2004; 2004WO-EP050082.  
XX 05-FEB-2003; 2003US-0445217P.  
XX (ISTP ) ARS APPLIED RES SYSTEMS HOLDING NV.  
XX Bienkowska J, Mcallister G;  
XX WPI; 2004-604324/58.  
XX



DR GENBANK; AAQ82434.

XX New isolated mucin-like polypeptides, useful for diagnosing or treating,

PT e.g. bacterial infections, allergic asthma, inflammation, allergic

PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung

PT cancer, or skin cancer.

XX Example 2; Fig 1; 170pp; English.

XX The present invention relates to novel mucin-like proteins (I) and their

CC coding sequences. The mucin-like proteins and coding sequences are useful

CC in the therapy or in the prevention of a disease when the increase in the

CC mucin-like activity of a polypeptide is needed e.g. bacterial infections,

CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced

CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial

CC wounding, inflammatory bowel disease, Crohn's disease, small

CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,

CC chronic cholecystitis, or skin cancer. The present sequence is a mucin

CC glycoprotein which was used in a sequence alignment with the mucin-like

CC proteins of the invention.

XX SQ Sequence 1569 AA;

Query Match 24.2%; Score 68.5; DB 8; Length 1569;

Best Local Similarity 45.2%; Pred. No. 50;

Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQ 38

Db |||:||||| :|||

1179 CSQDEYFDHEGVCVFCM-----PPTTPQ 1202

RESULT 66

ADRI8914

ID ADRI8914 standard; protein; 2240 AA.

AC ADRI8914;

XX 04-NOV-2004 (first entry)

XX Mature Human mucin-like protein, SCS0004, variant SEQ ID 4.

DE XX

DE Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;

KW Ophthalmological; Auditory; Vulnery; Gastrointestinal; Cytostatic;

KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;

KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;

KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;

KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;

KW gastric intestinal metaplasia; chronic cholecystitis; skin cancer.

XX OS Homo sapiens.

XX WO2004069136-A2.

XX 19-AUG-2004.

XX 04-FEB-2004; 2004WO-EP050082.

XX 05-FEB-2003; 2003US-0445217P.

XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Bienkowska J, Mcallister G;

XX WPI; 2004-604324/58.

XX New isolated mucin-like polypeptides, useful for diagnosing or treating,

PT e.g. bacterial infections, allergic asthma, inflammation, allergic

PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung

PT cancer, or skin cancer.

XX Claim 2; SEQ ID NO 4; 170pp; English.

CC The present invention relates to novel mucin-like proteins (I) and their

CC coding sequences. The present sequence is one such human mucin-like

CC protein. The mucin-like proteins and coding sequences are useful in the

CC therapy or in the prevention of a disease when the increase in the mucin-

CC like activity of a polypeptide is needed e.g. bacterial infections,

CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced

CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial

CC wounding, inflammatory bowel disease, Crohn's disease, small

CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,

CC chronic cholecystitis, or skin cancer.

XX SQ Sequence 2240 AA;

Query Match 24.2%; Score 68.5; DB 8; Length 2240;

Best Local Similarity 45.2%; Pred. No. 73;

Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQ 38

Db |||:||||| :|||

1161 CSQDEYFDHEGVCVFCM-----PPTTPQ 1184

RESULT 67

ADRI8913

ID ADRI8913 standard; protein; 2258 AA.

XX ADRI8913;

XX 04-NOV-2004 (first entry)

XX Human mucin-like protein, SCS0004, variant SEQ ID 3.

DE XX

DE Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;

KW Ophthalmological; Auditory; Vulnery; Gastrointestinal; Cytostatic;

KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;

KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;

KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;

KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;

KW gastric intestinal metaplasia; chronic cholecystitis; skin cancer.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..18

FT Protein /label= Signal\_peptide

FT 19..2258

FT /label= Mature\_protein

XX WO2004069136-A2.

XX 19-AUG-2004.

XX 04-FEB-2004; 2004WO-EP050082.

XX 05-FEB-2003; 2003US-0445217P.

XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Bienkowska J, Mcallister G;

XX WPI; 2004-604324/58.

XX New isolated mucin-like polypeptides, useful for diagnosing or treating,

PT e.g. bacterial infections, allergic asthma, inflammation, allergic

PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung

PT cancer, or skin cancer.

XX Claim 2; SEQ ID NO 3; 170pp; English.

XX The present invention relates to novel mucin-like proteins (I) and their

CC coding sequences. The present sequence is one such human mucin-like

CC protein. The mucin-like proteins and coding sequences are useful in the

CC therapy or in the prevention of a disease when the increase in the mucin-



CC like activity of a polypeptide is needed e.g. bacterial infections,  
 CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced  
 CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial  
 CC wounding, inflammatory bowel disease, Crohn's disease, small  
 CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,  
 CC chronic cholecystitis, or skin cancer.  
 XX  
 SQ Sequence 2258 AA;

Query Match 24.2%; Score 68.5; DB 8; Length 2258;  
 Best Local Similarity 45.2%; Pred. No. 73;  
 Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 8 CSQNEVFDLSLLHACIPQCLRCSSNTPTPTCO 38  
 ||||:||||| :|||  
 DB 1179 CSQDEYFDHEGVCVPCM-----PPTTPQ 1202

RESULT 68  
 ADR18915  
 ID ADR18915 standard; protein; 2264 AA.  
 XX  
 AC ADR18915;  
 XX  
 XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 DE His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.  
 XX  
 KW Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antinflammatory;  
 KW Ophthalmological; Auditory; Vulnerary; Gastrointestinal; Cytostatic;  
 KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;  
 KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;  
 KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;  
 KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;  
 KW gastric intestinal metaplasia; chronic cholecystitis; skin cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004069136-A2.  
 XX  
 PD 19-AUG-2004.  
 XX  
 PF 04-FEB-2004; 2004WO-EP050082.  
 XX  
 PR 05-FEB-2003; 2003US-0445217P.  
 XX  
 PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
 XX  
 PI Bienkowska J, Mcallister G;  
 XX  
 WPI; 2004-604324/58.

DR New isolated mucin-like polypeptides, useful for diagnosing or treating,  
 XX e.g. bacterial infections, allergic asthma, inflammation, allergic  
 PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung  
 PT cancer, or skin cancer.  
 XX  
 PS Claim 2; SEQ ID NO 5; 170pp; English.

XX The present invention relates to novel mucin-like proteins (I) and their  
 CC coding sequences. The present sequence is one such human mucin-like  
 CC protein. The mucin-like proteins and coding sequences are useful in the  
 CC therapy or in the prevention of a disease when the increase in the mucin-  
 CC like activity of a polypeptide is needed e.g. bacterial infections,  
 CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced  
 CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial  
 CC wounding, inflammatory bowel disease, Crohn's disease, small  
 CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,  
 CC chronic cholecystitis, or skin cancer.  
 XX

SQ Sequence 2264 AA;  
 Query Match 24.2%; Score 68.5; DB 8; Length 2264;

Best Local Similarity 45.2%; Pred. No. 73;  
 Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;  
 QY 8 CSQNEVFDLSLLHACIPQCLRCSSNTPTPTCO 38  
 ||||:||||| :|||  
 DB 1179 CSQDEYFDHEGVCVPCM-----PPTTPQ 1202

RESULT 69  
 AAU10951  
 ID AAU10951 standard; protein; 37 AA.  
 XX  
 AC AAU10951;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human AGP-3 receptor cysteine rich repeat region #1.

XX Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;  
 KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;  
 KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;  
 KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;  
 KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;  
 KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;  
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;  
 KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;  
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;  
 KW multiple sclerosis; Parkinson's disease; transgenic animal.

XX Homo sapiens.  
 OS  
 PN WO200185782-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 12-FEB-2001; 2001WO-US004568.  
 XX  
 PR 11-FEB-2000; 2000US-0181800P.

XX (AMGE-) AMGEN INC.  
 PA  
 PI Boyle WJ, Hsu H;  
 XX  
 WPI; 2002-049441/06.

XX Composition, useful for identifying modulator of receptor for treating  
 PT asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor  
 PT ligand family member) receptor and encoding nucleic acids.

XX Claim 1; Fig 18; 124pp; English.

XX The invention relates to a composition (I) comprising AGP-3 receptor  
 CC (tumour necrosis factor ligand family member) related protein (II)  
 CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related  
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in  
 CC assays to identify cells and tissues that express AGP-3R or proteins  
 CC related to AGP-3R-related protein and for identifying compounds (agonists  
 CC or antagonists) that interact with AGP-3R proteins. (II) is also useful  
 CC for identifying intracellular proteins that interact with the respective  
 CC cytoplasmic domains by yeast two-hybrid screening processes. (II) is  
 CC involved in B cell growth, survival and activation particularly in lymph  
 CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists  
 CC identified using (II) are used for modulating B cell response and are  
 CC used to treat diseases characterised by inflammatory processes or  
 CC deregulated immune response such as rheumatoid arthritis, graft-versus-  
 CC host disease, Crohn's disease, lupus, etc. (II) is also useful in the  
 CC production of hybridoma cells which are derived from B cells, which  
 CC involves treating the hybridoma cells with (II). (II) is useful in the  
 CC treatment of inflammatory conditions of joints, e.g., rheumatoid  
 CC arthritis, osteoarthritis, etc. (II), its agonists or antagonists are  
 CC useful for treating acute pancreatitis, amyotrophic lateral sclerosis  
 CC (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia,  
 CC diabetes, fever, glomerulonephritis, inflammatory bowel disease,







Query Match 23.9%; Score 67.5; DB 5; Length 59;  
Best Local Similarity 30.6%; Pred. No. 2.1;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEVFDLLHACIPCOLRCSSNTPPLTCORYCNA 43  
DB 34 CPBEQYWDPLLTGTCMSCKTICNHQS-QRTCAAFCS 68

RESULT 73  
AAE15494  
ID AAE15494 standard; protein; 166 AA.  
XX  
AC AAE15494;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human TAC1 extracellular domain.  
XX  
KW Human; transmembrane activator and intracellular CAML interact; TAC1;  
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200187979-A2.  
XX  
PD 22-NOV-2001.  
XX  
PF 14-MAY-2001; 2001WO-US015567.  
XX  
PR 12-MAY-2000; 2000US-0204039P.  
XX  
PR 27-JUN-2000; 2000US-0214591P.  
PR 14-MAY-2001; 2001US-00214591.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Theill LE, Yu G;  
XX  
DR WPI; 2002-066686/09.  
XX  
XX Inhibiting activity of B cell maturation protein and/or transmembrane  
PT activator and intracellular cyclophilin ligand interact, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX  
PS Claim 1; Fig 12A; 94pp; English.  
XX  
CC The invention relates to a method for inhibiting TAC1 (transmembrane  
CC activator and intracellular CAML interact) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is human TAC1 protein extracellular domain  
XX  
SQ Sequence 166 AA;

Query Match 23.9%; Score 67.5; DB 5; Length 166;  
Best Local Similarity 30.6%; Pred. No. 6.1;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEVFDLLHACIPCOLRCSSNTPPLTCORYCNA 43  
DB 1 CPBEQYWDPLLTGTCMSCKTICNHQS-QRTCAAFCS 35

RESULT 72  
AAW75785  
ID AAW75785 standard; protein; 166 AA.  
XX  
AC AAW75785;  
XX  
DT 18-JAN-1999 (first entry)  
XX  
DE Human lymphocyte surface receptor extracellular domain.  
XX  
KW TAC1; transmembrane activator and CAML-interactor;  
KW calcium signal-modulating cyclophilin ligand; human;  
KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;  
KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;  
KW immunosuppressive; graft versus host disease; transplant rejection;  
KW therapy; signal transduction.  
XX  
OS Homo sapiens.  
XX  
PN WO9839361-A1.  
XX  
PD 11-SEP-1998.  
XX  
PF 03-MAR-1998; 98WO-US004270.  
XX  
PR 03-MAR-1997; 97US-00810572.  
XX  
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.  
XX  
PI Bram RJ, Von Bulow G;  
XX  
DR WPI; 1998-S06346/43.  
DR N-PSDB; AAV57330.  
XX  
XX New isolated transmembrane activator protein - used to develop products  
PT for treating e.g. infections, cancers, autoimmune and inflammatory  
PT conditions, transplant rejection or graft-versus-host disease.  
XX  
PS Claim 8; Page 73; 89pp; English.  
XX  
CC This is the amino acid sequence of the N-terminal, i.e. the  
CC extracellular, domain of novel human transmembrane activator and CAML-  
CC interactor (TAC1) protein (see AAW75783). TAC1 is a lymphocyte receptor  
CC protein that is involved in the calcium activation pathway. It is  
CC normally present in B-lymphocytes, and to a much lesser extent in  
CC immature T-lymphocytes, and can therefore be targeted to specifically  
CC regulate B cell responses without affecting T cell activity. The  
CC extracellular domain of TAC1 functions as a binding site for a ligand  
CC that stimulates the activation of the cell by inducing the binding of the  
CC C-terminal portion (see AAW75784) of TAC1 to the N-terminal domain of  
CC CAML. A recombinant form of the extracellular portion of TAC1 acts as a  
CC dominant-negative or blocking agent and acts to suppress the immune  
CC system. It can be used to treat or prevent autoimmune disease, graft  
CC rejection or graft versus host disease. The extracellular region is also  
CC used in a claimed method for identifying a ligand for TAC1, in which  
CC binding of a candidate molecule is determined by detecting cellular  
CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription  
CC factor, or of NF-AT dependent transcription  
XX  
SQ Sequence 166 AA;

Query Match 23.9%; Score 67.5; DB 2; Length 166;  
Best Local Similarity 30.6%; Pred. No. 6.1;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;



Best Local Similarity 30.6%; Pred. No. 6.1; Mismatches 9; Conservative 15; Indels 1; Gaps 1;	
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;	
QY 8 CSONEYFDSLHACIPCOLRCSSNTFPLTCQRYCNA 43	
DB 34 CPEQYWDPLGLTGMSCSKTICNHQS-QRTCAAFCS 68	
RESULT 74	
ADN03188	ADN03188 standard; protein; 171 AA.
XX	
AC ADN03188;	
XX	
DT 15-JUL-2004 (first entry)	
XX	
DE Human TACI-HSBP fragment SEQ ID NO:18.	
XX	
KW transmembrane activator and CAML interactor; TACI; extracellular domain;	
KW trimerizing polypeptide; homotrimeric protein complex; antiinflammatory;	
KW antiarthritic; antirheumatic; immunosuppressive; antiarteriosclerotic;	
KW cytostatic; gene therapy; inflammatory disease; rheumatoid arthritis;	
KW inflammatory bowel disease; autoimmune disease; atherosclerosis;	
KW osteoporosis; allograft rejection; cancer; human;	
KW heat shock binding protein; HSBP; fusion protein.	
XX	
OS Homo sapiens.	
OS Synthetic.	
PN WO2004033486-A2.	
XX	
PD 22-APR-2004.	
XX	
PF 10-OCT-2003; 2003WO-US032878.	
XX	
PR 11-OCT-2002; 2002US-0417801P.	
XX	
PA (ZYMO ) ZYMOGENETICS INC.	
XX	
PI West JW, Brandt CS, Jaepers SR;	
XX	
DR WPI; 2004-364855/34.	
DR N-PSDB; ADN03187.	
XX	
PT New polypeptide comprising an extracellular domain of the transmembrane	
PT activator and calcium-signal modulating cyclophilin ligand (CAML)	
PT interactor (TACI), and a trimerizing polypeptide, useful for treating	
PT inflammatory diseases.	
XX	
PS Example 4; SEQ ID NO 18; 36pp; English.	
XX	
CC The present invention describes an isolated polypeptide comprising an	
CC extracellular domain of the transmembrane activator and calcium-signal	
CC modulating cyclophilin ligand (CAML) interactor (TACI), and a trimerizing	
CC polypeptide. Also described: (1) a homotrimeric protein complex	
CC comprising the polypeptide; (2) an expression vector comprising the	
CC following operably linked elements, a transcription promoter, the nucleic	
CC acid sequence encoding the polypeptide, and a transcription terminator;	
CC (3) a cultured cell into which has been introduced the expression vector,	
CC where the cell expresses the polypeptide; (4) producing a homotrimeric	
CC protein complex by culturing the cell, and recovering the homotrimeric	
CC protein complex; and (5) inhibiting tumour necrosis factor (TNF)/4-induced	
CC B cell proliferation by exposing the B cells to the homotrimeric protein	
CC complex. The polypeptide has antiinflammatory, antiarthritic,	
CC antirheumatic, immunosuppressive, antiarteriosclerotic and cytostatic	
CC activities, and can be used in gene therapy. The polypeptides are useful	
CC for treating and controlling inflammatory diseases, e.g. rheumatoid	
CC arthritis or inflammatory bowel disease, autoimmune disease,	
CC atherosclerosis, osteoporosis, allograft rejection and cancer. The	
CC present sequence represents a human TACI and heat shock binding protein	
CC (HSBP) fusion protein fragment, which is used in the exemplification of	
CC the present invention.	
XX	
SQ Sequence 171 AA;	
Query Match 23.9%; Score 67.5; DB 8; Length 171;	
Best Local Similarity 30.6%; Pred. No. 6.3;	
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;	
QY 8 CSONEYFDSLHACIPCOLRCSSNTFPLTCQRYCNA 43	
DB 6 CPEQYWDPLGLTGMSCSKTICNHQS-QRTCAAFCS 40	
RESULT 75	
AAE09244	AAE09244 standard; protein; 265 AA.
ID AAE09244	
XX	
AC AAE09244;	
XX	
DT 19-NOV-2001 (first entry)	
XX	
DE Human TACI splice variant protein.	
XX	
KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;	
KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;	
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.	
XX	
OS Homo sapiens.	
XX	
PN WO200160397-A1.	
XX	
PD 23-AUG-2001.	
XX	
PF 28-NOV-2000; 2000WO-US032378.	
XX	
PR 16-FEB-2000; 2000US-0182938P.	
XX	
PR 22-AUG-2000; 2000US-0226986P.	
XX	
PA (GETH ) GENENTECH INC.	
XX	
PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;	
PI Yan M;	
XX	
DR WPI; 2001-541628/60.	
XX	
PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological	
PT activity, for treating autoimmune disorders and cancer, comprises	
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or	
PT antagonists.	
XX	
PS Example 1; Fig 6; 160pp; English.	
XX	
CC The invention relates to methods of using one or more agonists or	
CC antagonists to modulate the activity of the members of TNF (tumour	
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.	
CC TACI or BCMA. The method is useful for treating pathological conditions	
CC or diseases associated with increased TALL-1 and APRIL expression or	
CC activity. TALL-1 and APRIL antagonists are used to block the interaction	
CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating	
CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,	
CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid	
CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The	
CC present sequence is human TACI splice variant protein	
XX	
Sequence 265 AA;	
Query Match 23.9%; Score 67.5; DB 4; Length 265;	
Best Local Similarity 30.6%; Pred. No. 10;	
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;	
QY 8 CSONEYFDSLHACIPCOLRCSSNTFPLTCQRYCNA 43	
DB 34 CPEQYWDPLGLTGMSCSKTICNHQS-QRTCAAFCS 68	



Search completed: December 21, 2005, 16:05:46  
Job time : 173.6 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 21, 2005, 15:57:04 ; Search time 28.2 Seconds  
(without alignments)  
174.009 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_1\_51  
Perfect score: 283

Sequence: 1 MLQWAGQCSQNEYFDSLHA.....TPPLTCQRCYNASVTNSYKG 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database :

PIR 80: \*  
1: Pirl: \*  
2: Pirl2: \*  
3: Pirl3: \*  
4: Pirl4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	283	100.0	184	2	S43486
2	70.5	24.9	1548	2	S34583
3	69.5	24.6	5376	2	T42215
4	68.5	24.2	1101	2	T16940
5	65.5	23.1	1299	2	T43251
6	62.5	22.1	999	2	T19275
7	62	21.9	330	2	T25169
8	61.5	21.7	483	2	T24856
9	61.5	21.7	483	2	G88946
10	61.5	21.7	520	2	T13954
11	60.5	21.4	1574	2	T14119
12	60.5	21.4	3034	2	T11887
13	59.5	21.0	388	2	T31888
14	59.5	21.0	388	2	T31889
15	59.5	21.0	438	2	T31898
16	59.5	21.0	445	2	T15577
17	59	20.8	758	2	T14558
18	59	20.8	1717	1	A45358
19	58.5	20.7	2533	2	T28675
20	58.5	20.7	2533	2	T28674
21	58	20.5	63	2	S07127
22	58	20.5	1513	2	T23681
23	58	20.5	1816	1	S68960
24	57.5	20.3	1680	2	A43434
25	57	20.1	502	2	T20130
26	57	20.1	653	2	G96675
27	57	20.1	838	2	T20125
28	56.5	20.0	701	2	S62460
29	56	19.8	2476	2	T34022

30	56	19.8	2824	2	T22759	hypothetical prote
31	55.5	19.6	339	1	KHRTB	cathepsin B (EC 3.
32	55.5	19.6	378	2	B99588	protein R09F10.7 (
33	55.5	19.6	815	1	T05754	S-receptor kinase
34	55.5	19.6	989	2	T01519	hypothetical prote
35	55	19.4	294	2	T23682	hypothetical prote
36	55	19.4	339	1	KHMSB	cathepsin B (EC 3.
37	55	19.4	758	2	S46625	finger protein XUL
38	55	19.4	1620	2	T27283	hypothetical prote
39	54.5	19.3	392	2	T27303	hypothetical prote
40	54.5	19.3	419	2	S6207	vascular endotheli
41	54.5	19.3	493	2	JC5486	membrane glycoprot
42	54.5	19.3	879	2	C90879	hypothetical prote
43	54.5	19.3	879	2	H64888	membrane protein y
44	54.5	19.3	879	2	G85739	hypothetical prote
45	54.5	19.3	2155	2	T30197	alpha tectorin - m
46	54	19.1	282	2	I48763	siah-1A protein -
47	54	19.1	282	2	S35754	siah-1B protein -
48	54	19.1	474	2	T27297	hypothetical prote
49	54	19.1	497	2	T27827	hypothetical prote
50	54	19.1	1099	2	T16822	hypothetical prote
51	54	19.1	1980	2	S54307	myosin heavy chain
52	54	19.1	2022	2	A59256	myosin-IXb [simila
53	53.5	18.9	255	2	A84544	hypothetical prote
54	53.5	18.9	332	2	T21458	hypothetical prote
55	53.5	18.9	356	2	T21681	hypothetical prote
56	53.5	18.9	915	2	T21773	hypothetical prote
57	53.5	18.9	927	2	T21772	hypothetical prote
58	53.5	18.9	1895	2	T15881	hypothetical prote
59	53.5	18.9	1935	2	T39411	RNA helicase - fla
60	53	18.7	98	2	C89046	protein C10G8.4 (i
61	53	18.7	274	2	F86276	F14L17.2 protein -
62	53	18.7	447	2	A96639	protein Tf9.18 (i
63	53	18.7	455	1	GOHUT1	tumor necrosis fac
64	53	18.7	592	1	JCL480	protein kinase C (
65	53	18.7	596	2	F88188	protein C18H9.7 (i
66	53	18.7	654	2	T30136	hypothetical prote
67	53	18.7	712	1	VCLJSA	env polyprotein pr
68	53	18.7	859	1	VCLJST	env polyprotein pr
69	53	18.7	1034	2	JC5598	mucin - rat
70	53	18.7	1077	2	T41146	probable cysteine-
71	53	18.7	1474	2	D88550	protein ZC84.6 (lm
72	53	18.7	2844	2	S28291	hypothetical prote
73	52.5	18.6	118	2	S61051	hypothetical prote
74	52.5	18.6	378	2	T51647	myb-related transc
75	52.5	18.6	389	2	T29488	hypothetical prote
76	52.5	18.6	397	2	F72072	probable transamin
77	52.5	18.6	563	2	C86552	aspartate aminotra
78	52.5	18.6	563	2	A36054	mucin homolog - bo
79	52.5	18.6	847	2	D72860	viral capsid assoc
80	52.5	18.6	1589	2	T42233	submaxillary mucin
81	52.5	18.6	3635	2	T10053	laminin alpha 5 ch
82	52	18.4	56	2	JN0380	trypsin inhibitor
83	52	18.4	141	2	S20915	lysozyme (EC 3.2.1
84	52	18.4	180	2	PC1305	genome polyprotein
85	52	18.4	181	2	T05301	hypothetical prote
86	52	18.4	304	1	JC2264	tissue factor path
87	52	18.4	420	2	T30507	probable alkaline
88	52	18.4	547	2	T34318	hypothetical prote
89	52	18.4	689	2	T52060	protein MEDEA (lmp
90	52	18.4	852	1	VCLJGG	env polyprotein pr
91	52	18.4	869	2	S53098	envelope polyprote
92	52	18.4	1115	2	S40241	G protein-coupled
93	52	18.4	1483	2	S30015	hypothetical prote
94	52	18.4	1747	2	T43162	antimicrobial pept
95	51.5	18.2	63	2	S57816	antimicrobial pept
96	51.5	18.2	424	2	T14525	S-locus-specific g
97	51.5	18.2	685	2	S78040	fibulin, splice fo
98	51.5	18.2	705	2	S34968	fibulin, splice fo
99	51.5	18.2	837	2	S43656	furin (EC 3.4.21.7
100	51.5	18.2	1808	2	T15099	hypothetical prote
101	51.5	18.2	2120	2	T30243	alpha tectorin - c
102	51	18.0	166	2	H89044	protein B0238.12 (







249 48 17.0 229 2 T22037  
250 48 17.0 266 2 T46314  
251 48 17.0 271 2 A70415  
252 48 17.0 304 1 THUGK  
253 48 17.0 317 2 A39935  
254 48 17.0 331 2 T26871  
255 48 17.0 367 2 S46336  
256 48 17.0 369 2 S21471  
257 48 17.0 371 2 T22652  
258 48 17.0 431 2 G75305  
259 48 17.0 450 1 TFEVNR  
260 48 17.0 479 2 T02623  
261 48 17.0 492 2 S41288  
262 48 17.0 539 2 T01513  
263 48 17.0 572 2 T29880  
264 48 17.0 597 2 T08681  
265 48 17.0 661 2 E71427  
266 48 17.0 666 2 T30098  
267 48 17.0 681 2 B53542  
268 48 17.0 697 2 E96752  
269 48 17.0 705 1 TFCHE  
270 48 17.0 788 2 I51530  
271 48 17.0 839 2 T41826  
272 48 17.0 888 2 A54280  
273 48 17.0 962 2 JC5571  
274 48 17.0 969 1 A39490  
275 48 17.0 975 2 JC5570  
276 48 17.0 1079 1 TVFVMI  
277 48 17.0 1189 2 T42726  
278 48 17.0 1203 2 A49175  
279 48 17.0 1852 1 VJCH2  
280 48 17.0 2215 2 T00348  
281 48 17.0 2219 2 T27684  
282 48 17.0 2395 1 S50820  
283 48 17.0 4543 1 A53102  
284 47.5 16.8 131 2 S53380  
285 47.5 16.8 160 2 I84444  
286 47.5 16.8 201 2 D71190  
287 47.5 16.8 202 2 T22237  
288 47.5 16.8 297 2 T28775  
289 47.5 16.8 319 2 F81319  
290 47.5 16.8 328 2 C86351  
291 47.5 16.8 354 2 R75630  
292 47.5 16.8 355 1 S22181  
293 47.5 16.8 370 2 E82369  
294 47.5 16.8 388 2 A88949  
295 47.5 16.8 390 2 T25642  
296 47.5 16.8 411 2 T29475  
297 47.5 16.8 427 2 T07811  
298 47.5 16.8 429 2 T14535  
299 47.5 16.8 431 2 T07812  
300 47.5 16.8 477 2 AG0765

ALIGNMENTS

RESULT 1  
S43486  
B-cell maturation factor - human  
N:Alternate names: BCM protein; BEL protein  
C:Species: Homo sapiens (man)  
C>Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S43486; S31208; S36661  
R:Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.  
Nucleic Acids Res. 22, 1147-1154, 1994  
A>Title: The BCM gene, preferentially expressed during B lymphoid maturation, is bidirectional  
A:Reference number: S43486; MUID:94218235; PMID:8165126  
A:Accession: S43486  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-184 <LAA>  
A:Cross-references: UNIPROT:Q02223; UNIPARC:UPI0000034D1B; EMBL:Z29574; NID:g471244; PID:

R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.  
EMBO J. 11, 3897-3904, 1992  
A>Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)  
A:Reference number: S31208; MUID:93010984; PMID:1396583  
A:Accession: S31208  
A:Molecule type: mRNA  
A:Residues: 1-184 <LAA>  
A:Cross-references: UNIPARC:UPI0000034D1B; EMBL:Z14954; NID:g29407; PIDN:CAA78679.1; PID:  
A:Accession: S36661  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 4-184 <LAA>  
A:Cross-references: UNIPARC:UPI0000046868; EMBL:Z14955  
C:Genetics:  
A:Gene: GDB:BCMA  
A:Cross-references: GDB:135977; OMIM:109545  
A:Map position: 16p13.1-16p13.1  
A:Introns: 44/1; 93/1  
C:Superfamily: human B-cell maturation factor  
Query Match 100.0%; Score 283; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 8.5e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVK 51  
Db 1 MLQWAGQCSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVK 51  
RESULT 2  
S34583  
serine proteinase (EC 3.4.21.-) PC6B - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S34583  
R:Nakagawa, T.; Murakami, K.; Nakayama, K.  
FEBS Lett. 327, 165-171, 1993  
A>Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a t  
A:Reference number: S34583; MUID:93327934; PMID:8335106  
A:Accession: S34583  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1548 <NAK>  
A:Cross-references: UNIPROT:Q04592; UNIPARC:UPI000016CF9E; GB:D17583; NID:g407344; PIDN:  
C:Keywords: hydrolase; serine proteinase  
Query Match 24.9%; Score 70.5; DB 2; Length 1548;  
Best Local Similarity 34.7%; Pred. No. 4.2;  
Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;  
Qy 7 QCSQNEYFDSLHACIPCOLRCSSNTPP-----LTCORYCNASVTNSVK 50  
Db 1151 ECAAVEYWDGSHRQPCCHKRCSCGSPSEDQCYTCPRETFLNTTCVK 1199  
RESULT 3  
T42215  
zonadhesin - mouse  
N:Alternate names: sperm-specific membrane protein  
C:Species: Mus musculus (house mouse)  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T42215  
R:Gao, Z.; Garbers, D.L.  
J. Biol. Chem. 273, 3415-3421, 1998  
A>Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane prot  
A:Reference number: Z22080; MUID:98123114; PMID:9452463  
A:Accession: T42215  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-5376 <GAO>  
A:Cross-references: UNIPROT:O88799; UNIPARC:UPI000002A15E; EMBL:U97068; NID:g3327420; PI  
C:Genetics:  
A:Gene: Zan



A;Map position: 5

C;Function:

A;Description: functions in multiple cell adhesion processes

A;Note: found exclusively on the apical region of the sperm head

C;Keywords: cell adhesion

Query Match 24.6%; Score 69.5; DB 2; Length 5376;

Best Local Similarity 36.8%; Pred. No. 16;

Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIP-CQLRCSNTP--PLTCQRYC 41

DB 3299 QCPNTSQFTDCLPSCVPCSNRCEVTSPPVSSCREGC 3336

RESULT 4

T16840

hypothetical protein T10E10.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C;Accession: T16840

R;Geisels, C.

submitted to the EMBL Data Library, October 1995

A;Description: The sequence of C. elegans cosmid T10E10.

A;Reference number: Z18588

A;Accession: T16840

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1101 <GRI>

A;Cross-references: UNIPROT:Q22378; UNIPARC:UPI000017BB8F; EMBL:U39644; NID:g1049339; PI

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:T10E10.4

A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match

Best Local Similarity 24.2%; Score 68.5; DB 2; Length 1101;

Matches 17; Conservative 10; Mismatches 15; Indels 5; Gaps 3;

QY 7 QCSQNEYFDSLHACIPQLR--CSSNTPLTCQRYCNASVTSVKG 51

DB 350 QCSQSTVFNSDLNVCPLAIGNCSDSSSTQQPVCS--C-SQVSSSCPG 393

RESULT 5

T43251

furin (EC 3.4.21.75) - fall armyworm

N;Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin

C;Species: Spodoptera frugiperda (fall armyworm)

C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004

C;Accession: T43251

R;Cioplik, M.; Klenk, H.

submitted to the EMBL Data Library, January 1996

A;Description: Cloning and functional characterization of FURIN from Spodoptera frugiper

A;Reference number: Z22368

A;Accession: T43251

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1299 <CIE>

A;Cross-references: UNIPROT:Q26489; UNIPARC:UPI0000083055; EMBL:Z68888; NID:g1167859; PI

A;Experimental source: clone Sfurin 6; ovary

C;Function:

A;Description: responsible for the endoproteolytic processing of proproteins with specif

C;Keywords: hydrolase; serine proteinase

Query Match

Best Local Similarity 23.1%; Score 65.5; DB 2; Length 1299;

Matches 18; Conservative 8; Mismatches 14; Indels 13; Gaps 4;

QY 8 CSQNEYFDSLHACIPQLRCS-----SNTPLTCQRYCNAS-----VTNSVKG 51

DB 1150 CSRPLRIDRLNQCVCPC---CSERGVTNSTPTDC-CHCNPNBNGRCINSSVAG 1198

RESULT 6

T19275

hypothetical protein F34D10.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T19275; T21723

R;Harris, B.

submitted to the EMBL Data Library, September 1994

A;Reference number: Z19099

A;Accession: T19275

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-999 <WIL>

A;Cross-references: UNIPROT:Q17969; UNIPARC:UPI0000079A41; EMBL:Z37139; PIDN:CAA85494.1;

A;Experimental source: clone C14B1

R;Kershaw, J.

submitted to the EMBL Data Library, June 1994

A;Reference number: Z19464

A;Accession: T21723

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-999 <WIZ>

A;Cross-references: UNIPARC:UPI0000079A41; EMBL:Z34799; PIDN:CAA84320.1; GSPDB:GN00021; C

A;Experimental source: clone F34D10

C;Genetics:

A;Gene: CESP:F34D10.2

A;Map position: 3

A;Introns: 20/3; 40/3; 72/1; 234/3; 387/3; 457/1; 523/2; 541/3; 682/1; 784/2; 822/2; 870/

Query Match

Best Local Similarity 22.1%; Score 62.5; DB 2; Length 999;

Matches 17; Conservative 2; Mismatches 20; Indels 1; Gaps 1;

QY 13 YFDSLHACIPQQL-RCSSNTPLTCQRYCNASVTSVKG 51

DB 516 YEDSLNTCIGRAPEVKVMTPLRLIQSYFVSSTPNGLDG 555

RESULT 7

T25169

hypothetical protein T23F1.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T25169

R;Wilkinson, J.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19990

A;Accession: T25169

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-330 <WIL>

A;Cross-references: UNIPROT:O18118; UNIPARC:UPI000006118C; EMBL:Z81129; PIDN:CAB03405.1;

A;Experimental source: clone T23F1

C;Genetics:

A;Gene: CESP:T23F1.6

A;Map position: 5

A;Introns: 16/3

C;Superfamily: gliadin

Query Match

Best Local Similarity 21.9%; Score 62; DB 2; Length 330;

Matches 14; Conservative 7; Mismatches 19; Indels 8; Gaps 2;

QY 8 CSQNEYFDSLHACIP-----CQLRCSNTPPL---TCQRYCNASVTN 47

DB 59 CASSQYQLQTSQCMWPCACQSCSQCCOSQNTTQCQPTCCQSCQTSSCN 106

RESULT 8

S60231

gibberellin-regulated protein GASA3 precursor - Arabidopsis thaliana

N;Alternate names: GAST1 protein homolog



C:Genetics:  
A:Gene: T12A7.2  
A:Map position: 4

Query Match 21.7%; Score 61.5; DB 2; Length 520;  
Best Local Similarity 31.8%; Pred. No. 17;  
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;

Qy 8 CSQNEYFDSLHACIPCOLRCSSNTPLTCORYCNASVTNSVKG 51  
Db 145 CMNDGYFNHTLGRCV-----CTSNWVGHCIFRCNSGVVNTKTS 183

RESULT 11

T13954  
MEGF6 protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T13954  
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.  
Genomics 51, 27-34, 1998  
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs  
A:Reference number: Z14126; MUID:98360089; PMID:9693030  
A:Accession: T13954  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1574 <NAK>  
A:Cross-references: UNIPROT:O88281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:G3449293;  
A:Experimental source: strain Sprague-Dawley; brain  
C:Genetics:  
A:Gene: MEGF6

Query Match 21.4%; Score 60.5; DB 2; Length 1574;  
Best Local Similarity 32.2%; Pred. No. 56;  
Matches 19; Conservative 8; Mismatches 19; Indels 13; Gaps 4;

Qy 5 AGQCSQNEYFDSLHACIPCOL-----RCSSNTPLT----CORYC---NASVTNSVKG 51  
Db 963 ACNCSAGAPCDVATGSCICAPGRWGPCAQSCPLPTFGLNCSQICTCFNGACDSVTG 1020

RESULT 12

T14119  
seven-pass transmembrane receptor protein precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T14119  
R:Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R.  
submitted to the EMBL Data Library, October 1997  
A:Description: The Celsr family of novel evolutionarily conserved seven-pass transmembrane  
A:Reference number: Z17881  
A:Accession: T14119  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-3034 <HAD>  
A:Cross-references: UNIPROT:O35161; UNIPARC:UPI000002931C; EMBL:AF031572; NID:G3800735;  
C:Genetics:  
A:Gene: Celsr1  
A:Map position: 15  
C:Keywords: transmembrane protein  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:27-3034/Product: seven-pass transmembrane receptor protein #status predicted <MAT>

Query Match 21.4%; Score 60.5; DB 2; Length 3034;  
Best Local Similarity 28.3%; Pred. No. 99;  
Matches 17; Conservative 5; Mismatches 19; Indels 19; Gaps 3;

Qy 7 QCSQNEYFDSLHACIPCOL-----RCSSNTPLTCCO-----RYCN-----ASVTN 47  
Db 2001 QCKENYKPPAQDAQLPCDFPHGSHSRACDMDTGQACKPGVIGQCNCNDPFAEVT 2060

RESULT 13



T31887  
hypothetical protein C03A7.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
R:Accession: T31887  
R:Greco, T.; Bradshaw, H.; Elliott, G.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid C03A7.  
A:Reference number: Z21096  
A:Accession: T31887  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-388 <GRE>  
A:Cross-references: UNIPROT:O16500; UNIPARC:UPI000007BC52; EMBL:AF016451; PIDN:AAB66001.  
A:Experimental source: strain Bristol N2; clone C03A7  
C:Genetics:  
A:Gene: CESP:C03A7.4  
A:Map position: 5  
A:Introns: 75/3  
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 388;  
Best Local Similarity 31.9%; Pred. No. 22;  
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

QY 3 QWAGCCSQNEYFDSLHACIPCOLRC-SSNTPPLTCORYCNASVTNS 48  
Db 316 QCAPQCEQS-----CQQCCVQQQPPAAQCQTACQSSCSNS 350

RESULT 14  
T31888  
hypothetical protein C03A7.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
R:Accession: T31888  
R:Greco, T.; Bradshaw, H.; Elliott, G.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid C03A7.  
A:Reference number: Z21096  
A:Accession: T31888  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-388 <GRE>  
A:Cross-references: UNIPROT:O16501; UNIPARC:UPI0000077D46; EMBL:AF016451; PIDN:AAB65996.  
A:Experimental source: strain Bristol N2; clone C03A7  
C:Genetics:  
A:Gene: CESP:C03A7.7  
A:Map position: 5  
A:Introns: 75/3  
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 388;  
Best Local Similarity 31.9%; Pred. No. 22;  
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

QY 3 QWAGCCSQNEYFDSLHACIPCOLRC-SSNTPPLTCORYCNASVTNS 48  
Db 316 QCAPQCEQS-----CQQCCVQQQPPAAQCQTACQSSCSNS 350

RESULT 15  
T31889  
hypothetical protein C03A7.8 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
R:Accession: T31889  
R:Greco, T.; Bradshaw, H.; Elliott, G.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid C03A7.  
A:Reference number: Z21096  
A:Accession: T31889  
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
A:Residues: 1-438 <GRE>  
A:Cross-references: UNIPROT:O16502; UNIPARC:UPI000007AF62; EMBL:AF016451; PIDN:AAB65995.1  
A:Experimental source: strain Bristol N2; clone C03A7  
C:Genetics:  
A:Gene: CESP:C03A7.8  
A:Map position: 5  
A:Introns: 75/3  
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 438;  
Best Local Similarity 31.9%; Pred. No. 24;  
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

QY 3 QWAGCCSQNEYFDSLHACIPCOLRC-SSNTPPLTCORYCNASVTNS 48  
Db 366 QCAPQCEQS-----CQQCCVQQQPPAAQCQTACQSSCSNS 400

RESULT 16  
T31898  
hypothetical protein C03A7.14 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
R:Accession: T31898  
R:Greco, T.; Bradshaw, H.; Elliott, G.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid C03A7.  
A:Reference number: Z21096  
A:Accession: T31898  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-445 <GRE>  
A:Cross-references: UNIPROT:O16511; UNIPARC:UPI000007B691; EMBL:AF016451; PIDN:AAB66007.1  
A:Experimental source: strain Bristol N2; clone C03A7  
C:Genetics:  
A:Gene: CESP:C03A7.14  
A:Map position: 5  
A:Introns: 18/3; 75/3  
C:Superfamily: gliadin

Query Match 21.0%; Score 59.5; DB 2; Length 445;  
Best Local Similarity 31.9%; Pred. No. 25;  
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;

QY 3 QWAGCCSQNEYFDSLHACIPCOLRC-SSNTPPLTCORYCNASVTNS 48  
Db 373 QCAPQCEQS-----CQQCCVQQQPPAAQCQTACQSSCSNS 407

RESULT 17  
T15577  
hypothetical protein C23G10.8 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 31-Dec-2004  
C:Accession: T15577  
R:Latreille, P.  
submitted to the EMBL Data Library, November 1995  
A:Description: The sequence of C. elegans cosmid C23G10.  
A:Reference number: Z18372  
A:Accession: T15577  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-758 <LAT>  
A:Cross-references: UNIPROT:Q9GYR5; UNIPARC:UPI000017925B; EMBL:U39851; NID:g1055062; PIDN:g1055062; PII  
C:Genetics:  
A:Gene: CESP:C23G10.8  
A:Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3

Query Match 20.8%; Score 59; DB 2; Length 758;  
Best Local Similarity 42.9%; Pred. No. 44;  
Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;



```
QY 15 DSLHACIPQLRCSNTTPEL 35
Db 260 ESVFHPYPAIRCSADGPPL 280

RESULT 18
A45558
epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Schistosoma mansoni
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A45558; S27836
R;Shoemaker, C.B.; Ramachandran, H.; Landa, A.; dos Reis, M.G.; Stein, L.D.
Mol. Biochem. Parasitol. 53, 17-32, 1992
A;Title: Alternative splicing of the Schistosoma mansoni gene encoding a homologue of ep
A;Reference number: A45558; MUID:92365727; PMID:1501637
A;Accession: A45558
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1717 <SHO>
A;Cross-references: UNIPROT:Q26566; UNIPARC:UPI000007DCD7; EMBL:M86396; NID:g160957; PID
A;Note: sequence extracted from NCBI backbone (NCBI:P:111129)
C;Genetics:
A;Gene: SER
C;Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology
C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1717/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F;1018-1323/Domain: protein kinase homology <KIN>
F;1026-1034/Region: protein kinase ATP-binding motif

Query Match 20.8%; Score 59; DB 1; Length 1717;
Best Local Similarity 39.1%; Pred. No. 89;
Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 7 QCSONEYFDSLHACIPQLRCS 29
Db 645 ECPNTYIDQTRHCLFCNESCS 667

RESULT 19
T28675
alpha-51D immobilization antigen - Paramesidium tetraurelia
C;Species: Paramesidium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28675
R;Schwegmann, K.J.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z20506
A;Accession: T28675
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-2533 <SCH>
A;Cross-references: UNIPROT:P90589; UNIPARC:UPI0000078A73; EMBL:X96400; PIDN:CAA65264.1
C;Genetics:
A;Gene: alpha-51D
A;Genetic code: SGC5
A;Introns: 280/3; 538/2; 1248/2
C;Superfamily: G surface protein

Query Match 20.7%; Score 58.5; DB 2; Length 2533;
Best Local Similarity 20.7%; Pred. No. 1.4e+02;
Matches 17; Conservative 7; Mismatches 23; Indels 35; Gaps 2;

QY 5 AGQCSONEYF-----DSLHACIPQLRCSNTTPTLTCOR----- 39
Db 1661 AGACTNKKCYDNVTATSDSECDYLSGCVTRGTGTCIPNSEPCTSYRGTKLQCELFKKFTG 1720

QY 40 -----YCNASVTVNSVKG 51
Db 1721 LDANKNPIYECGSDATNTATG 1742

Query Match 20.8%; Score 59; DB 1; Length 1717;
Best Local Similarity 39.1%; Pred. No. 89;
Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 7 QCSONEYFDSLHACIPQLRCS 29
Db 645 ECPNTYIDQTRHCLFCNESCS 667

RESULT 19
T28675
alpha-51D immobilization antigen - Paramesidium tetraurelia
C;Species: Paramesidium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28675
R;Schwegmann, K.J.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z20506
A;Accession: T28675
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-2533 <SCH>
A;Cross-references: UNIPROT:P90589; UNIPARC:UPI0000078A73; EMBL:X96400; PIDN:CAA65264.1
C;Genetics:
A;Gene: alpha-51D
A;Genetic code: SGC5
A;Introns: 280/3; 538/2; 1248/2
C;Superfamily: G surface protein

Query Match 20.7%; Score 58.5; DB 2; Length 2533;
Best Local Similarity 20.7%; Pred. No. 1.4e+02;
Matches 17; Conservative 7; Mismatches 23; Indels 35; Gaps 2;

QY 5 AGQCSONEYF-----DSLHACIPQLRCSNTTPTLTCOR----- 39
Db 1661 AGACTNKKCYDNVTATSDSECDYLSGCVTRGTGTCIPNSEPCTSYRGTKLQCELFKKFTG 1720

QY 40 -----YCNASVTVNSVKG 51
Db 1721 LDANKNPIYECGSDATNTATG 1742
```

```
RESULT 20
T28674
alpha-51D-immobilization antigen - Paramesidium tetraurelia
C;Species: Paramesidium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28674
R;Schmidt, H.J.
submitted to the EMBL Data Library, March 1995
A;Reference number: Z20505
A;Accession: T28674
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-2533 <SCH>
A;Cross-references: UNIPROT:Q27183; UNIPARC:UPI000007E3B2; EMBL:X85135; NID:g728634; PID:
C;Genetics:
A;Genetic code: SGC5
A;Note: alpha-51D
C;Superfamily: G surface protein

Query Match 20.7%; Score 58.5; DB 2; Length 2533;
Best Local Similarity 20.7%; Pred. No. 1.4e+02;
Matches 17; Conservative 7; Mismatches 23; Indels 35; Gaps 2;

QY 5 AGQCSONEYF-----DSLHACIPQLRCSNTTPTLTCOR----- 39
Db 1661 AGACTNKKCYDNVTATSDSECDYLSGCVTRGTGTCIPNSEPCTSYRGTKLQCELFKKFTG 1720

QY 40 -----YCNASVTVNSVKG 51
Db 1721 LDANKNPIYECGSDATNTATG 1742

RESULT 21
S07127
chymotrypsin/elastase inhibitor - common roundworm
C;Species: Ascaris lumbricoideis (common roundworm)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S07127
R;Babin, D.R.; Peanasky, R.J.; Goos, S.M.
Arch. Biochem. Biophys. 232, 143-161, 1984
A;Title: The isoforms of chymotrypsin/elastase from Ascaris lumbricoideis: the prima
A;Reference number: S07127; MUID:84255715; PMID:6564898
A;Accession: S07127
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-63 <BAB>
A;Cross-references: UNIPARC:UPI000012D146
C;Superfamily: roundworm trypsin inhibitor

Query Match 20.5%; Score 58; DB 2; Length 63;
Best Local Similarity 36.6%; Pred. No. 6.9;
Matches 15; Conservative 5; Mismatches 13; Indels 8; Gaps 4;

QY 8 CSQNEYFDSLHACIPQLRCS--SSNTP-PLTCOR-YNAS 44
Db 5 CGPNEVWTE----CTGCENKCGPDENTPCPLMCRPSCECS 41

RESULT 22
T23681
hypothetical protein M02G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23681
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19781
A;Accession: T23681
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1513 <WIL>
A;Cross-references: UNIPROT:O17970; UNIPARC:UPI000007686D; EMBL:Z81573; PIDN:CAB04625.1;
A;Experimental source: clone M02G9
```







[illegible]







```
Qy 24 COLRCSSTPPLTCQRYCNASVTNSVKG 51
Db 378 CKIKCSN---CCTAYANTDREGKG 402

RESULT 34
T01519
hypotheical protein Tl0M13.17.1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01519
R;Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gott
Martensen, R.; McCombie, W.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of the Arabidopsis thaliana Tl0M13 BAC.
A;Reference number: Z14346
A;Accession: T01519
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-989 <JOH>
A;Cross-references: UNIPROT:Q9ZU00; UNIPARC:UPI000000A0E3D; EMBL:AF001308; NID:G2104523;
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4S
A;Introns: 31/3
A;Note: Tl0M13.17.1

Query Match 19.6%; Score 55.5; DB 2; Length 989;
Best Local Similarity 41.9%; Pred. No. 1.4e+02;
Matches 13; Conservative 3; Mismatches 10; Indels 5; Gaps 2;

Qy 8 CSQNEYFDSLHACIPC-----QLRCSSTP 34
Db 540 CARN-IDRLFFYHCSPCNFTDLRCVLNPPP 569

RESULT 35
T23682
hypotheical protein M02G9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23682
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19781
A;Accession: T23682
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-294 <WIL>
A;Cross-references: UNIPROT:Q9XUS0; UNIPARC:UPI00000076A8F; EMBL:Z81573; PIDN:CAB04626.1;
A;Experimental source: clone M02G9
C;Genetics:
A;Gene: CESP:M02G9.3
A;Map position: 2
A;Introns: 20/3; 76/2; 182/3; 223/3

Query Match 19.4%; Score 55; DB 2; Length 294;
Best Local Similarity 37.3%; Pred. No. 56;
Matches 22; Conservative 3; Mismatches 20; Indels 14; Gaps 5;

Qy 3 QMAGCQSQ--NEYFDSLHACIPCQLRCS--NTFPPL--TCOR-----YCNA---SVTN 47
Db 72 QCSNQCNQOQTSITISGFCSCQSCACSACTTTCIRTQRCNSCLNLTGNSCTN 130

RESULT 36
KM5B
cathepsin B (EC 3.4.22.1) precursor - mouse
N;Alternate names: preprocathepsin B
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 26-Apr-1996 #text_change 09-Jul-2004
C;Accession: A38458; A49826; B26498; S12901; PS0360
R;Qian, F.; Frankfater, A.; Chan, S.J.; Steiner, D.F.
```

```
DNA Cell Biol. 10, 159-168, 1991
A;Title: The structure of the mouse cathepsin B gene and its putative promoter.
A;Reference number: A38458; MUID:91190267; PMID:2012677
A;Accession: A38458
A;Molecule type: DNA
A;Residues: 1-339 <QIA>
A;Cross-references: UNIPROT:PI0605; UNIPARC:UPI00000018A4; GB:M63999
R;Qian, F.; Frankfater, A.; Steiner, D.F.; Bajkowski, A.S.; Chan, S.J.
Anticancer Res. 11, 1445-1451, 1991
A;Title: Characterization of multiple cathepsin B mRNAs in murine B16a melanoma.
A;Reference number: A49826; MUID:92082172; PMID:1746902
A;Accession: A49826
A;Molecule type: mRNA
A;Residues: 1-339 <QI2>
A;Cross-references: UNIPARC:UPI00000018A4; GB:S69034; NID:G239906; PIDN:AAB20536.1; PID:
A;Experimental source: B16a melanoma
A;Note: sequence extracted from NCBI backbone (NCBI:69034, NCBI:P:69039)
A;Note: three mRNA forms from B16a melanoma cells were found to have identical coding seq
R;Chan, S.J.; San Segundo, B.; McCormick, M.B.; Steiner, D.F.
Proc. Natl. Acad. Sci. U.S.A. 83, 7721-7725, 1986
A;Title: Nucleotide and predicted amino acid sequences of cloned human and mouse preproc
A;Reference number: A26498; MUID:87017021; PMID:3463996
A;Accession: B26498
A;Molecule type: mRNA
A;Residues: 1-159, 'N', 161-173, 'D', 175-176, 'I', 178-283, 'V', 285-339 <CHA>
A;Cross-references: UNIPARC:UPI000016CCB0; GB:M14222; NID:G192841; PIDN:AAA37494.1; PID:
R;Ferrara, M.; Wojcik, F.; Rhaisel, H.; Mordier, S.; Roux, M.P.; Bechet, D.
FEBS Lett. 273, 195-199, 1990
A;Title: Gene structure of mouse cathepsin B.
A;Reference number: S12901; MUID:91032179; PMID:2226854
A;Accession: S12901
A;Molecule type: DNA
A;Residues: 1-159, 'N', 161-173, 'D', 175-176, 'I', 178-283, 'V', 285-339 <PER>
A;Cross-references: UNIPARC:UPI000016CCB0; GB:M14222; NID:G192841; PIDN:AAA37494.1; PID:
R;Fremont, C.; Closs, E.I.; Silbermann, M.; Erfle, V.; Strauss, P.G.
Gene 103, 259-261, 1991
A;Title: Isolation of a cathepsin B-encoding cDNA from murine osteogenic cells.
A;Reference number: PS0360; MUID:91365255; PMID:1889751
A;Accession: PS0360
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 314-339 <FRI>
A;Cross-references: UNIPARC:UPI000016CCB1; EMBL:X54966; NID:G50596; PIDN:CAA38713.1; PID
C;Genetics:
A;Note: single copy gene
C;Function:
A;Description: broad specificity endopeptidase and peptidyl dipeptidase
A;Pathway: intracellular protein degradation
C;Superfamily: papain
C;Keywords: cysteine proteinase; glycoprotein; hydrolase; lysosome; protein degradation
F;1-17/Domain: signal sequence #status predicted <SIG>
F;80-339/Product: cathepsin B #status predicted <MAT>
F;38,192/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;93,122,105-150,141-207,142-146,179-211,187-198/Disulfide bonds: #status predicted
F;108,278,298/Active site: Cys, His, Asn #status predicted

Query Match 19.4%; Score 55; DB 1; Length 339;
Best Local Similarity 25.0%; Pred. No. 63;
Matches 16; Conservative 7; Mismatches 17; Indels 24; Gaps 2;

Qy 11 NEYFDSLHACIPCQLRCSNTPTPLT-----CQRYCNA-----SVT 46
Db 174 NSHVGCLPYTIPCEHHVNGSRPCTGEGTTPRCNKSCAGSPSYKEDKHGFTYSYS 233

Qy 47 NSVK 50
Db 234 NSVK 237

RESULT 37
S46625
finger protein YJL206c - yeast (Saccharomyces cerevisiae)
N;Alternate names: probable membrane protein YJL206c; protein J0316
```



C;Species: Saccharomyces cerevisiae  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Oct-2004  
 A;Accession: S46625; S56993  
 R;Purnelle, B.; Coster, F.; Goffeau, A.  
 Yeast 10, 1235-1249, 1994  
 A;Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identified as gene ACO1 and two homologues to chromosome III genes.  
 A;Reference number: S46621; MUID:95214326; PMID:7754713  
 A;Accession: S46625  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: DNA  
 A;Residues: 1-758 <P>  
 A;Cross-references: UNIPROT:P39529; UNIPARC:UPI000013B60A; EMBL:X77688; NID:gl103992; P; R;Purnelle, B.; Coster, F.; Goffeau, A.  
 submitted to the Protein Sequence Database, September 1995  
 A;Reference number: S56977  
 A;Accession: S56993  
 A;Molecule type: DNA  
 A;Residues: 1-758 <P>  
 A;Cross-references: UNIPARC:UPI000013B60A; EMBL:Z49481; NID:gl015584; PIDN:CAA89502.1; F; C;Genetics:  
 A;Cross-references: SGD:S0003741  
 A;Map position: 10L  
 C;Keywords: DNA binding; nucleus; transcription regulation; transmembrane protein; zinc F; 42-78/Domain: GAL4 zinc nuclear cluster homology <GAL4>  
 Query Match 19.4%; Score 55; DB 2; Length 758;  
 Best Local Similarity 43.8%; Pred. No. 1.3e+02;  
 Matches 14; Conservative 2; Mismatches 6; Indels 10; Gaps 2;  
 QY 20 ACIPC---QLRCSSTPPLTCORYCNASVTNS 48  
 |||||::|||::|||  
 Db 46 ACTACRKRKRCSGNTPCRLCQ-----TNS 70  
 RESULT 38  
 T27283  
 hypothetical protein Y64G10A.f - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C;Accession: T27283  
 R;Kinscough, R.  
 submitted to the EMBL Data Library, September 1999  
 A;Reference number: Z20336  
 A;Accession: T27283  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-1620 <WIL>  
 A;Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:el1542303; PIDN:CAB54471.1;  
 A;Experimental source: clone Y64G10A  
 C;Genetics:  
 A;Gene: CESP:Y64G10A.f  
 A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7  
 Query Match 19.4%; Score 55; DB 2; Length 1620;  
 Best Local Similarity 25.6%; Pred. No. 2.4e+02;  
 Matches 11; Conservative 7; Mismatches 17; Indels 8; Gaps 1;  
 QY 8 CSQNEYFDSLHACI-----PCQLRCSSTPPLTCORYCN 42  
 |||||::|||::|||  
 Db 1409 CENGGVDSSTGSCVCPGPYIGTKCEIACQSDRFGPTCEKICN 1451  
 RESULT 39  
 T27303  
 hypothetical protein Y68A4A.10 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T27303  
 R;Steward, C.  
 submitted to the EMBL Data Library, January 1998  
 A;Reference number: Z20340  
 A;Accession: T27303

A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-392 <WIL>  
 A;Cross-references: UNIPROT:Q9XXP6; UNIPARC:UPI000007EED1; EMBL:AL021503; PIDN:CAA16424.1  
 A;Experimental source: clone Y68A4A  
 C;Genetics:  
 A;Gene: CESP:Y68A4A.10  
 A;Map position: 5  
 A;Introns: 45/2; 74/3; 139/3; 175/2; 190/3; 241/3; 305/3; 356/3  
 Query Match 19.3%; Score 54.5; DB 2; Length 392;  
 Best Local Similarity 40.0%; Pred. No. 81;  
 Matches 10; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
 QY 20 ACIPCQLRCSSTPPLTCORYCNAS 44  
 |||||::|||::|||  
 Db 189 SCLPCQ-TCASFTDPMSEKATCTAT 212  
 RESULT 40  
 S69207  
 vascular endothelial growth factor C precursor - human  
 N;Alternate names: FLT4 ligand DHM  
 C;Species: Homo sapiens (man)  
 C;Date: 27-Apr-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
 C;Accession: S69207; S61795; S71443; S69208; G02659  
 R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chllov, D.; Lahtinen, I.; Kuk, E.; Saksela, C.  
 EMBO J. 15, 1751, 1996  
 A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand for  
 A;Reference number: S69207; MUID:96203094; PMID:8612600  
 A;Accession: S69207  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-419 <JOU>  
 A;Cross-references: UNIPROT:P49767; UNIPARC:UPI000001C2A; EMBL:X94216; NID:gl177488; P; R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chllov, D.; Lahtinen, I.; Kuk, E.; Saksela, C.  
 EMBO J. 15, 290-298, 1996  
 A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (V  
 A;Reference number: S61795; MUID:96178224; PMID:8617204  
 A;Accession: S61795  
 A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 70-419 <JOU1>  
 A;Cross-references: UNIPARC:UPI0000150795  
 A;Note: this sequence has been revised in reference S69207  
 A;Accession: S71443  
 A;Molecule type: protein  
 A;Residues: 'X',104-120 <JOU2>  
 A;Cross-references: UNIPARC:UPI000014E2AF  
 R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.  
 submitted to the EMBL Data Library, December 1995  
 A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and sp  
 A;Reference number: S69208  
 A;Accession: S69208  
 A;Molecule type: mRNA  
 A;Residues: 1-419 <LEE>  
 A;Cross-references: UNIPARC:UPI0000001C2A; EMBL:U43142; NID:gl150988; PIDN:AAA85214.1; P; R;Morris, J.C.  
 submitted to the EMBL Data Library, May 1996  
 A;Reference number: H01557  
 A;Accession: G02659  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-419 <MOR>  
 A;Cross-references: UNIPARC:UPI0000001C2A; EMBL:U58111; NID:gl1373426; PIDN:AAB02909.1; P; C;Genetics:  
 A;Gene: GDB:VEGFC; VRP  
 A;Cross-references: GDB:3890883; OMIM:601528  
 F;1-12/Domain: signal sequence #status predicted <SIG>  
 F;13-102/Domain: propeptide #status predicted <PRO>



F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>

Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 86;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QCSQNEVFDLSLLHACIPQQLRCSSTNP--PLTCQRYCNAS 44  
Db 327 QCGANREFDENTOCV--CKRTCPRNQPLNFKGKACETES 365

RESULT 41  
JC5486  
membrane glycoprotein CD30 homolog precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
R;Accession: JC5486  
R;Alzawa, S.; Satcho, H.; Horie, R.; Ito, K.; Choi, S.H.; Takeuchi, H.; Watanabe, T.  
Gene 182, 155-162, 1996  
A;Title: Cloning and characterization of a cDNA for rat CD30 homolog and chromosomal assignment  
A;Reference number: JC5486; MUID:97136705; PMID:8982082  
A;Contents: T cell  
A;Accession: JC5486  
A;Molecule type: mRNA  
A;Residues: 1-493 <AIZ>  
A;Cross-references: UNIPROT:P97525; UNIPARC:UPI00001370F0; DBJ:D42117; NID:gl817523; P  
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-493/Product: membrane glycoprotein CD30 homolog #status predicted <MAT>  
F;278-304/Domain: transmembrane #status predicted <TMM>  
F;305-493/Domain: intracellular #status predicted <INT>

Query Match 19.3%; Score 54.5; DB 2; Length 493;  
Best Local Similarity 32.7%; Pred. No. 99;  
Matches 16; Conservative 6; Mismatches 16; Indels 11; Gaps 4;

Qy 9 SQNEVFDLSLLHACIPQ-----QLRCSSTNPPL--TCO--RYCNASVTNS 48  
Db 74 TSNE--DGKCTACVTCLPLGLVEKAPCSGNSPRICECPGMVCSPTAVNS 120

RESULT 42  
C90879  
hypothetical protein ECS2003 [imported] - Escherichia coli (strain O157:H7, substrain R  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C;Accession: C90879  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: C90879  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-879 <HAY>  
A;Cross-references: UNIPROT:Q8X9R3; UNIPARC:UPI00000D07BA; GB:BA000007; PIDN:BA035426.1;  
A;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: ECS2003  
C;Superfamily: Escherichia coli membrane protein ydbH

Query Match 19.3%; Score 54.5; DB 2; Length 879;  
Best Local Similarity 40.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 6; Mismatches 12; Indels 3; Gaps 1;

Qy 2 LQWAGQCSQNEVFDLSLLHACIPQQLRCSSTNPPLT 36  
Db 330 LQLTGEAKQ---ADLLILYARLPAQLSGSLSDPTLT 361

RESULT 43  
H64886  
alpha tectorin - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T30197  
R;Legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.  
J. Biol. Chem. 272, 8791-8801, 1997  
A;Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to com  
A;Reference number: 220771; MUID:97236843; PMID:9079715  
A;Accession: T30197  
A;Status: preliminary; translated from GB/EMBL/DBDJB  
A;Molecule type: mRNA  
A;Residues: 1-2155 <LEG>

membrane protein ydbH - Escherichia coli (strain K-12)  
C;Species: Escherichia coli  
C;Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004  
C;Accession: H64888  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: H64888  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-879 <BLAT>  
A;Cross-references: UNIPROT:P52645; UNIPARC:UPI000013A90E; GB:AE000235; GB:U000096; NID:9  
C;Experimental source: strain K-12, substrain MG1655  
C;Genetics:  
A;Gene: ydbH  
C;Superfamily: Escherichia coli membrane protein ydbH  
F;8-24/Domain: transmembrane #status predicted <TMO1>

Query Match 19.3%; Score 54.5; DB 2; Length 879;  
Best Local Similarity 40.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 6; Mismatches 12; Indels 3; Gaps 1;

Qy 2 LQWAGQCSQNEVFDLSLLHACIPQQLRCSSTNPPLT 36  
Db 330 LQLTGEAKQ---ADLLILYARLPAQLSGSLSDPTLT 361

RESULT 44  
G85739  
hypothetical protein ydbH [imported] - Escherichia coli (strain O157:H7, substrain EDL93:  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: G85739  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: G85739  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-879 <STO>  
A;Cross-references: UNIPROT:Q8X9R3; UNIPARC:UPI00001657C5; GB:AE005174; NID:gl2515319; P  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: ydbH  
C;Superfamily: Escherichia coli membrane protein ydbH

Query Match 19.3%; Score 54.5; DB 2; Length 879;  
Best Local Similarity 40.0%; Pred. No. 1.6e+02;  
Matches 14; Conservative 6; Mismatches 12; Indels 3; Gaps 1;

Qy 2 LQWAGQCSQNEVFDLSLLHACIPQQLRCSSTNPPLT 36  
Db 330 LQLTGEAKQ---ADLLILYARLPAQLSGSLSDPTLT 361

RESULT 45  
T30197  
alpha tectorin - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T30197  
R;Legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.  
J. Biol. Chem. 272, 8791-8801, 1997  
A;Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to com  
A;Reference number: 220771; MUID:97236843; PMID:9079715  
A;Accession: T30197  
A;Status: preliminary; translated from GB/EMBL/DBDJB  
A;Molecule type: mRNA  
A;Residues: 1-2155 <LEG>







QY 2 LQWAGCQNEYFDSLHACIPCOLRCSNTTPTLTTCORYCNASVTNSV 49  
 Db 707 LKKKGQLS-----FTPVSDAGIECHSRNKNKTPRQICDQWNVSVFVISV 750

RESULT 51  
 S54307  
 myosin heavy chain - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
 C:Accession: S54307  
 R:Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.  
 EMBO J. 14, 697-704, 1995  
 A:Title: A novel type of myosin implicated in signalling by rho family GTPases.  
 A:Reference number: S54307; MUID:95188874; PMID:7882973  
 A:Accession: S54307  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1980 <REI>  
 A:Cross-references: UNIPROT:Q63358; UNIPARC:UPI000012PAD6; EMBL:X77609; NID:9639998; PID:1980  
 C:Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C zeta  
 C:Keywords: nucleotide binding; P-loop  
 F:149-942/Domain: myosin motor domain homology <MMOT>  
 F:239-246/Region: nucleotide-binding motif A (P-loop)  
 F:1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 19.1%; Score 54; DB 2; Length 1980;  
 Best Local Similarity 52.9%; Pred. No. 3.7e+02;  
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 23 PCQLRCSNTTPTLTTCOR 39  
 Db 1812 PCLLRCPDNDPLTSMK 1828

RESULT 52  
 A59256  
 myosin-IXb [similarity] - human  
 C:Species: Homo sapiens (man)  
 C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 31-Dec-2004  
 C:Accession: A59256; I61700  
 R:Wirth, J.A.; Jensen, K.A.; Post, P.L.; Bement, W.M.; Mooseker, M.S.  
 J. Cell Sci. 109, 653-661, 1996  
 A:Title: Human myosin-IXb, an unconventional myosin with a chimerin-like rho/rac GTPase-  
 A:Reference number: A59256; MUID:97063843; PMID:8907710  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-2022 <WIR>  
 A:Cross-references: UNIPROT:Q14788; UNIPARC:UPI00000161189; GB:U42391; NID:g1147782; PID:1980  
 R:Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994  
 A:Title: Identification and overlapping expression of multiple unconventional myosin gen  
 A:Reference number: A55758; MUID:94294418; PMID:8022818  
 A:Accession: I61700  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 234-322 <RES>  
 A:Cross-references: UNIPARC:UPI0000073918; GB:L29149; NID:g457257; PIDN:AAA20912.1; PID:1980  
 C:Genetics:  
 A:Gene: GDB:MYO9B; OMIM:602129  
 A:Map position: 19p13.1  
 C:Superfamily: myosin motor domain homology; protein kinase C zinc-binding repeat homolo  
 C:Keywords: nucleotide binding; P-loop  
 F:149-941/Domain: myosin motor domain homology #status atypical <MMO>  
 F:239-246/Region: nucleotide-binding motif A (P-loop)

Query Match 19.1%; Score 54; DB 2; Length 2022;  
 Best Local Similarity 52.9%; Pred. No. 3.7e+02;  
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 23 PCQLRCSNTTPTLTTCOR 39  
 Db 1812 PCLLRCPDNDPLTSMK 1828

Db 1852 PCLLRCPDNDPLTSMK 1868

## RESULT 53

A84544

hypothetical protein At2g16770 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C:Accession: A84544

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84544

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-255 &lt;STO&gt;

A:Cross-references: UNIPROT:Q9SLE1; UNIPARC:UPI00000A1869; GB:AE002093; NID:g4581120; PID:

C:Genetics:

A:Gene: At2g16770

A:Map position: 2

Query Match 18.9%; Score 53.5; DB 2; Length 255;

Best Local Similarity 37.2%; Pred. No. 73;

Matches 16; Conservative 3; Mismatches 15; Indels 9; Gaps 3;

QY 4 MAGQ---CSQNYFDSL---HACT---PCQLRCSNTTPTLTTC 37

Db 13 MGGELPSCSMDSFDFDLRLDSHACTHTTCTCPGPTHTTTC 55

## RESULT 54

T21458

hypothetical protein F27E5.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T21458

R:Wilkinson, J.

submitted to the EMBL Data Library, March 1995

A:Reference number: Z19425

A:Accession: T21458

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-332 &lt;WIL&gt;

A:Cross-references: UNIPROT:Q09553; UNIPARC:UPI000008359F; EMBL:Z48582; PIDN:CAA88466.1;

A:Experimental source: clone F27E5

C:Genetics:

A:Gene: CESP:F27E5.4

A:Map position: 2

A:Introns: 87/3; 101/2; 152/2; 236/1; 284/3

Query Match 18.9%; Score 53.5; DB 2; Length 332;

Best Local Similarity 28.6%; Pred. No. 91;

Matches 14; Conservative 6; Mismatches 20; Indels 9; Gaps 2;

QY 8 CSQNEYFDSLHACIPCO--LRCSNTTPTL-----TCORYCNASVTN 47

Db 119 CLAQEASEACTKALTDCNDLECONRLAPLMACSTNTCOPQCRSAVLN 167

## RESULT 55

T21681

hypothetical protein F32H5.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T21681

R:Steward, C.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19458

A:Accession: T21681

A:Status: preliminary; translated from GB/EMBL/DBJ







C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: A96639  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: A96639  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-98 <STO>  
A:Cross-references: UNIPROT:Q94162; UNIPARC:UPI000007C506; GB:chr\_V; PIDN:AAB09171.1; PI  
C:Genetics:  
A:Gene: C10G8.4  
A:Map position: 5

Query Match 18.7%; Score 53; DB 2; Length 98;  
Best Local Similarity 34.8%; Pred. No. 37;  
Matches 16; Conservative 3; Mismatches 21; Indels 6; Gaps 2;

QY 7 QCSQNEYFDSLLHACIP-COLRCSSNTPPLTCORYCNASVTSVKG 51  
DB 39 RCPSENEFRSCGTAPEFTCO-----NPNPOVCTLQCILNVCCSQG 79

RESULT 61  
F86276  
F14L17.2 protein - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: F86276  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: F86276  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-274 <STO>  
A:Cross-references: UNIPROT:Q9M9T6; UNIPARC:UPI00000A27A8; GB:ABE005172; NID:97262667; PI  
C:Genetics:  
A:Map position: 1

Query Match 18.7%; Score 53; DB 2; Length 274;  
Best Local Similarity 30.2%; Pred. No. 88;  
Matches 16; Conservative 5; Mismatches 16; Indels 16; Gaps 3;

QY 6 GQCSQNEYFDSLLHA--CIPOLRCSSNT--PPLTC-----ORYCN 42  
DB 40 GDTTNEBEDSLISSAECRICQDECDIKNLESPCACNGSLKYAHKRCVQRWCN 92

RESULT 62  
A96639  
protein TIF9.18 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2004  
C:Accession: A96639  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: A96639  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-447 <STO>  
A:Cross-references: UNIPROT:O64787; UNIPARC:UPI000009F9F6; GB:ABE005173; NID:93056597; PI  
C:Genetics:  
A:Gene: TIF9.18  
A:Map position: 1  
C:Superfamily: Arabidopsis thaliana hypothetical protein F17J16.30

Query Match 18.7%; Score 53; DB 2; Length 447;  
Best Local Similarity 28.3%; Pred. No. 1.3e+02;  
Matches 15; Conservative 10; Mismatches 22; Indels 6; Gaps 1;

QY 3 QWAGO-----CSQNEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTSV 49  
DB 194 QMSGNGILTIYAHDKFKSLVSCMPNLLSIFLDAPLTCEYKYDGYAKTINV 246

RESULT 63  
GQHUT1  
tumor necrosis factor receptor 1 precursor [validated] - human  
N:Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1  
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38;  
R:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.  
Genomics 13, 215-224, 1992  
A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to chr  
A:Reference number: A38208; MUID:92250049; PMID:1315717  
A:Accession: A38208  
A:Molecule type: DNA  
A:Residues: 1-455 <PUC>  
A:Cross-references: UNIPROT:P19438; UNIPARC:UPI000002CE11; GB:M75864; GB:M75865; GB:M7586  
R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau  
Cell 61, 351-359, 1990  
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recept  
A:Reference number: A34899; MUID:90235284; PMID:2158862  
A:Accession: A34899  
A:Molecule type: mRNA  
A:Residues: 1-455 <LOE>  
A:Cross-references: UNIPARC:UPI000002CE11; GB:M58286; GB:M33480; NID:9339753; PIDN:AAA36  
A:Experimental source: placenta, including the amino end of the mature protein, confirmed t  
R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.,  
Cell 61, 361-370, 1990  
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.  
A:Reference number: A34900; MUID:90235285; PMID:2158863  
A:Accession: A34900  
A:Molecule type: mRNA  
A:Residues: 1-455 <SCH>  
A:Cross-references: UNIPARC:UPI000002CE11; GB:M33294; NID:9339744; PIDN:AAA03210.1; PID:  
R:Himmler, A.; Maurer-Egry, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; C  
DNA Cell Biol. 9, 705-715, 1990  
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor;  
A:Reference number: A36555; MUID:91090841; PMID:1702293  
A:Accession: A36555  
A:Molecule type: mRNA



A:Residues: 1-455 <HIM>  
A:Cross-references: UNIPARC:UPI0000002CE11; GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:  
A:Accession: C36555  
A:Molecule type: protein  
A:Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;107-128;162-167,'X',169-2  
A:Cross-references: UNIPARC:UPI000002D398; UNIPARC:UPI000002D836; UNIPARC:UPI00001736DE;  
A:Note: the purified protein, called tumor necrosis factor binding protein, is a soluble  
R:Gray, P.W.; Barrett, K.; Chanzy, D.; Turner, M.; Feldmann, M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990  
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re  
A:Reference number: A38281; NID:91017509; PMID:2170974  
A:Accession: A38281  
A:Molecule type: mRNA  
A:Residues: 1-455 <GRA>  
A:Cross-references: UNIPARC:UPI000002CE11; GB:M37764  
A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372  
R:Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann  
EMBO J. 9, 3269-3278, 1990  
A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type  
I form of the receptor.  
A:Reference number: S12057; MUID:91006021; PMID:1698610  
A:Accession: S12057  
A:Molecule type: mRNA  
A:Residues: 1-455 <NOP>  
A:Cross-references: UNIPARC:UPI000002CE11; EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID  
A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w  
R:Kemper, O.; Wallach, D.  
Gene 134, 209-216, 1993  
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne  
A:Reference number: J70758; MUID:94085779; PMID:8262379  
A:Accession: J70758  
A:Molecule type: DNA  
A:Residues: 1-13 <REM>  
A:Cross-references: UNIPARC:UPI0000155CFB  
R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
Eur. J. Immunol. 20, 1167-1174, 1990  
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc  
A:Reference number: A60231; MUID:902922116; PMID:2113477  
A:Accession: A60231  
A:Molecule type: protein  
A:Residues: 41-43,'X',45-53,'X',55-57 <SEC>  
A:Cross-references: UNIPARC:UPI0000072FDB  
R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le  
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto  
tients.  
A:Reference number: A38258; MUID:91062364; PMID:2174164  
A:Accession: A38258  
A:Molecule type: protein  
A:Residues: 41-60 <GAT>  
A:Cross-references: UNIPARC:UPI00001736E1  
A:Experimental source: cancer patient serum  
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.  
Eur. J. Haematol. 42, 270-275, 1989  
A:Title: Isolation and characterization of a tumor necrosis factor binding protein from  
A:Reference number: A60594; MUID:89171156; PMID:2924890  
A:Accession: A60594  
A:Molecule type: protein  
A:Residues: 41-43,'X',45-53,'V',55-57,'XX',60 <OLS>  
A:Cross-references: UNIPARC:UPI00001736E2  
A:Experimental source: renal failure patient urine  
R:Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A:Reference number: A35010; MUID:90110215; PMID:2153136  
A:Accession: A35010  
A:Molecule type: protein  
A:Residues: 41-45 <ENG>  
A:Cross-references: UNIPARC:UPI00001736E3  
A:Experimental source: normal urine  
R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994  
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f

A:Reference number: JC2404; MUID:95128033; PMID:7765720  
A:Accession: JC2404  
A:Molecule type: protein  
A:Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>  
A:Cross-references: UNIPARC:UPI00001736E4  
A:Experimental source: urine  
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
C:Genetics:  
A:Gene: GDB:TNPR1  
A:Cross-references: GDB:125913; OMIM:191190  
A:Map position: 12p13.2-12p13.2  
A:Introns: 13/3; 65/1; 108/1; 184/2; 209/1; 247/1; 256/3; 353/1  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>  
F:30-211/Domain: extracellular #status predicted <EXT>  
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
F:44-82/Domain: NGF receptor repeat homology <NG1>  
F:84-126/Domain: NGF receptor repeat homology <NG2>  
F:127-167/Domain: NGF receptor repeat homology <NG3>  
F:168-196/Domain: NGF receptor repeat homology <NG4>  
F:212-234/Domain: transmembrane #status predicted <MEM>  
F:235-455/Domain: intracellular #status predicted <INT>  
F:54,145,151/Binding site: carboxydrate (Asn) (covalent) #status predicted  
Query Match 18.7%; Score 53; DB 1; Length 455;  
Best Local Similarity 33.3%; Pred. No. 1.4e+02;  
Matches 14; Conservative 5; Mismatches 19; Indels 4; Gaps 2;  
QY 8 CSQNE--YEDSLHACIPCOLRCSSNTPTLTTCORYCNASVT 46  
DB 127 CRKNQRYHWSNLFQCFNCSL-CLNGTVHLSCOEKQNTVCT 167  
RESULT 64  
JC1480  
protein kinase C (EC 2.7.1.1-) zeta - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 05-Oct-2004  
C:Accession: JC1480  
R:Goodnight, J.; Kazanietz, M.G.; Blumberg, P.M.; Mushinski, J.F.; Mischak, H.  
Gene 122, 305-311, 1992  
A:Title: The cDNA sequence, expression pattern and protein characteristics of mouse prote  
A:Reference number: JC1480; MUID:93138400; PMID:1487145  
A:Accession: JC1480  
A:Molecule type: mRNA  
A:Residues: 1-592 <GOO>  
A:Cross-references: UNIPROT:Q02956; UNIPARC:UPI0000029ADD; GB:M94632; NID:g200498; PIDN:  
A:Experimental source: brain  
C:Superfamily: protein kinase C, zeta/iota types; protein kinase C zinc-binding repeat  
C:Keywords: ATP; phorbol ester binding; phosphotransferase; serine/threonine-specific pr  
F:131-180/Domain: protein kinase C zinc-binding repeat homology <KZ1>  
F:250-518/Domain: protein kinase homology <KIN>  
F:258-266/Region: protein kinase ATP-binding motif  
F:281/Active site: Lys #status predicted  
Query Match 18.7%; Score 53; DB 1; Length 592;  
Best Local Similarity 34.9%; Pred. No. 1.7e+02;  
Matches 15; Conservative 8; Mismatches 14; Indels 6; Gaps 3;  
QY 6 GQCSQNEY-FDSLHACIPCOL----RCSSNTPTLTTCORYCNA 43  
DB 145 GQCSERINGLSRQYRCINCCKLVHKRCHV-LVPLTCRRHMD 186  
RESULT 65  
F88188  
protein C18H9.7 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C:Accession: F88188  
R:anonymous, The C. elegans Sequencing Consortium.







ntestinal tract and reproductive tract.

C:Genetics:

A:Gene: Muc5A

F:45-149/Domain: cysteine-rich <CYS>

F:762-830/Domain: von Willebrand factor type C repeat homology <VMC>

Query Match 18.7%; Score 53; DB 2; Length 1034;

Best Local Similarity 40.0%; Pred. No. 2.7e+02;

Matches 16; Conservative 5; Mismatches 15; Indels 4; Gaps 2;

QY 1 LMQAGCQSQNEYFDSLLHA---CIPCOLRCSSTNPPLTLC 37

DB 560 MLDLEWVCSGLELYASLCAGQGVCIPIWRSH-TNNTCPFTC 598

RESULT 70

T41146

probable cysteine-rich transcription regulator - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: T41146

R:Hubert, H.; Dueterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, October 1998

A:Reference number: Z21973

A:Accession: T41146

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1077 <HIL>

A:Cross-references: UNIPROT:O74853; UNIPARC:UPI000006A9D7; EMBL:AL031907; PIDN:CAA21417.

A:Experimental source: strain 972h-; cosmid c18

C:Genetics:

A:Gene: SPDB:SPCC18.03

A:Map position: 3

F:193-252/Domain: RING finger homology <RRN>

Query Match

Best Local Similarity 18.7%; Score 53; DB 2; Length 1077;

Matches 13; Conservative 7; Mismatches 14; Indels 10; Gaps 2;

QY 2 LQAGCQSQNEYFDSLLHACIPCOLRCSSTNPPLTCORYCNASV 45

DB 495 LSGCTGCTSET-----LTIPC--RCTANEVQVTCQLQNGFI 528

RESULT 71

D88550

protein ZC84.6 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

C:Accession: D88550

R:anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; PMID:99069613; PMID:9851916

A:Note: see websites genome.wustl.edu/sec/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele

A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: D88550

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1474 <STO>

A:Cross-references: UNIPROT:O62504; UNIPARC:UPI00000781E7; GB:chr\_III; PIDN:CAA79570.1;

C:Genetics:

A:Gene: ZC84.6

A:Map position: 3

Query Match

Best Local Similarity 18.7%; Score 53; DB 2; Length 1474;

Matches 14; Conservative 5; Mismatches 16; Indels 4; Gaps 3;

QY 3 QMAGCQSQNE--YFDSLHACIPCO-LRCS-SNTPPLTLC 37

DB 518 QSSSCPANFECYFDGNHGCCPTKRAFTCSLSPSFGKTC 556

RESULT 72

S28291

hypothetical protein ZC84.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C:Accession: S28291

R:Thomas, K.

submitted to the EMBL Data Library, December 1992

A:Reference number: S28285

A:Accession: S28291

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2844 <THO>

A:Cross-references: UNIPROT:Q03610; UNIPARC:UPI000017BCE9; EMBL:Z19157

C:Genetics:

A:Introns: 14/1; 32/3; 57/1; 192/3; 277/1; 398/1; 439/1; 474/1; 497/1; 813/1; 1135/1; 121

493/1; 2555/1; 2730/1; 2739/3; 2819/1

F:220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPI1>

F:343-395/Domain: animal Kunitz-type proteinase inhibitor homology <BPI2>

F:442-492/Domain: animal Kunitz-type proteinase inhibitor homology <BPI3>

F:546-598/Domain: animal Kunitz-type proteinase inhibitor homology <BPI4>

F:654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPI5>

F:1662-1716/Domain: animal Kunitz-type proteinase inhibitor homology <BPI6>

F:1787-1839/Domain: animal Kunitz-type proteinase inhibitor homology <BPI7>

F:1845-1895/Domain: animal Kunitz-type proteinase inhibitor homology <BPI8>

F:1952-2004/Domain: animal Kunitz-type proteinase inhibitor homology <BPI9>

F:2097-2152/Domain: animal Kunitz-type proteinase inhibitor homology <BPI10>

Query Match 18.7%; Score 53; DB 2; Length 2844;

Best Local Similarity 35.9%; Pred. No. 6.5e+02;

Matches 14; Conservative 5; Mismatches 16; Indels 4; Gaps 3;

QY 3 QMAGCQSQNE--YFDSLHACIPCO-LRCS-SNTPPLTLC 37

DB 1924 QSSSCPANFECYFDGNHGCCPTKRAFTCSLSPSFGKTC 1962

RESULT 73

S61051

hypothetical protein YDL162c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein D1510

C:Species: Saccharomyces cerevisiae

C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C:Accession: S61051; S67714

R:Pohl, T.M.

submitted to the EMBL Data Library, November 1995

A:Reference number: S61010

A:Accession: S61051

A:Molecule type: DNA

A:Residues: 1-118 <POH>

A:Cross-references: UNIPROT:Q12307; UNIPARC:UPI000006A6BC; EMBL:Z67750; NID:g1061256; PII

R:Pohl, T.M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67708

A:Accession: S67714

A:Molecule type: DNA

A:Residues: 1-118 <POW>

A:Cross-references: UNIPARC:UPI000006A6BC; EMBL:Z74210; NID:g1431255; PIDN:CAA98735.1; P1

A:Experimental source: strain S288C

C:Genetics:

A:Cross-references: SGD:S0002321

A:Map position: 4L

C:Superfamily: Saccharomyces hypothetical protein YDL162c

Query Match

Best Local Similarity 18.6%; Score 52.5; DB 2; Length 118;

Matches 11; Conservative 4; Mismatches 10; Indels 7; Gaps 2;

QY 8 CSONEYFDSLHACIP-----COLRCSSTNPPL 35

DB 72 CNRNSYCSRWYFCCLTLSSFCGLRC---VPPL 100



Thu Dec 22 14:13:29 2005

RESULT 74

T51647

myb-related transcription factor MYB33 [imported] - Arabidopsis thaliana (fragment)

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004

C/Accession: T51647

R/Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; Paz-Ares, J.; Weishaar, B.

Plant J. 16, 263-276, 1998

A/Title: Towards functional characterisation of the members of the R2R3-MYB gene from Arabidopsis thaliana

A/Reference number: Z14349; MUID:9839469; PMID:9839469

A/Accession: T51647

A>Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-378 <KRA>

A/Cross references: UNIPROT:Q9ZTE7; UNIPARC:UPI00000A77EF; EMBL:AF062875; PIDN:AAC83597.

A/Experimental source: cultivar Columbia

C/Genetics:

A/Gene: MYB33

A/Map position: III

C/Keywords: transcription factor

```

Query Match      18.6%; Score 52.5; DB 2; Length 378;
Best Local Similarity 23.5%; Pred. No. 1.3e+02;
Matches 16; Conservative 9; Mismatches 20; Indels 23; Gaps 2;

Qy      6  GQCSQNYFDSLHACIPCOLR-----CSS-----NTPPLTCQRYCN 42
      ||| : :: : ||| ||| ||| : ||| :
Db 136  GNCASSPRYENFMTPTIPSSKRLWESELLYPGCSSTIKQEFSSPEQPRNTSPQISKTCS 195
      ||| : ||| : ||| : ||| : ||| : ||| :

Qy      43  ASVTNSYVK 50
      ||| :
Db 196  FSVPCDVE 203

```

RESULT 75

T29488  
hypothetical protein M01H9.2 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T29488  
R:Pauley, A.; Gattung, S.  
submitted to the EMBL Data Library, September 1996  
A:Description: The sequence of *C. elegans* cosmid M01H9.  
A:Reference number: Z20626  
A:Accession: T29488  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-389 <PAU>  
A:Cross-references: UNIPROT:Q95018; UNIPARC:UPI000007DA14; EMBL:U70853; PIDN:AAB09143.1;  
A:Experimental source: strain Bristol N2; clone M01H9  
C:Genetics:  
A:Gene: CESP:M01H9.2  
A:Map position: 4  
A:Introns: 51/1; 96/1; 121/3; 209/2; 319/1

Query Match	18.6%	Score 52.5;	DB 2;	Length 389;
Best Local Similarity	34.1%	Pred. No. 1.4e+02;		
Matches 14;	Conservative	5;	Mismatches 15;	Indels 7; Gaps 2;
QY	8	CSQNEYFDLSLHACI-----PCQLRCSSNTPTLCORYCN	42	
DB	317	CSGYOCIDSIKIDCAEVKAQACGLSVASVCPRTCE-YCN	356	

Search completed: December 21, 2005, 16:11:34  
Job time : 38.2 secs



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 21, 2005, 15:56:49 ; Search time 175.8 Seconds  
(without alignments)  
204.675 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_1\_51  
Perfect score: 283  
Sequence: 1 MLOMAGQCSQNYFDSLHA.....TPPLTCQRCYNASVTNSVKG 51

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	283	100.0	184	1	TNR17_HUMAN	Q02233 homo sapien
2	283	100.0	184	2	G6P546_HUMAN	G6pe46 homo sapien
3	181	64.0	185	1	TNR17_MOUSE	O88472 mus musculus
4	78	27.6	184	2	Q4S4Q3_TETNG	Q4s4q3 tetraodon n
5	73	25.8	178	2	Q9BI07_ENTHI	Q9bi07 entamoeba h
6	73	25.8	1113	2	Q511P5_ENTHI	O511p5 entamoeba h
7	72.5	25.6	499	2	O88714_MOUSE	O88714 mus musculus
8	72.5	25.6	1674	2	Q80218_MOUSE	Q80218 mus musculus
9	72.5	25.6	2850	2	Q80T03_MOUSE	Q80t03 mus musculus
10	71.5	25.3	74	2	O5S084_MOUSE	O5su84 mus musculus
11	71.5	25.3	140	2	O5S083_MOUSE	O5su83 mus musculus
12	71.5	25.3	249	1	TR13B_MOUSE	O9et35 mus musculus
13	71.5	25.3	249	2	O5S082_MOUSE	O5su82 mus musculus
14	71	25.1	1150	2	Q50PT4_ENTHI	O50pt4 entamoeba h
15	71	25.1	3005	2	G6BF04_PARTE	G6bfr4 paramacium
16	70.5	24.9	1877	1	PCSK5_MOUSE	Q04592 mus musculus
17	70	24.7	1025	2	Q7R6J7_GIALA	Q7r6j7 giardia lam
18	69.5	24.6	5374	2	Q99ND0_MOUSE	O99nd0 mus musculus
19	69.5	24.6	5376	1	ZAN_MOUSE	O88799 mus musculus
20	68.5	24.2	966	2	Q22378_CABEL	Q22378 caenorhabdi
21	68.5	24.2	1569	2	Q6W4X9_HUMAN	Q6w4x9 homo sapien
22	67.5	23.9	293	1	TR13B_HUMAN	O14836 homo sapien
23	67.5	23.9	293	2	O53F36_HUMAN	O53f36 homo sapien
24	67	23.7	135	2	O60WC9_CAEHR	O60wc9 caenorhabdi
25	67	23.7	532	2	O17496_ASCSU	O17496 ascaris suu
26	67	23.7	574	2	Q54XU6_DICDI	Q54xu6 dictyosteli
27	66.5	23.5	1562	2	Q4N599_THEPA	Q4n599 theileria p
28	66	23.3	861	2	O55NL5_CRYNE	O55nl5 cryptococcu
29	65.5	23.1	1299	2	Q26489_SPOFR	Q26489 spodoptera
30	65	23.0	2551	1	STAB2_HUMAN	O8wv8 h stabilin-
31	64.5	22.8	484	2	Q5CZ66_HUMAN	Q5cz66 homo sapien

32	64.5	22.8	581	2	Q8NAV8_HUMAN	Q8nav8 homo sapien
33	64.5	22.8	799	2	Q50LY7_ENTHI	Q50ly7 entamoeba h
34	64.5	22.8	802	2	O50Y51_ENTHI	O50y51 entamoeba h
35	64.5	22.8	852	2	O5CZB3_HUMAN	O5czb3 homo sapien
36	64.5	22.8	880	2	Q8NAU9_HUMAN	O8nau9 homo sapien
37	64.5	22.8	919	2	Q61V24_CAEHR	Q61v24 caenorhabdi
38	64.5	22.8	992	2	Q86U29_HUMAN	Q86u29 homo sapien
39	64.5	22.8	993	2	Q8IX30_HUMAN	Q8ix30 homo sapien
40	64.5	22.8	1294	2	Q7QGV0_ANOGA	Q7qgv0 anopheles p
41	64.5	22.8	1532	2	Q4N9U5_THEPA	Q4n9u5 theileria p
42	64	22.6	494	2	Q729F0_DESVH	Q729f0 deulfovibr
43	64	22.6	762	2	Q4I0V5_GIBZE	Q4i0v5 gibberella
44	63.5	22.4	300	2	Q54KF9_DICDI	Q54kf9 dictyosteli
45	63.5	22.4	548	2	Q9GQ45_GIALA	Q9gq45 giardia lam
46	63.5	22.4	827	2	Q68FG9_MOUSE	Q68fg9 mus musculus
47	63.5	22.4	993	2	Q66PY1_MOUSE	Q66py1 mus musculus
48	63.5	22.4	1563	2	Q4UE95_THEAN	Q4ue95 theileria a
49	63	22.3	175	1	TR13C_MOUSE	Q948d0 mus musculus
50	63	22.3	175	2	Q8R4W8_MOUSE	Q8r4w8 mus musculus
51	63	22.3	289	2	Q678B7_9VIRU	Q678b7 lymphocyti
52	63	22.3	341	2	Q8CFA7_MOUSE	Q8cfa7 mus musculus
53	63	22.3	341	2	Q9D351_MOUSE	Q9d351 mus musculus
54	63	22.3	341	2	Q6P233_MOUSE	Q6p233 mus musculus
55	63	22.3	1560	2	Q5USG7_HUMAN	Q5jg97 homo sapien
56	62.5	22.1	974	2	Q4UHW4_THEAN	Q4uhw4 theileria a
57	62.5	22.1	985	2	Q8IZ06_HUMAN	Q8iz06 homo sapien
58	62.5	22.1	985	2	Q7Z5T8_HUMAN	Q7z5t8 homo sapien
59	62.5	22.1	995	2	Q5HYA8_HUMAN	Q5hya8 homo sapien
60	62.5	22.1	999	2	Q17968_CAEEL	Q17969 caenorhabdi
61	62.5	22.1	1917	2	Q5IED6_ENTHI	Q5ied6 entamoeba h
62	62	21.9	330	2	O18118_CABEL	O18118 caenorhabdi
63	62	21.9	1592	1	SORL_CHICK	Q98930 g sortilin-
64	62	21.9	3622	2	O6BG85_PARTE	O6bg85 paramacium
65	61.5	21.7	99	1	GAS3_ARATH	P46687 arabidopsis
66	61.5	21.7	353	2	Q8SZ58_DROME	O8sz58 drosophila
67	61.5	21.7	353	2	Q9VW81_DROME	Q9vw81 drosophila
68	61.5	21.7	432	2	Q61L29_CAEHR	Q61l29 caenorhabdi
69	61.5	21.7	483	2	Q22423_CABEL	Q22423 caenorhabdi
70	61.5	21.7	491	2	O5UOL4_MIMIV	Q5uol4 mimivirus
71	61.5	21.7	798	2	Q9VTR9_DROME	Q9vtr9 drosophila
72	61	21.6	263	2	Q9WEJ8_9HIV1	Q9wej8 human immun
73	61	21.6	354	2	Q4RNR8_TETNG	Q4rnr8 tetraodon n
74	61	21.6	815	2	Q4ZLE4_PSESY	Q4zle4 pseudomonas
75	60.5	21.4	339	2	Q61S18_CAEHR	Q61s18 caenorhabdi
76	60.5	21.4	412	2	Q6DEJ5_BRARE	Q6dej5 brachydanio
77	60.5	21.4	710	2	O5OM54_ENTHI	O5om54 entamoeba h
78	60.5	21.4	1083	2	O5ICE3_ENTHI	O5ice3 entamoeba h
79	60.5	21.4	1100	2	Q5OS60_ENTHI	Q5os60 entamoeba h
80	60.5	21.4	1155	2	Q6B534_WHEAT	Q6b534 triticum ae
81	60.5	21.4	1155	2	Q717V9_WHEAT	Q717v9 triticum ae
82	60.5	21.4	1516	2	Q4UFT2_THEAN	Q4uft2 theileria a
83	60.5	21.4	1529	2	Q4NOV0_THEPA	Q4nov0 theileria p
84	60.5	21.4	1545	2	Q4K3N8_THEPA	Q4k3n8 theileria p
85	60.5	21.4	1574	1	EGFL3_RAT	O88281 rattus norv
86	60.5	21.4	1656	2	Q5OSS7_ENTHI	O5oss7 entamoeba h
87	60.5	21.4	1671	2	Q571L9_MOUSE	Q571l9 mus musculus
88	60.5	21.4	1866	2	Q4SVV9_TETNG	Q4svv9 tetraodon n
89	60.5	21.4	3034	1	CELR1_MOUSE	O35161 mus musculus
90	60.5	21.4	3667	2	Q5JAV9_RAT	O5jav9 rattus norv
91	60	21.2	262	2	Q9WDX2_9HIV1	Q9wdx2 human immun
92	60	21.2	356	2	Q6NE22_CAEHR	Q6ne22 caenorhabdi
93	60	21.2	525	1	ALO_KLULA	Q6c9y3 kluyveromyc
94	60	21.2	673	2	O86WK8_HUMAN	Q86wk8 homo sapien
95	60	21.2	830	2	Q4RTY8_TETNG	Q4rty8 tetraodon n
96	60	21.2	867	1	SSPO_BOVIN	P98167 bos taurus
97	60	21.2	955	2	Q96DN2_HUMAN	Q96dn2 homo sapien
98	60	21.2	1431	2	Q4S9D3_TETNG	Q4s9d3 tetraodon n
99	60	21.2	5146	2	Q8SPM4_BOVIN	Q8spm4 bos taurus
100	59.5	21.0	102	2	Q6PIK8_HUMAN	Q6pik8 homo sapien
101	59.5	21.0	248	2	O5DDB6_SCHJA	O5ddb6 schistosoma
102	59.5	21.0	383	2	Q6IM00_CAEHR	Q6im00 caenorhabdi
103	59.5	21.0	388	2	O16500_CABEL	O16500 caenorhabdi
104	59.5	21.0	388	2	O16501_CABEL	O16501 caenorhabdi



105	59.5	21.0	426	2	Q519S8_ENTHI	Q519S8	entamoeba h	178	58	20.5	923	2	Q17970_CAEEL	O17970	caenorhabdi
106	59.5	21.0	436	2	Q61J22_CABER	Q61J22	caenorhabdi	179	58	20.5	1013	2	Q41F99_GIBZE	Q41F99	gibberella
107	59.5	21.0	448	2	Q16502_CAEEL	Q16502	caenorhabdi	180	58	20.5	1293	2	Q5B0C3_EMENI	Q5B0C3	aspergillus
108	59.5	21.0	435	2	Q16511_CAEEL	Q16511	caenorhabdi	181	58	20.5	1360	2	Q620M9_CABER	Q620M9	caenorhabdi
109	59.5	21.0	445	2	Q6BJV7_DEBHA	Q6BJV7	debaromyce	182	58	20.5	1816	1	LAMA4_HUMAN	LAMA4	homo sapien
110	59.5	21.0	741	2	Q4RLP8_TETNG	Q4RLP8	tetraodon n	183	58	20.5	1816	2	Q5D044_HUMAN	Q5D044	homo sapien
111	59.5	21.0	856	2	Q945R4_HORVU	Q945R4	hordeum vul	184	58	20.5	1823	2	Q5SZG8_HUMAN	Q5SZG8	homo sapien
112	59.5	21.0	1155	2	Q56S01_HORVD	Q56S01	hordeum vul	185	58	20.5	1852	2	Q4LE44_HUMAN	Q4LE44	homo sapien
113	59.5	21.0	1155	2	Q56S02_HORVD	Q56S02	hordeum vul	186	57.5	20.3	146	2	Q9ENZ4_9HEPC	Q9ENZ4	hepatitis c
114	59	20.8	127	1	ACPS_ONYPE	Q6Yqd4	onion yello	187	57.5	20.3	146	2	Q9EP23_9HEPC	Q9EP23	hepatitis c
115	59	20.8	147	1	MSRB_VIBPA	Q6Yme5	vibrio para	188	57.5	20.3	159	2	Q5ALV1_CANAL	Q5ALV1	candida alb
116	59	20.8	263	2	Q9WDU5_9HIV1	Q9wdus	human immun	189	57.5	20.3	159	2	Q61R18_CABER	Q61R18	caenorhabdi
117	59	20.8	263	2	Q9WDV0_9HIV1	Q9wdv0	human immun	190	57.5	20.3	266	2	Q9WDV9_9HIV1	Q9WDV9	human immun
118	59	20.8	263	2	Q9WDV0_9HIV1	Q9wdv0	human immun	191	57.5	20.3	266	2	Q9WDW1_9HIV1	Q9WDW1	human immun
119	59	20.8	263	2	Q9WDV8_9HIV1	Q9wdv8	human immun	192	57.5	20.3	675	2	Q94LU3_ORISA	Q94LU3	oryza sativ
120	59	20.8	263	2	Q9WDV8_9HIV1	Q9wdv8	human immun	193	57.5	20.3	881	2	Q94LU6_ORISA	Q94LU6	oryza sativ
121	59	20.8	263	2	Q9WDW7_9HIV1	Q9wdw7	human immun	194	57.5	20.3	1061	2	Q5B110_DROME	Q5B110	drosophila
122	59	20.8	263	2	Q9WDW8_9HIV1	Q9wdw8	human immun	195	57.5	20.3	1153	2	Q6B535_WHEAT	Q6B535	triticum ae
123	59	20.8	263	2	Q9WDW9_9HIV1	Q9wdw9	human immun	196	57.5	20.3	1452	2	Q4SS61_TETNG	Q4SS61	tetraodon n
124	59	20.8	263	2	Q9WDX0_9HIV1	Q9wdx0	human immun	197	57.5	20.3	1511	2	Q4UF82_THEAN	Q4UF82	theileria a
125	59	20.8	263	2	Q9WDX6_9HIV1	Q9wdx6	human immun	198	57.5	20.3	1527	2	Q4UHS5_THEAN	Q4UHS5	theileria a
126	59	20.8	263	2	Q9WE18_9HIV1	Q9we18	human immun	199	57.5	20.3	1679	1	FUR2_DROME	FUR2	drosophila
127	59	20.8	263	2	Q9WE19_9HIV1	Q9we19	human immun	200	57	20.1	292	1	KR109_HUMAN	KR109	homo sapien
128	59	20.8	263	2	Q9WEJ0_9HIV1	Q9wej0	human immun	201	57	20.1	294	2	Q620N2_CABER	Q620N2	caenorhabdi
129	59	20.8	263	2	Q9WEJ1_9HIV1	Q9wej1	human immun	202	57	20.1	321	2	Q9MAM0_ARATH	Q9MAM0	arabidopsis
130	59	20.8	263	2	Q9WEJ2_9HIV1	Q9wej2	human immun	203	57	20.1	355	2	Q41BL3_GIBZE	Q41BL3	gibberella
131	59	20.8	263	2	Q9WEJ3_9HIV1	Q9wej3	human immun	204	57	20.1	355	2	Q899P5_CLOTE	Q899P5	clostridium
132	59	20.8	263	2	Q9WEJ5_9HIV1	Q9wej5	human immun	205	57	20.1	364	2	Q41LX2_GIBZE	Q41LX2	gibberella
133	59	20.8	263	2	Q9WEJ7_9HIV1	Q9wej7	human immun	206	57	20.1	388	2	Q4X6L2_PLACH	Q4X6L2	plasmodium
134	59	20.8	263	2	Q9WEJ9_9HIV1	Q9wej9	human immun	207	57	20.1	428	2	Q4Y0X1_PLACH	Q4Y0X1	plasmodium
135	59	20.8	263	2	Q9WEL3_9HIV1	Q9wel3	human immun	208	57	20.1	436	2	Q41FW6_GIBZE	Q41FW6	gibberella
136	59	20.8	304	2	Q5IAP4_ENTHI	Q5iap4	entamoeba h	209	57	20.1	440	2	Q8BU58_MOUSE	Q8BU58	mus musculus
137	59	20.8	379	1	PE48_CHRBE	O17450	chrysomya b	210	57	20.1	554	2	Q4KFP5_PSEF5	Q4KFP5	pseudomonas
138	59	20.8	596	2	Q4HZ82_GIBZE	Q4hz82	gibberella	211	57	20.1	653	2	Q9S9J8_ARATH	Q9S9J8	arabidopsis
139	59	20.8	663	2	Q9LT87_ARATH	Q9lt87	arabidopsis	212	57	20.1	663	2	Q81YJ8_HUMAN	Q81YJ8	homo sapien
140	59	20.8	937	2	Q9GVR5_CABER	Q9gvr5	caenorhabdi	213	57	20.1	686	2	Q6POM3_HUMAN	Q6POM3	homo sapien
141	59	20.8	1455	2	Q85FJ9_CABER	Q85fj9	caenorhabdi	214	57	20.1	752	2	Q9C091_HUMAN	Q9C091	homo sapien
142	59	20.8	1717	2	Q28566_SCHMA	Q28566	schistosoma	215	57	20.1	838	2	Q27422_CAEEL	Q27422	caenorhabdi
143	58.5	20.7	146	2	Q9EP28_9HEPC	Q9ep28	hepatitis c	216	57	20.1	858	2	Q18761_CAEEL	Q18761	caenorhabdi
144	58.5	20.7	276	2	Q4QJH5_LEIMA	Q4qjh5	leishmania	217	57	20.1	881	2	TTC7A_HUMAN	TTC7A	homo sapien
145	58.5	20.7	438	2	Q510V0_ENTHI	Q510v0	entamoeba h	218	57	20.1	911	2	Q68KF8_XENLA	Q68KF8	xenopus lae
146	58.5	20.7	476	2	Q4KZ32_ECOLI	Q4kz32	escherichia	219	57	20.1	911	2	Q5EE49_XENLA	Q5EE49	xenopus lae
147	58.5	20.7	626	2	Q5SSV4_CRYNE	Q5sav4	cryptococcus	220	57	20.1	938	2	Q60K18_CABER	Q60K18	caenorhabdi
148	58.5	20.7	626	2	Q5KH88_CRYNE	Q5kh88	cryptococcus	221	57	20.1	1174	2	Q5EE44_XENLA	Q5EE44	xenopus lae
149	58.5	20.7	657	2	Q518K7_ENTHI	Q518k7	entamoeba h	222	57	20.1	1185	2	Q5EE45_XENLA	Q5EE45	xenopus lae
150	58.5	20.7	796	2	Q8MRG9_DROME	Q8mr9	drosophila	223	57	20.1	1210	2	Q7R165_GIALA	Q7R165	giardia lam
151	58.5	20.7	796	2	Q9VTR4_DROME	Q9vtr4	drosophila	224	57	20.1	1394	2	Q8MST1_DROME	Q8MST1	drosophila
152	58.5	20.7	830	2	Q9IV27_9HIV1	Q9iv27	human immun	225	57	20.1	1511	2	Q9VB21_DROME	Q9VB21	xenopus lae
153	58.5	20.7	949	2	Q452B5_TETNG	Q452b5	tetraodon n	226	57	20.1	1546	2	Q5EE46_XENLA	Q5EE46	xenopus lae
154	58.5	20.7	1010	2	Q53166_BRARE	Q53166	brachydanio	227	57	20.1	1632	2	Q5EE47_XENLA	Q5EE47	xenopus lae
155	58.5	20.7	1010	2	Q5G872_BRARE	Q5g872	brachydanio	228	57	20.1	1704	2	Q51EF3_ENTHI	Q51EF3	entamoeba h
156	58.5	20.7	1079	2	Q4SSN7_TETNG	Q4ssn7	tetraodon n	229	57	20.1	1849	2	Q5EE48_XENLA	Q5EE48	xenopus lae
157	58.5	20.7	1240	2	Q50RH2_ENTHI	Q50rh2	tetraodon n	230	56.5	20.0	117	2	Q5HBX1_HUMAN	Q5HBX1	homo sapien
158	58.5	20.7	1491	2	Q4UD49_THEAN	Q4ud49	theileria a	231	56.5	20.0	150	2	Q31476_ONCGO	Q31476	oncorhynch
159	58.5	20.7	1525	2	Q4UD47_THEAN	Q4ud47	theileria a	232	56.5	20.0	313	1	STAH2_XENLA	STAH2	xenopus lae
160	58.5	20.7	1527	2	Q4UAR4_THEAN	Q4uar4	theileria a	233	56.5	20.0	358	2	Q7QEX5_ANOGA	Q7QEX5	anopheles g
161	58.5	20.7	2533	2	P90589_PARTE	P90589	paramesicium	234	56.5	20.0	549	2	Q8E940_SHEON	Q8E940	shewanella
162	58.5	20.7	2533	2	Q27183_PARTE	Q27183	paramesicium	235	56.5	20.0	608	2	Q4XTN2_PLACH	Q4XTN2	plasmodium
163	58	20.5	63	1	ICEL_ASCSU	P07851	ascaris suu	236	56.5	20.0	701	1	PALA_SCHPO	PALA	schizosacch
164	58	20.5	101	2	Q8BR19_MOUSE	Q8br19	mus musculus	237	56.5	20.0	974	2	Q4N7P5_THEPA	Q4N7P5	theileria p
165	58	20.5	104	2	Q5DBU1_SCHJA	Q5dbu1	schistosoma	238	56.5	20.0	1084	2	Q61RM7_XENLA	Q61RM7	xenopus lae
166	58	20.5	158	2	Q5XQY7_9HEPC	Q5xqy7	hepatitis c	239	56.5	20.0	1476	2	Q8WRFA_MONBE	Q8wrfa	monosiga br
167	58	20.5	244	2	Q4R6M0_MACFA	Q4r6m0	macaca fasc	240	56.5	20.0	1792	2	Q57484_CHICK	Q57484	gallus gall
168	58	20.5	271	1	KR105_HUMAN	P60370	homo sapien	241	56.5	20.0	1883	2	Q50PC6_ENTHI	Q50PC6	entamoeba h
169	58	20.5	387	2	Q9PVD4_XENLA	Q9pvd4	xenopus lae	242	56.5	20.0	2898	2	Q9VLT6_DROME	Q9VLT6	drosophila
170	58	20.5	387	2	Q4KLX7_XENLA	Q4klx7	xenopus lae	243	56	19.8	76	2	Q7YWT3_CAEEL	Q7YWT3	caenorhabdi
171	58	20.5	392	2	Q6NUF1_XENLA	Q6nuf1	xenopus lae	244	56	19.8	146	2	Q9EP06_9HEPC	Q9EP06	hepatitis c
172	58	20.5	414	2	Q68790_9HEPC	Q68790	hepatitis c	245	56	19.8	158	2	Q5XQ21_9HEPC	Q5XQ21	hepatitis c
173	58	20.5	415	2	Q81552_9HEPC	Q81552	hepatitis c	246	56	19.8	181	2	Q4SS63_TETNG	Q4SS63	tetraodon n
174	58	20.5	464	2	Q511H8_ENTHI	Q511h8	entamoeba h	247	56	19.8	185	2	Q8X1W9_DROYA	Q8X1W9	drosophila
175	58	20.5	667	2	Q60K86_CABER	Q60k86	caenorhabdi	248	56	19.8	221	2	Q8AXC1_XENLA	Q8AXC1	xenopus lae
176	58	20.5	721	2	Q6SSH4_ORISA	Q6esh4	oryza sativ	249	56	19.8	337	2	Q9VHP7_DROME	Q9VHP7	drosophila
177	58	20.5	911	2	Q5PQ96_XENLA	Q5pq96	xenopus lae	250	56	19.8	342	2	Q6H7U0_ORISA	Q6H7U0	oryza sativ



251	56	19.8	380	2	Q74432	9HIV2	human immun
252	56	19.8	380	2	Q93017	9HIV2	human immun
253	56	19.8	415	2	Q68791	9HEPC	hepatitis c
254	56	19.8	489	2	Q4WLA5	ASgFPU	aspergillus
255	56	19.8	490	2	Q88120	SIVCZ	chimpanzee
256	56	19.8	522	2	Q90521	SIVCZ	chimpanzee
257	56	19.8	522	2	Q90527	SIVCZ	chimpanzee
258	56	19.8	550	2	Q4J2W3	AZOVI	azotobacter
259	56	19.8	760	1	EZ_DROME		drosophila
260	56	19.8	819	2	Q6DDW2	XENLA	xenopus lae
261	56	19.8	1090	2	Q50RX4	ENTHI	entamoeba h
262	56	19.8	1093	2	Q50X86	ENTHI	entamoeba h
263	56	19.8	1277	2	Q50RX0	ENTHI	entamoeba h
264	56	19.8	1489	2	Q50Y64	ENTHI	entamoeba h
265	56	19.8	1668	2	Q6SZU6	MOUSE	mus musculus
266	56	19.8	2397	2	Q6Q7Y4	PARPR	paramcium
267	56	19.8	2476	1	ZAN_PIG		sus scrofa
268	56	19.8	2855	2	Q61DQ8	CAEBR	caenorhabdi
269	56	19.8	2972	2	Q90891	CAEBL	caenorhabdi
270	55.5	19.6	103	2	Q4J2Z2	9VIRU	microplitis
271	55.5	19.6	116	2	Q8RYA8	HEVR	hevea bras
272	55.5	19.6	142	2	Q50SR1	ENTHI	entamoeba h
273	55.5	19.6	146	2	Q9ENZ5	9HEPC	hepatitis c
274	55.5	19.6	146	2	Q9EP09	9HEPC	hepatitis c
275	55.5	19.6	225	2	Q9VE40	DROSOPH	drosophila
276	55.5	19.6	269	2	Q7PRQ7	ANOGA	anopheles g
277	55.5	19.6	334	2	Q8SZ02	DROME	drosophila
278	55.5	19.6	334	2	Q9VW95	DROME	drosophila
279	55.5	19.6	339	1	CATB_RAT		rattus norv
280	55.5	19.6	339	2	Q6IN22	RAT	rattus norv
281	55.5	19.6	377	2	Q6ONE3	CAEBR	caenorhabdi
282	55.5	19.6	378	2	Q27183	CAEBL	caenorhabdi
283	55.5	19.6	419	2	Q6FH59	HUMAN	homo sapien
284	55.5	19.6	473	2	Q93CT0	SHIBO	shigella bo
285	55.5	19.6	806	2	Q4N023	THELIERIA	theileria p
286	55.5	19.6	815	2	O81833	ARATH	arabidopsis
287	55.5	19.6	989	2	Q9ZU00	ARATH	arabidopsis
288	55.5	19.6	1433	2	Q9B1H9	ANOGA	anopheles g
289	55.5	19.6	1531	2	Q4NSA0	THEPRA	theileria p
290	55.5	19.6	1807	2	Q55GM7	DICDI	dictyostel
291	55.5	19.6	2843	2	Q9Y6R7	HUMAN	homo sapien
292	55.5	19.6	3695	1	LAMA5	HUMAN	homo sapien
293	55.5	19.6	4260	2	Q4T3T2	TETNG	tetraodon n
294	55	19.4	62	2	Q6VON8	CRAVI	crassostrea
295	55	19.4	62	2	Q6MUZ6	CRAVI	crassostrea
296	55	19.4	89	1	VPI_MESMA		mesobuthus
297	55	19.4	137	2	Q5FXF2	9HEPC	hepatitis c
298	55	19.4	137	2	Q5FXF9	9HEPC	hepatitis c
299	55	19.4	137	2	Q5FXH0	9HEPC	hepatitis c
300	55	19.4	186	2	Q4LIQ3	9BURK	burkholderi

## ALIGNMENTS

RESULT 1  
TNR17 HUMAN  
ID TNR17 HUMAN STANDARD; PRT; 184 AA.

AC Q02223;  
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 17 (B-cell

DE maturation protein).

GN Name=TNFRSF17; Synonyms=BCM, BCMA;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OC NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE, AND CHROMOSOMAL TRANSLOCATION.

RC TISSUE=Lymph node, and Peripheral blood leukocyte;

RX MEDLINE=93010984; PubMed=1396583;  
RA Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,  
RA Larsen C.-J., Tsapis A.;  
RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene  
RL by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";  
RN EMBO J. 11:3897-3904(1992).  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94218235; PubMed=8165126;  
RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.-J., Tsapis A.;  
RT "The BCMA gene, preferentially expressed during B lymphoid maturation,  
RL is bidirectionally transcribed.";  
RN Nucleic Acids Res. 22:1147-1154(1994).  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX MEDLINE=94218235; PubMed=10493829; DOI=10.1006/geno.1999.5927;  
RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,  
RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,  
RA DeLattre Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,  
RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;  
RT "Genome duplications and other features in 12 Mb of DNA sequence from  
RL human chromosome 16p and 16q.";  
RN Genomics 60:295-308(1999).  
RP NUCLEOTIDE SEQUENCE, AND VARIANT THR-153.  
RX MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770;  
RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;  
RT "Presence of four major haplotypes in human BCMA gene: lack of  
RL association with systemic lupus erythematosus and rheumatoid  
RN arthritis.";  
RP Genes Immun. 2:276-279(2001).  
RX NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-54; VAL-65;  
RA VAL-75; ASN-81 AND SER-165.  
RP Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,  
RA Nguyen C.P., Nguyen D.A., Foel C.L., Robertson P.D., Schekwitz W.S.,  
RA Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;  
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department  
RL of Genome Sciences, Seattle, WA (URL: //egp.gs.washington.edu).";  
RN Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
RP FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.  
RX MEDLINE=20363816; PubMed=10903733;  
RA Hatzoglou A., Roussel J., Bourgeois M.-F., Rogier E., Madry C.,  
RA Inoue J.-I., Devergne O., Tsapis A.;  
RT "TNF receptor family member BCMA (B cell maturation) associates with  
RL TNF receptor associated factor (TRAF) 1, TRAF2, and TRAF3 and  
RN activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-  
RP activated protein kinase.";  
RX J. Immunol. 165:1322-1330(2000).  
RN [7]  
RP FUNCTION  
RX MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;  
RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,  
RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,  
RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,  
RA Harrison K., Kindavogel W., Clegg C.H.;  
RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell  
RL autoimmune disease.";  
RN Nature 404:995-999(2000).  
RP [8]  
RN FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.  
RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;  
RA Yu G., Boone T., Delaney J.J., Hawkins N., Kelley M.J., Ramakrishnan M.,  
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,  
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Thell L.E.;  
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating  
RN humoral immunity.";  
RP Nat. Immunol. 1:252-256(2000).  
RN [9]  
RP INTERACTIONS WITH TRAF5 AND TRAF6.  
RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;  
RA Shu H.-B., Johnson H.;



"B cell maturation protein is a receptor for the tumor necrosis factor family member TAL-1.";  
 Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).  
 CC -!- FUNCTION: Receptor for TNFSF13B/BlYS/BAFF and TNFSF13/APRIL.  
 CC Promotes B-cell survival and plays a role in the regulation of  
 CC humoral immunity. Activates NF-kappa-B and JNK.  
 CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
 CC -!- INTERACTION:  
 CC Q9Y275:TNFSF13B; NbExp1; IntAct=EBI-519945, EBI-519169;  
 CC -!- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane  
 CC and perinuclear Golgi-like structures.  
 CC -!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-  
 CC cells or monocytes.  
 CC -!- DISEASE: A chromosomal aberration involving TNFRSF17 is found in a  
 CC form of T-cell acute lymphoblastic leukemia (T-ALL). Translocation  
 CC t(4;16)(q26;pl3) with 11L2.  
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; Z14954; CAA78679.1; -; mRNA.  
 CC EMBL; Z29575; CAA82691.1; -; mRNA.  
 CC EMBL; Z29574; CAA82690.1; -; Genomic DNA.  
 CC EMBL; U95742; AAB67251.1; -; Genomic DNA.  
 CC EMBL; AB052772; BAB60895.1; -; Genomic DNA.  
 CC EMBL; AY059112; AAR84240.1; -; Genomic DNA.  
 CC PIR; S43486; S43486.  
 CC PDB; 1QOD; X-ray; K/L/M/N/O/P/Q/R-S-46.  
 CC PDB; 1XU2; X-ray; R/S/T-S-51.  
 CC InterAct; Q02223; -.  
 CC Ensembl; ENSG0000048462; Homo sapiens.  
 CC HGNC; HGNC:11513; TNFRSF17.  
 CC MIM; 109545; -.  
 CC GO; GO:0016021; C:integral to membrane; TAS.  
 CC GO; GO:0005886; C:plasma membrane; TAS.  
 CC GO; GO:0004872; F:receptor activity; TAS.  
 CC GO; GO:0008283; P:cell proliferation; TAS.  
 CC GO; GO:0007275; P:development; TAS.  
 CC GO; GO:0007165; P:signal transduction; TAS.  
 CC InterPro; IPR001368; TNFR\_c6.  
 CC PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.  
 CC PROSITE; PS00500; TNFR\_NGFR\_2; FALSE\_NEG.  
 CC 3D-structure; Chromosomal translocation; Immune response;  
 CC Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.  
 KW TOPO\_DOM 1 54 Extracellular (Potential).  
 FT TRANSMEM 55 77 Signal-anchor for type III membrane  
 FT TOPO\_DOM 78 184 Cytoplasmic (Potential).  
 FT REPEAT 7 41 TNFR-Cys.  
 FT SITE 3 4 Breakpoint for translocation to form  
 FT IL2/TNFSF17 oncogene.  
 FT DISULFID 8 21 By similarity.  
 FT DISULFID 24 37 By similarity.  
 FT DISULFID 28 41 By similarity.  
 FT VARIANT 54 54 A -> V.  
 FT VARIANT 65 65 I -> V.  
 FT VARIANT 75 75 /FTID=VAR\_018756.  
 FT VARIANT 81 81 S -> N (in dbSNP:373496).  
 FT VARIANT 153 153 A -> T.  
 FT VARIANT 165 165 C -> S.  
 FT SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;  
 SQ Query Match 100.0%; Score 283; DB 1; Length 184;

Best Local Similarity 100.0%; Pred. No. 7.6e-27;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKG 51  
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKG 51  
 RESULT 2  
 Q6PE46 HUMAN PRELIMINARY; PRT; 184 AA.  
 AC Q6PE46  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily, member 17.  
 GN Name=TNFRSF17;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Poolled;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshilyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Poolled;  
 RA Strausberg R.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC058291; AAH58291.1; -; mRNA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 SQ SEQUENCE 184 AA; 20139 MW; C7ACFPB40FC5531A CRC64;  
 Query Match 100.0%; Score 283; DB 2; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-27;  
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKG 51  
 DB 1 MLQWAGQCSQNEYFDSLHACIPQLRCSSNTPLTCORYCNASVTNSVKG 51  
 RESULT 3  
 TNR17 MOUSE  
 ID TNR17\_MOUSE STANDARD; PRT; 185 AA.  
 AC O88472;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell











RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RC NUCLEOTIDE SEQUENCE.

RP TISSUE=Stomach;

RA Tomasetto C.L.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ010752; CAA09343.1; -; mRNA.

DR HSP; P56682; ICCV

DR Ensemble; ENSMUSG0000048191; Mus musculus.

DR MGI; MGI:2663233; Muc6.

DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.

DR InterPro; IPR001846; VWF\_D.

DR Pfam; PF01826; TIL; 1.

DR Pfam; PF00094; VWD; 1.

DR SMART; SM00216; VWD; 1.

DR NON TER 1

FT NON TER 499

FT NON TER 499

SQ SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;

Query Match 25.6%; Score 72.5; DB 2; Length 499;

Best Local Similarity 48.3%; Pred. No. 1.9;

Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Query 8 CSQNEFDLSLLHACIPQCLRCSSNTPLT 36

Db 430 CSQNEFDHSEGTVCPC-----APPTT 451

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AC Q80T03;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE MUC6.

GN Name=Muc6;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J;

RX MEDLINE=22563400; PubMed=12676567; DOI=10.1016/S0888-7543(03)00036-3;

RA Desseyn J.-L., Laine A.;

RT "Characterization of mouse muc6 and evidence of conservation of the

gel-forming mucin gene cluster between human and mouse.";

RL Genomics 81:433-436(2003).

DR EMBL; AY184388; AAO47735.1; -; Genomic\_DNA.

DR EMBL; AY184385; AAO47735.1; JOINED; Genomic\_DNA.

DR EMBL; AY184387; AAO47735.1; JOINED; Genomic\_DNA.

DR EMBL; AY184386; AAO47735.1; JOINED; Genomic\_DNA.

DR HSP; O46162; IKJ0.

DR Ensemble; ENSMUSG0000048191; Mus musculus.

DR MGI; MGI:2663233; Muc6.

DR InterPro; IPR006207; Cys\_knot\_C.

DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.

DR InterPro; IPR001846; VWF\_D.

DR Pfam; PF01826; TIL; 2.

DR Pfam; PF00094; VWD; 3.

DR SMART; SM00216; VWD; 3.

DR PROSITE; PS01225; CTCK 2; 1.

SQ SEQUENCE 2850 AA; 300398 MW; 9CD95F0845C79C9D CRC64;

Query Match 25.6%; Score 72.5; DB 2; Length 2850;

Best Local Similarity 48.3%; Pred. No. 12;

Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Query 8 CSQNEFDLSLLHACIPQCLRCSSNTPLT 36

Db 1222 CSQNEFDHSEGTVCPC-----APPTT 1243

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RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RC NUCLEOTIDE SEQUENCE.

RP TISSUE=Stomach;

RA Tomasetto C.L.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ010752; CAA09343.1; -; mRNA.

DR HSP; P56682; ICCV

DR Ensemble; ENSMUSG0000048191; Mus musculus.

DR MGI; MGI:2663233; Muc6.

DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.

DR InterPro; IPR001846; VWF\_D.

DR Pfam; PF01826; TIL; 1.

DR Pfam; PF00094; VWD; 1.

DR SMART; SM00216; VWD; 1.

DR NON TER 1

FT NON TER 499

FT NON TER 499

SQ SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;

Query Match 25.6%; Score 72.5; DB 2; Length 1674;

Best Local Similarity 48.3%; Pred. No. 6.8;

Matches 14; Conservative 1; Mismatches 7; Indels 7; Gaps 1;

Query 8 CSQNEFDLSLLHACIPQCLRCSSNTPLT 36

Db 1181 CSQNEFDHSEGTVCPC-----APPTT 1202

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RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RC NUCLEOTIDE SEQUENCE.

RP TISSUE=Stomach;

RA Tomasetto C.L.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ010752; CAA09343.1; -; mRNA.

DR HSP; P56682; ICCV

DR Ensemble; ENSMUSG0000048191; Mus musculus.

DR MGI; MGI:2663233; Muc6.

DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.

DR InterPro; IPR001846; VWF\_D.

DR Pfam; PF01826; TIL; 1.

DR Pfam; PF00094; VWD; 1.

DR SMART; SM00216; VWD; 1.

DR NON TER 1

FT NON TER 499

FT NON TER 499

SQ SEQUENCE 499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;

Query Match 25.6%; Score 71.5; DB 2; Length 74;

Best Local Similarity 35.3%; Pred. No. 0.36;

Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Query 8 CSQNEFDLSLLHACIPQCLRCSSNTPLT 36

Db 1181 CSQNEFDHSEGTVCPC-----APPTT 1202

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QY 8 CSQNEVFDLHACIPQLRCSNTPLTCQRYC 41
DB 6 CPKQDQWDSRSKSCVSCALTCQSORS-QRTCTDFC 38

RESULT 11
QSSU83 MOUSE
ID QSSU83_MOUSE PRELIMINARY; PRT; 140 AA.
AC QSSU83;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 13b
DE (fragment).
GN Name=Tnfrsf13b; ORFNames=RP23-5512.2-003;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL646093; CAI25895.1; -; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 140
SQ SEQUENCE 140 AA; 15672 MW; 005D8CDF4E8E3D15 CRC64;

Query Match 25.3%; Score 71.5; DB 2; Length 140;
Best Local Similarity 35.3%; Pred. No. 0.69; 13; Indels 1; Gaps 1;
Matches 12; Conservative 8; Mismatches 13;

QY 8 CSQNEVFDLHACIPQLRCSNTPLTCQRYC 41
DB 6 CPKQDQWDSRSKSCVSCALTCQSORS-QRTCTDFC 38

RESULT 12
TR13B MOUSE
ID TR13B_MOUSE STANDARD; PRT; 249 AA.
AC Q9ET35; Q9DBZ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN Name=Tnfrsf13b; Synonyms=Taci;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tissue=Splice;
RC MEDLINE=2117254; PubMed=10881172; DOI=10.1038/76889;
RA Van M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
RT "Identification of a receptor for Blys demonstrates a crucial role in
RT humoral immunity";
RL Nat. Immunol. 1:37-41(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gyojbori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

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GAasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
GRimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
KANai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
KOnagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
MAGlott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G.,
PETrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RAVASI T., Reed J.C., Reed D.J., Reid J., King B.Z., Ringwald M.,
Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
SULTana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
VERardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
WILming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
YUAN Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
HIROZAKI-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
SHIRAKI T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
HARA A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
MIYAZAKI A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
YASUNISHI A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
BIRNEY E., Hayashizaki Y.,
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP FUNCTION.
RX MEDLINE=20341628; PubMed=10880535; DOI=10.1084/jem.192.1.137;
XIA X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
THEILL L.E., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R.,
MINER K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
MENG S.-Y., Boyle W.J., Hsu H.;
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT factor family member involved in B cell regulation.";
J. Exp. Med. 192:137-143(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21322748; PubMed=11429548; DOI=10.1038/89782;
WANG H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
VAN M., Dixit V.M., Ashkenazi A., Grewal I.S.;
RT "TACI-ligand interactions are required for T cell activation and
RT collagen-induced arthritis in mice.";
RL Nat. Immunol. 2:632-637(2001).
CC -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity (By
CC similarity).
CC -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAMLG with its C-terminus (By similarity).
CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF257673; AAG00081.1; -; mRNA.
CC EMBL; AK004668; BAB23457.1; -; mRNA.
CC Ensembl; ENSMUSG00000010142; Mus musculus.
CC MGI; MGI:1889411; Tnfrsf13b.
CC GO; GO:0009897; C:external side of plasma membrane; IDA.
CC GO; GO:0005887; C:integral to plasma membrane; IDA.
CC GO; GO:0001782; P:B cell homeostasis; IMP.
CC GO; GO:0030889; P:negative regulation of B cell proliferation; IMP.
CC InterPro; IPR001368; TNFR_C6.
CC PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
CC PROSITE; PS00505; TNFR_NGFR_2; FALSE_NEG.
KW Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.
FT TOPO_DOM 1 128
FT Extracellular (Potential).
FT TRANSMEM 129 149
FT Signal-anchor for type III membrane
FT protein (Potential).
FT TOPO_DOM 150 249
FT Cytoplasmic (Potential).

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FT REPEAT      5 38      TNFR-Cys 1.
FT REPEAT      42 76      TNFR-Cys 2.
FT FT DISULFID 6 19      By similarity.
FT FT DISULFID 22 34      By similarity.
FT FT DISULFID 26 38      By similarity.
FT FT DISULFID 43 58      By similarity.
FT FT DISULFID 61 72      By similarity.
FT FT DISULFID 65 76      By similarity.
FT FT CONFLICT 137 137   I -> F (in Ref. 2).
SQ SEQUENCE    249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match
Best Local Similarity 25.3%; Score 71.5; DB 1; Length 249;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 8 CSONEYFDSLHACIPCOLRCSNSTPPLTCORYC 41
Db 6 CPKQYWDSSRKSCVSCALTCQRS-QRTCTDFC 38

RESULT 13
Q5SU82_MOUSE PRELIMINARY; PRT; 249 AA.
AC Q5SU82;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 13b.
GN Name=TNFRsf13b; ORFNames=RP23-55I2.2-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Holt K.;
RR Submitted (FEB-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AL646093; CAI25896.1; -, Genomic_DNA.
KW Receptor.
SQ SEQUENCE    249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match
Best Local Similarity 25.3%; Score 71.5; DB 2; Length 249;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 8 CSONEYFDSLHACIPCOLRCSNSTPPLTCORYC 41
Db 6 CPKQYWDSSRKSCVSCALTCQRS-QRTCTDFC 38

RESULT 14
Q5OPT4_ENTHI PRELIMINARY; PRT; 1150 AA.
AC Q5OPT4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Receptor protein kinase, putative.
GN ORFNames=359.t00009;
OS Entamoeba histolytica HM-1.1MS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1.1MS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Barriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoef U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

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PCSK5_MOUSE
ID PCSK5_MOUSE STANDARD; PRT; 1877 AA.
AC Q04592; Q62040;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Protein convertase subtilisin/kexin type 5 precursor (EC 3.4.21.-)
DE (Protein convertase PCS5) (Subtilisin/kexin-like protease PCS) (PC6)
DE (Subtilisin-like proprotein convertase 6) (SPC6).
GN Name=PCSK5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE OF 330-1877 (ISOFORM PCS5B).
RC STRAIN=ICR; TISSUE=Intestine;
RX MEDLINE=93327934; PubMed=8335106; DOI=10.1016/0014-5793(93)80163-O;
RA Nakagawa T., Murakami K., Nakayama K.;
RT "Identification of an isoform with an extremely large Cys-rich region
of PC6, a Kex2-like processing endoprotease.";
RL FEBS Lett. 327:165-171(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM PCSA).
RC TISSUE=Brain, and Intestine;
RX MEDLINE=93224489; PubMed=8468318;
RA Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
RA Nakayama K.;
RT "Identification and functional expression of a new member of the
mammalian Kex2-like processing endoprotease family: its striking
structural similarity to PACE4.";
RL J. Biochem. 113:132-135(1993).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM PCSA).
RC TISSUE=Adrenal cortex;
RX MEDLINE=93342056; PubMed=8341687;
RA Lussan J., Vieau D., Hamelin J., Day R., Christien M., Seidah N.G.;
RT "cDNA structure of the mouse and rat subtilisin/kexin-like PC5: a
candidate proprotein convertase expressed in endocrine and
nonendocrine cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).
RN [4]
RP PARTIAL PROTEIN SEQUENCE, AND SUBCELLULAR LOCATION.
RX MEDLINE=97103178; PubMed=8947550; DOI=10.1083/jcb.135.5.1261;
RA De Bie T., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,
RA Bendayan M., Seidah N.G.;
RT "The isoforms of proprotein convertase PCS are sorted to different
subcellular compartments.";
RL J. Cell Biol. 135:1261-1275(1996).
RN [5]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=96293359; PubMed=8698813; DOI=10.1083/jcb.134.1.181;
RA Constam D.B., Calton M., Robertson E.J.;
RT "SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
morphogenetic proteins at distinct sites during embryogenesis.";
RL J. Cell Biol. 134:181-191(1996).
RN [6]
RP DEVELOPMENTAL EXPRESSION.
RX MEDLINE=97436919; PubMed=9291583;
RX DOI=10.1002/(SICI)1520-6408(1997)21:1<75::AID-DVG9>3.3.CO;2-T;
RA Rancourt S.L., Rancourt D.E.;
RT "Murine subtilisin-like proteinase SPC6 is expressed during embryonic
implantation, somitogenesis, and skeletal formation.";
RL Dev. Genet. 21:75-81(1997).
CC -!- FUNCTION: Likely to represent a widespread endoprotease activity
within the constitutive and regulated secretory pathway. Capable
of cleavage at the RX(K/R)R consensus motif. May be responsible
for the maturation of gastrointestinal peptides. May be involved
in the cellular proliferation of adrenal cortex via the activation
of growth factors.
CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their
proteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa

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CC can be any amino acid and Yaa is Arg or Lys.
CC -!- SUBCELLULAR LOCATION: PCSA is secreted through the regulated
CC secretory pathway. PCSB is a type I membrane protein localized to
CC a paranuclear post-Golgi network compartment in communication with
CC early endosomes.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=PCSB; Synonyms=Long;
CC IsoID=Q04592-1; Sequences=Displayed;
CC Name=PCSA; Synonyms=Short;
CC IsoID=Q04592-2; Sequence=VSP_005438, VSP_005439;
CC TISSUE SPECIFICITY: PCSA is expressed in most tissues but is most
CC abundant in the intestine and adrenals. PCSB is expressed in the
CC intestine, adrenals and lung but not in the brain.
CC -!- DEVELOPMENTAL STAGE: Weakly expressed throughout the embryo,
CC except in the developing nervous system, the ribs and the liver,
CC but markedly up-regulated at discrete sites during development. At
CC E6.5, prominent expression observed in differentiated decidua. At
CC E7.5, intense expression in extraembryonic endoderm, amnion and
CC nascent mesoderm. At E8.5, abundant expression in somites and yolk
CC sac followed by a confinement to dermamyotome compartment. Between
CC E9.5 and E11.5, abundant expression in AER (thickened ectodermal
CC cells of limb buds). At E12.5, expression in the limbs is confined
CC to the condensing mesenchym surrounding the cartilage. At this
CC stage, strong expression also detected in vertebral and facial
CC cartilage primordia and in the muscle of the tongue. At E16.5,
CC abundant expression in epithelial cells of the intestinal villi.
CC Isoform A is most abundant at all stages but significant levels of
CC isoform B occur at E12.5.
CC -!- DOMAIN: The propeptide domain acts as an intramolecular chaperone
CC assisting the folding of the zymogen within the endoplasmic
CC reticulum.
CC -!- DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain
CC sorting information. AC 1 directs TGN localization and interacts
CC with the TGN sorting protein PACS-1.
CC -!- SIMILARITY: Belongs to the peptidase S8 family.
CC -!- SIMILARITY: Contains 1 homo B/P domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; D17583; BAA04507.1; -; mRNA.
CC EMBL; D12619; BAA02143.1; -; mRNA.
CC EMBL; L14932; AAA74636.1; -; mRNA.
CC PIR; A48225; A48225.
CC PIR; S34583; S34583.
CC HSP; P23188; IP80.
CC MEROPS; S08.076; -.
CC Ensembl; ENSMUSG00000024713; Mus musculus.
CC MGI; MGI:97515; Pcsks.
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0015021; C:integral to membrane; TAS.
CC InterPro; IPR003460; AFP.
CC InterPro; IPR00209; Pept_S8_S53.
CC InterPro; IPR002884; PpProtnConvertsp.
CC Pfam; PF02420; AFP; 1.
CC Pfam; PF01483; P_protein; 1.
CC Pfam; PF00082; Peptidase_S8; 1.
CC PRINTS; PD00723; SUBTILISIN.
CC ProDom; PD000717; PpProtnConvertsp; 1.
CC PROSITE; PS00136; SUBTILASE ASP; 1.
CC PROSITE; PS00137; SUBTILASE HIS; 1.
CC PROSITE; PS00138; SUBTILASE_SER; 1.
CC Alternative splicing. Cleavage on pair of basic residues;
CC Direct protein sequencing; Glycoprotein; Hydrolase; Protease; Repeat;
CC Serine protease; Signal; Transmembrane; Zymogen.
CC SIGNAL 1 34
CC PROPEP 35 116
CC CHAIN 117 1877 Proprotein convertase subtilisin/kexin

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Matches 15; Conservative 8; Mismatches 19; Indels 20; Gaps 2

QY 4 MAGCQSQNYFDSLHACIPQLCRSS-----NTPPLTCQRYNASV 45  
Db : : | ||| :|| : : || : :  
75 ICSSCTDDFYLSLFGCFSCSHSSCSCTGSPSHDFCLTCRVGELESSPPSACP--CDLQJ 132

QY 46 TN 47  
Db |||  
133 TN 134

RESULT 18  
Q99ND0\_MOUSE  
ID Q99ND0\_MOUSE PRELIMINARY; PRT; 5374 AA.  
AC Q99ND0\_ MOUSE PRELIMINARY;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE ZAN [Zonadhesin].  
GN Name=Zan;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN NCBI [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/Sv;  
RX MEDLINE=211138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;  
RA Wilson M.D., Riemer D.C., Martindale D.W., Schnupf P., Boright A.P.,  
Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,  
Miller W., Koop B.F.;  
RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human  
chromosome 7q22 with the orthologous region on mouse chromosome 5.";  
RL Nucleic Acids Res. 29:1352-1365(2001).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/Sv;  
RA Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF312033; AAC28824.1; -; Genomic DNA.  
DR EMBL; AY046056; AAL04416.1; -; Genomic DNA.  
DR HSP; AY0248; IHX2.  
DR MG1; MG1.106656; Zan.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0007339; P:binding of sperm to zona pellucida; IEA.  
DR GO; GO:0007155; P:cell adhesion; IEA.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR003645; Fol\_N.  
DR InterPro; IPR006210; LEGF.  
DR InterPro; IPR000998; NAM.  
DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.  
DR InterPro; IPR003328; TILA\_Cyrich.  
DR InterPro; IPR001007; VMF\_C.  
DR InterPro; IPR001846; VWF\_D.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00629; NAM; 3.  
DR Pfam; PF01826; TIL; 25.  
DR Pfam; PF02345; TIL\_assoc; 25.  
DR Pfam; PF00094; VND; 4.  
DR SMART; SM00181; EGF; 2.  
DR SMART; SM00274; FOLN; 20.  
DR SMART; SM00137; NAM; 3.  
DR SMART; SM00214; VWC; 18.  
DR SMART; SM00216; VND; 4.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 18.  
DR PROSITE; PS50026; EGF\_3; 1.  
DR PROSITE; PS00740; NAM\_1; 1.  
DR PROSITE; PS50060; NAM\_2; 3.  
SQ SEQUENCE 5374 AA; 579545 MW; 90D2D8CFE5DE24EB CRC64;







FT CARBOHYD 3065 3065 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 3144 3144 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 3172 3172 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 3288 3288 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 3292 3292 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 3782 3782 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4005 4005 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4136 4136 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4243 4243 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4254 4254 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4335 4335 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4376 4376 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 4586 4586 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 5136 5136 N-linked (GlcNAc. . .) (Potential).  
FT CARBOHYD 5252 5252 N-linked (GlcNAc. . .) (Potential).  
FT DISULFID 5263 5274 By similarity.  
FT DISULFID 5268 5283 By similarity.  
FT DISULFID 5285 5294 By similarity.  
SQ SEQUENCE 5376 AA; 579913 MW; 0E44DB77DF2A2620 CRC64;

Query Match 24.6%; Score 69.5; DB 1; Length 5376;  
Best Local Similarity 36.8%; Pred. No. 54;  
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

QY 7 QCSQNEFYDLSLHACIP-CQLRCSNTP--PLTCQRYC 41  
DB 3299 QCTNSQFTDCLPSCVPCNSRCVTSVPSSCREGC 3336

RESULT 20  
Q22378 CASEL  
ID Q22378 CASEL PRELIMINARY; PRT; 966 AA.  
AC Q22378;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Hypothetical protein T10E10.4.  
GN ORFNames=T10E10.4;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Bristol N2;  
RG MEDLINE=99069613; PubMed=9851916;  
RX The C. elegans sequencing consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology";  
RL Science 282:2012-2018(1998).  
DR EMBL; U39644; AAA80360.2; -; Genomic\_DNA.  
DR PIR; T16840; T16840.  
DR HSSP; P10969; 1WGT.  
DR IntAct; Q22378; -.  
DR Ensembl; T10E10.4; Caenorhabditis elegans.  
DR WormBase; WBGene00020421; T10E10.4.  
DR WormPep; T10E10.4; CE25989.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008061; F:chitin binding; IEA.  
DR GO; GO:0006030; P:chitin metabolism; IEA.  
DR InterPro; IPR002557; Chitin bind\_Pera.  
DR InterPro; IPR006149; EB\_region.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR000794; Ketoacyl synth.  
DR InterPro; IPR003571; Snake toxin.  
DR InterPro; IPR006150; Worm\_Repeat\_1.  
DR Pfam; PF01607; CBM\_14; 2.  
DR Pfam; PF01683; EB; 1.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00289; WRI; 12.  
DR PROSITE; PS00606; B\_KETOACYL SYNTHASE; UNKNOWN\_1.  
DR PROSITE; PS00272; SNAKE TOXIN; UNKNOWN\_1.  
KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 966 AA; 102461 MW; B565A3CDD2521D9 CRC64;  
Query Match 24.2%; Score 68.5; DB 2; Length 966;  
Best Local Similarity 36.2%; Pred. No. 12;  
Matches 17; Conservative 10; Mismatches 15; Indels 5; Gaps 3;  
QY 7 QCSQNEFYDLSLHACIPCOLR--CSSNTPPLTCQRYCNASVTNSVKG 51  
DB 215 QCSQSTVFNSDLNVCVPLAIQNCDSSTQQPVC--C-SQVSSSCPG 258

RESULT 21  
Q6W4X9 HUMAN  
ID Q6W4X9 HUMAN PRELIMINARY; PRT; 1569 AA.  
AC Q6W4X9;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
DE Mucin glycoprotein (Fragment).  
GN Name=MUC6;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15081123; DOI=10.1016/j.ygeno.2003.11.003;  
RA Rousseau K., Byrne C., Kim Y.S., Gum J.R., Swallow D.M.,  
RA Toribara N.W.;  
RT "The complete genomic organization of the human MUC6 and MUC2 mucin genes";  
RL Genomics 83:936-939(2004).  
DR EMBL; AY312160; AAQ82434.1; -; mRNA.  
DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.  
DR InterPro; IPR006552; VWC\_out.  
DR InterPro; IPR001846; VWF\_D.  
DR Pfam; PF01826; TIL; 2.  
DR Pfam; PF00094; VMD; 3.  
DR SMART; SM00215; VWC\_out; 2.  
DR SMART; SM00216; VMD; 3.  
FT NON\_TER 1569 1569  
SQ SEQUENCE 1569 AA; 168065 MW; 6AEDBE143ECB855B CRC64;

Query Match 24.2%; Score 68.5; DB 2; Length 1569;  
Best Local Similarity 45.2%; Pred. No. 20;  
Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 8 CSQNEFYDLSLHACIPCOLRCSNTPPLTCQ 38  
DB 1179 CSQDEYFDHEEGVCVFCM-----PPTTPQ 1202

RESULT 22  
T13B HUMAN  
ID T13B HUMAN STANDARD; PRT; 293 AA.  
AC O14836; Q7Z6F5;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).  
DE Name=TNFRSF13B; Synonyms=TACI;  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).  
RC TISSUE=B-cell;  
RX MEDLINE=97458245; PubMed=9311921; DOI=10.1126/science.278.5335-138; von Buelow G.-U., Bram R.J.;







RC	TISSUE=Small intestine;
RA	Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;
RL	Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
RW	EMBL; AK223453; BAD97173.1; -; mRNA.
KW	Receptor.
FT	NON TER
SQ	SEQUENCE 293 AA; 31846 MW; D9EA2F2B83BF466D CRC64; Query Match 23.9%; Score 67.5; DB 2; Length 293; Best Local Similarity 30.6%; Pred.No.4.6; Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
Qy	8 CSQNEYFDLSLLHACIPCOLRCSSNTPPLTCORYCNA 43   : :           : : : : :   : :           : : : : :
Dd	34 CPBEQYWDPLLGTGCMCKTICNHQS-QRTCAAFCRS 68   : :           : : : : :   : :           : : : : :
RESULT 24	
QIDWC9 CAEBR PRELIMINARY;	PRT; 135 AA.
ID Q6OWC9; AC Q6OWC9;	
DT 25-OCT-2004 (TrEMBLrel. 28, Created)	
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)	
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)	
DE Hypothetical protein CBGI9174.	
GN Name=CBGI9174;	
OS Caenorhabditis briggsae.	
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;	
OC Rhabditidae; Peloderinae; Caenorhabditis.	
OX NCBI_TaxID=6238;	
RN [1]	
CC NUCLEOTIDE SEQUENCE.	
RP The C.briggsae Sequencing Consortium;	
RG Submitted (SPR-2003) to the EMBL/GenBank/DBJ databases.	
CC -!- CAUTION: The sequence shown here is derived from an	
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is	
CC preliminary data.	
CC EMBL; CAAC0100098; CAF72086.1; -; Genomic_DNA.	
DR InterPro; IPR006209; EGF like.	
DR InterPro; IPR002919; Prot_Inh_CR_TIL.	
DR Pfam; PF01826; TIL; 2.	
DR PROSITE; PS01186; EGF_2; UNKOWN 2.	
KW Hypothetical protein.	
SQ SEQUENCE 135 AA; 14981 MW; 74B21060EAF539B6 CRC64; Query Match 23.7%; Score 67; DB 2; Length 135; Best Local Similarity 34.8%; Pred.No.2.4; Matches 16; Conservative 5; Mismatches 19; Indels 6; Gaps 2;	
Qy	7 QCSENYFDSLHLHACIP-CQLRCSSNTPLTCORYCNASVTNSVKG 51   : :           : : : : :   : :           : : : : :
Dd	79 KCPNEQFRGGCTACEPTCE-----NPKPMACTKCQIINVQCCKG 119   : :           : : : : :   : :           : : : : :
RESULT 25	
O17496 ASCSU PRELIMINARY;	PRT; 532 AA.
ID O17496; AC O17496;	
DT 01-JAN-1998 (TrEMBLrel. 05, Created)	
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)	
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)	
DE Serotonin receptor.	
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoide).	
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;	
OC Ascarididae; Ascaris.	
OX NCBI_TaxID=6253;	
RN [1]	
CC NUCLEOTIDE SEQUENCE.	
RP MEDLINE=9933991; PubMed=10413046; DOI=10.1016/S0166-6851(99)00059-6;	
RA Huang X., Duran B., Diaz F., Xiao H., Messer W.S. Jr., Komuniecki R.;	
RT "Alternative-splicing of serotonin receptor isoforms in the pharynx	
RL and muscle of the parasitic nematode, Ascaris suum.";	
RT Mol. Biochem. Parasitol. 101:95-106(1999).	



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CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AF01000053; BAF68033.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0008468; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein.
SQ SEQUENCE 574 AA; 64223 MW; 9D344378077A91C8 CRC64;

Query Match 23.7%; Score 67; DB 2; Length 574;
Best Local Similarity 35.7%; Pred. No. 11;
Matches 20; Conservative 6; Mismatches 16; Indels 14; Gaps 3;

QY 7 QCSQNEYFDS-LLHACIPQLR-----CSSNTP-----PLTCORYCNASVTNS 48
DB 359 QAKKNYIVSHLLHGLTPCEDRYRESMPASSNTPSPDSRSPSPHYHNGNVNS 414

RESULT 27
Q4N599_THEPA
ID Q4N599_THEPA PRELIMINARY; PRT; 1562 AA.
AC Q4N599;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE ABC transporter, putative.
DE ORFNames=TF02_0391;
GN Theileria parva.
OS Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC Theileria.
OX NCBI_TaxID=5875;
RN [1]_TaxID=5875;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
RA Silva J.C., Utterback T.R., Feldblyum T.V., Perlea M., Allen J.,
RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA Venter J.C., Fraser C.M., Nene V.;
RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
RT lymphocytes.";
RL Science 309:134-137(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muguga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utterback T., Feldblyum T., Perlea M., Allen J., Taracha E.L.,
RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA Fraser C.M., Nene V.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAGK0100002; EAN32674.1; -; Genomic DNA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.
DR GO; GO:0004674; F:ATP binding; IEA.
DR GO; GO:0005524; F:peptidase activity; IEA.
DR GO; GO:0008468; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004674; F:ATP binding; IEA.
DR GO; GO:0005524; F:peptidase activity; IEA.
DR GO; GO:0008468; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.

Query Match 23.5%; Score 66.5; DB 2; Length 1562;
Best Local Similarity 30.9%; Pred. No. 35;
Matches 17; Conservative 12; Mismatches 9; Indels 17; Gaps 4;

QY 6 GQCSQNEYF-----DSLHACIPQLCRSSNTPPLTC--QRYCNASVT 46
DB 233 GLCYRRKFFNNVKGSLNVCNLSVHSCSP-ESKCSN--PLYCPRARRFQNSDIT 284

RESULT 28
Q55NL5_CRYNE
ID Q55NL5_CRYNE PRELIMINARY; PRT; 861 AA.
AC Q55NL5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
DE ORFNames=CNBH0730;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A; Bruno D., Miranda M., Fukushima M.,
RA Fung E., Hyman R.W., Rowley D., Davis R.W.;
RA Wickes B.L., Fu J.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAEY0100041; EAL19380.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 861 AA; 93346 MW; 8745729FBD869366 CRC64;

Query Match 23.3%; Score 66; DB 2; Length 861;
Best Local Similarity 34.8%; Pred. No. 22;
Matches 16; Conservative 6; Mismatches 24; Indels 0; Gaps 0;

QY 6 GQCSQNEYFDSLHACIPQLCRSSNTPPLTCQRYCNASVTNSVKG 51
DB 319 GTCSSGLYDSTSSCSCSPACSTCTGPTGSDCLSCASPRVNLQ 364

RESULT 29
Q26489_SPOFR
ID Q26489_SPOFR PRELIMINARY; PRT; 1299 AA.
AC Q26489;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endoprotease FURIN.
GN Name=FURIN;
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyrae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Sf9;
RA Cieplik M., Klenk H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z68888; CAA93116.1; -; mRNA.
DR F01; T43251; T43251.
DR HSSP; P23188; 1P8J.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; IEA.
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RP NUCLEOTIDE SEQUENCE.  
RX PubMed=14702039; DOI=10.1038/ng1285;  
RA Oka T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Iehi S.,  
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,  
RA Nagahori K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
RA Shirokari A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,  
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,  
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,  
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,  
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,  
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
RA Nomura Y., Togiyama S., Komai F., Hara R., Takeuchi K., Arita M.,  
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
RA Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isoqai T., Sugano S.,  
RA "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45(2004).  
DR EMBL; AK092010; BAC03789.1; -; mRNA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR011641; GCC2\_GCC3.  
DR Pfam; PF00431; CUB; 1; GCC2\_GCC3; 3.  
DR Pfam; PF07699; GCC2\_GCC3; 3.  
DR SMART; SM00042; CUB; 1.  
DR PROSITE; PS01180; CUB; 1.  
SQ SEQUENCE 581 AA; 64343 MW; D17BC28CDA1E4E1 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 581;  
Best Local Similarity 30.8%; Pred. No. 22;  
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;  
QY 7 QCSQNEYFDSLHACIPQL-----RCSNNT 32  
DB 336 QCSQHYNTSIHRCMGSYQDFRQNFCSRCPGNT 374

RESULT 33  
ID Q50LY7\_ENTHI PRELIMINARY; PRT; 799 AA.  
AC Q50LY7;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Protein kinase, putative (Fragment).  
GN ORFNames=650.t00003;  
OS Entamoeba histolytica HM-1:IMSS.  
OC Eukaryota; Entamoebidae; Entamoeba.  
OX NCBI\_TaxID=294381;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HM-1:IMSS;  
RX PubMed=15729342; DOI=10.1038/nature03291;  
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,  
RA Amadeo P., Rongaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,  
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,  
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,  
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,  
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,  
RA Eukaryota; Entamoebidae; Entamoeba.  
OX NCBI\_TaxID=294381;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HM-1:IMSS;  
RX PubMed=15729342; DOI=10.1038/nature03291;  
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,  
RA Amadeo P., Rongaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,  
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,  
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,  
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,  
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,

RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,  
RA Guillen N.G., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,  
RA Foster P.G., Sichert-Ponten T., Weber C., Singh U., Mukherjee C.,  
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,  
RA Fraser C.M., Hall N.;  
RT "The genome of the protist parasite Entamoeba histolytica.";  
RL Nature 433:865-868(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; AAFB01001427; EAL42605.1; -; Genomic\_DNA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR InterPro; IPR006212; Fuxin repeat.  
DR InterPro; IPR000719; Prot Kinase.  
DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
DR InterPro; IPR0022390; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00261; FU; 4.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00219; TYRK; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR ATP-binding; Kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; transferase.  
FT NON\_TER 1  
SQ SEQUENCE 799 AA; 91662 MW; D8BFE2F2E235989E CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 799;  
Best Local Similarity 34.3%; Pred. No. 31;  
Matches 12; Conservative 6; Mismatches 14; Indels 3; Gaps 1;  
QY 7 QCSQNEYFDSLHACIPQC---LRCSNTPPLTQC 38  
DB 136 RCDNYYDKELQSCVCSSECLTCSNKDICFTCK 170

RESULT 34  
ID Q50Y51\_ENTHI PRELIMINARY; PRT; 802 AA.  
AC Q50Y51;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE CXC-rich protein (Fragment).  
GN ORFNames=141.t00017;  
OS Entamoeba histolytica HM-1:IMSS.  
OC Eukaryota; Entamoebidae; Entamoeba.  
OX NCBI\_TaxID=294381;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=HM-1:IMSS;  
RX PubMed=15729342; DOI=10.1038/nature03291;  
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,  
RA Amadeo P., Rongaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,  
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,  
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,  
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,  
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,  
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,  
RA Guillen N.G., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,  
RA Foster P.G., Sichert-Ponten T., Weber C., Singh U., Mukherjee C.,  
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,  
RA Fraser C.M., Hall N.;  
RT "The genome of the protist parasite Entamoeba histolytica.";  
RL Nature 433:865-868(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.



DR	ENBL; AAFB01000471; EAL46536.1; -; Genomic_DNA.
FT	NON TER
SQ	SEQUENCE      802 AA;            91026 MW;    1425BF8514DED237 CRC64;
 Query Match                  22.8%; Score 64.5; DB 2; Length Best Local Similarity       34.3%; Pred No. 31; Matches     12; Conservative     6; Mismatches    14; Indels	
Oy	7 QCSONEYFDSLHACIPQC---LRCSNWTPLTCQ 38
Dd	: ::   ::   : 653 RCDDNYYYDKELQSCVGSSECLTCSNKDICFTCK 687
 RESULT 35	
QSCZB3_HUMAN	
ID	QSCZB3 HUMAN PRELIMINARY; PRT; 852 AA.
AC	QSCZB3;
DT	10-MAY-2005 (TrEMBLrel. 30, Created)
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DS	Hypothetical protein DKFP686B1223 [Fragment].
GN	Name=DKFP686B1223;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu-
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarr-
OC	Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Testis;
RG	The German cDNA Consortium;
RA	Poustka A., Albert R., Moosmayer P., Schupp I., Wellen-
RA	Mewes H.W., Weib B., Anid C., Osanger A., Fobo G., Han-
RL	Submitted (FEJ-2005) to the ENBL/GenBank/DBSJ database
DR	ENBL; CR36607; CAI56752.1; -; mRNA.
DR	GO; GO:0016020; C-membrane; IEA.
DR	GO; GO:0005509; F:calcium ion binding; IEA.
DR	GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR	GO; GO:0007596; P:blood coagulation; IEA.
DR	InterPro; IPRO00152; Asx_hydroxyl_S.
DR	InterPro; IPRO00859; CUB.
DR	InterPro; IPRO00742; EGF_2.
DR	InterPro; IPRO01881; EGF_Ca.
DR	InterPro; IPRO06209; EGF like.
DR	InterPro; IPRO11641; GCC2_GCC3.
DR	InterPro; IPRO06210; IEGF
DR	InterPro; IPRO01491; Thrombomodulin.
DR	Fam; PF00431; CUB; 1.
DR	Fam; PF00008; EGF; 5.
DR	Fam; PF07645; EGF_CA; 1.
DR	Fam; PF07699; GCC2_GCC3; 3.
DR	PRINTS; PRO0907; THROMBOMODULN.
DR	SMART; SM00042; CUB; 1.
DR	SMART; SM00181; EGF; 7.
DR	SMART; SM00179; EGF_CA; 4.
DR	PROSITE; PS00010; ASX_HYDROXYL; 3.
DR	PROSITE; PS01180; CUB; 1.
DR	PROSITE; PS01186; EGF_2; 4.
DR	PROSITE; PS50026; EGF_3; 3.
DR	PROSITE; PS01187; EGF_CA; 3.
KW	EGF-like domain; Hypothesized protein.
FT	NON TER
SQ	SEQUENCE      852 AA;            93812 MW;    514918COD126C7B2 CRC64;
 Query Match                  22.8%; Score 64.5; DB 2; Length Best Local Similarity       30.8%; Pred. No. 33; Matches     12; Conservative     5; Mismatches    9; Indels	
Oy	7 QCSONEYFDSLHACIPQCL-----RCSNNT 32
Dd	:: ::   : 607 CCSPGHYNTYSIHRCIRCAMGSOYDPFRQNCFSCPNGT 645

RESULT 36

Q8NAU9_HUMAN	Q8NAU9_HUMAN PRELIMINARY;	PRT;	880 AA.
AC	Q8NAU9;		
AD	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Hypothetical protein FLJ37473.		
GN	Name=SCUBE3;		
OS	homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	PubMed=14702039; DOI=10.1038/ngl1285;		
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,		
RA	Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,		
RA	Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,		
RA	Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,		
RA	Negahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,		
RA	Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., E.,		
RA	Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,		
RA	Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,		
RA	Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,		
RA	Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,		
RA	Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Horuta T.,		
RA	Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,		
RA	Nomura Y., Togliya S., Komai F., Hara K., Takeuchi K., Arita M.,		
RA	Imose N., Musahishino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,		
RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,		
RA	Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O.,		
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,		
RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,		
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,		
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,		
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,		
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,		
RA	Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,		
RA	Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,		
RA	Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,		
RA	Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,		
RA	Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,		
RA	Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;		
RT	"Complete sequencing and characterization of 21,243 full-length human		
RT	cDNAs."		
EL	Nat. Genet. 36:40-45(2004).		
DR	EMBL; AK092062; BAC03798.1; -; mRNA.		
DR	HSP; P35555; IMAGE.		
DR	Ensembl; ENSG00000146197; Homo sapiens.		
DR	HGNC; HGNC:13655; SCUBE3.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0005509; F:calcium ion binding; IEA.		
DR	GO; GO:0004988; F:transmembrane receptor activity; IEA.		
DR	GO; GO:0007596; P:blood coagulation; IEA.		
DR	InterPro; IPRO00152; Asx_hydroxyl_S.		
DR	InterPro; IPRO00859; CUB.		
DR	InterPro; IPRO00742; EGF 2.		
DR	InterPro; IPRO01881; EGF_Ca.		
DR	InterPro; IPRO06209; EGF_like.		
DR	InterPro; IPRO11641; GCC2 GCC3.		
DR	InterPro; IPRO01491; Thrombomodulin.		
DR	Pfam; PF00431; CUB; 1.		
DR	Pfam; PF00008; EGF; 4.		
DR	Pfam; PF07645; EGF CA; 2.		
DR	Pfam; PF07699; GCC2 GCC3; 3.		
DR	PRINTS; PR00907; THROMBOMODULN.		
DR	SMART; SM00042; CUB; 1.		
DR	SMART; SM00179; EGF CA; 3.		
DR	PROSITE; PS00010; ASX HYDROXYL; 3.		
DR	PROSITE; PS01180; CUB; 1.		
DR	PROSITE; PS01186; EGF 2; 5.		



```
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 3.
SQ SEQUENCE 880 AA; 97239 MW; F0BDE6B85266FDD60 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 880;
Best Local Similarity 30.8%; Pred. No. 34;
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 7 QCSQNEVFDLSLHACIPCOL-----RCSNT 32
||| : : : : :
Db 635 QCSQNEVFDLSLHACIPCOL-----RCSNT 32

RESULT 37
Q61V24 CAEBR PRELIMINARY; PRT; 919 AA.
AC Q61V24;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG05036.
GN Name=CBG05036;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; CAAC01000022; CAE61236.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR InterPro; IPR006149; EB_region.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR003571; Snake_toxin.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01607; CBM_14; 2.
DR Pfam; PF01683; EB_1.
DR SMART; SM00289; WRI_14.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 919 AA; 96816 MW; BE3EFC096CE53DFD CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 919;
Best Local Similarity 34.0%; Pred. No. 36;
Matches 16; Conservative 10; Mismatches 16; Indels 5; Gaps 3;

QY 7 QCSQNEVFDLSLHACIPCOLR--CSSNTPPLTCQYCNASVTNSVKG 51
||||| : : : : :
Db 163 QCSQSTVFNELSVCVPLATQNSDSTQPVCS--C-SQVSSSCP 206

RESULT 38
Q86U29 HUMAN
ID Q86U29_HUMAN PRELIMINARY; PRT; 992 AA.
AC Q86U29;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Signal peptide, CUB domain, EGF-like 3.
GN Name=SCUBE3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.

TISSUE=Pancreas;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Rosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bhak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052263; AAH52263.2; -; mRNA.
DR HSSP; P35555; IEMN.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB_2.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR011641; GCC2_GCC3.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF07645; EGF_CA; 4.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 10.
DR SMART; SM00179; EGF_CA; 7.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01186; CUB; 1.
DR PROSITE; PS01187; EGF_3; 6.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 6.
SQ SEQUENCE 992 AA; 109165 MW; 24093050738932E1 CRC64;

Query Match 22.8%; Score 64.5; DB 2; Length 992;
Best Local Similarity 30.8%; Pred. No. 38;
Matches 12; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 7 QCSQNEVFDLSLHACIPCOL-----RCSNT 32
||||| : : : : :
Db 747 QCSQGHYNTSIHRCIRCMGSIQDPFRQNFCSRCPGNT 785

RESULT 39
Q8IX30 HUMAN
ID Q8IX30_HUMAN PRELIMINARY; PRT; 993 AA.
AC Q8IX30;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE CUB and EGF containing protein (Signal peptide, CUB and EGF-like
domain containing protein 3 precursor) (ORTHUMP00000016250).
GN Name=SCUBE3; Synonyms=CEGF3; ORFNames=RP3-329A5.4-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
```







RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=Muga;	
RA	Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J., Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R., Haas B., Angiuoli S., Cresay T.H., Lu C., Suh B., Silva J.C., Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L., Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C., Fraser C.M., Nene V.;	
RL	Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.	
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.	
CC	EMBL; AAGK01000001; EAN33255.1; -; Genomic DNA.	
DR	SEQUENCE 1532 AA; 175403 MW; 33652005EAD2774 CRC64;	
Query Match	22.8%; Score 64.5; DB 2; Length 1532;	
Best Local Similarity	32.7%; Pred. No. 60;	
Matches	18; Conservative 7; Mismatches 13; Indels 17; Gaps 4;	
Qy	6 GQCQNEYFDSL-----LHACIPQLRCSNTPLTC--ORYCNASVT 46	
Db	223 GWCYRRKYFNNGSNLSVCGVLTCTSP--DSDCSRN--PLFCPARRYQNKDIT 274	
RESULT 42		
Q729F0 DESVH	PRELIMINARY; PRT; 494 AA.	
AC	Q729F0	
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE	Hydrogenase, iron-sulfur cluster-binding subunit, putative.	
GN	OrderedLocustNames=DVU2401;	
OS	Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303).	
OC	Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobibrionales;	
OC	Desulfobibrionaceae; Desulfobivrio.	
OC	NCBI_TaxID=882;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RX	PubMed=15077118; DOI=10.1038/nbt959;	
RA	Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Kolonay J.F., Eisen J.A., Ward N.D., Methe B.A., Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;	
RA	"The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough."	
RL	Nat. Biotechnol. 22:554-559(2004).	
DR	EMBL; AE017317; AAS96874.1; -; Genomic DNA.	
DR	TIGR; DVU2401; -	
DR	GO; GO:0005489; F:electron transporter activity; IEA.	
DR	GO; GO:0005506; F:iron ion binding; IEA.	
DR	GO; GO:0006118; P:electron transport; IEA.	
DR	GO; GO:0015948; P:methanogenesis; IEA.	
DR	InterPro; IPR001450; 4Fe4S_Fe_S_bd.	
DR	InterPro; IPR003813; FlpD.	
DR	InterPro; IPR006662; Thioredoxin.	
DR	Pfam; PF02662; FlpD; 1.	
DR	PRINTS; PR00421; THIOREDOXIN.	
DR	PROSITE; PS00198; 4Fe4S_FEREDOXIN; 2.	
KW	Complete proteome.	
SEQ	SEQUENCE 494 AA; 54143 MW; 904B524BF3BB118E CRC64;	
Query Match	22.6%; Score 64; DB 2; Length 494;	
Best Local Similarity	31.8%; Pred. No. 22;	
Matches	14; Conservative 7; Mismatches 13; Indels 10; Gaps 1;	
Qy	2 LOMAGQCSQNEYFDSLHACIPQLRCSNTPLTCORYCNASV 45	
Db	428 LHLAGRCTE-----CGECRACPVNIPVLALKQWNRSV 461	
RESULT 43		
Q410Y5 GIBZE	PRELIMINARY; PRT; 762 AA.	
ID	Q410Y5	
AC	Q410Y5	
DT	13-SEP-2005 (TrEMBLrel. 31, Created)	
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)	
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)	
DE	Hypothetical protein.	
GN	ORFNames=FG09123.1;	
OS	Gibberella zeae PH-1.	
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
OC	Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.	
OC	NCBI_TaxID=229533;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=PH-1;	
RA	Birren B., Nusbaum C., Abouelheil A., Allen N., Anderson S., Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L., Boukhalgalter B., Butler J., Calvo S.E., Camarata J., Chang J., Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArelano K., Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R., Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J., Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N., Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A., Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J., Matthews C., Mauceli E., McCarthy M., Meldrim J., Maneus L., Minova I., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R., Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D., Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S., Raghupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P., Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M., Talamas J., Tesfaye S., Theodore J., Topham K., Travers M., Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B., Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M., Lander E.;	
RA	"Fusarium graminearum genome sequence."	
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.	
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.	
CC	EMBL; AACM01000370; EAA78173.1; -; Genomic DNA.	
KW	Hypothetical protein.	
SEQ	SEQUENCE 762 AA; 84756 MW; 55B25D037F21A35A CRC64;	
Query Match	22.6%; Score 64; DB 2; Length 762;	
Best Local Similarity	43.3%; Pred. No. 34;	
Matches	13; Conservative 3; Mismatches 6; Indels 8; Gaps 2;	
Qy	20 ACIPQ---LRCSNTPLTCOR-----YC 41	
Db	17 ACVPCQSKKRCDSQSPCANCRRRDCIPYC 46	
RESULT 44		
Q54KF9 DICDI	PRELIMINARY; PRT; 300 AA.	
ID	Q54KF9	
AC	Q54KF9	
DT	13-SEP-2005 (TrEMBLrel. 31, Created)	
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)	
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)	
DE	Hypothetical protein.	
GN	ORFNames=DDB0219228;	
OS	Dictyostelium discoideum (slime mold).	
OC	Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.	
OC	NCBI_TaxID=44689;	



```

RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AX4;
RA Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA Sugngan R., Beriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA Loulsegged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA Urushihara H., Hernandez J., Rabinowitsch E., Steffen D., Sanders M.,
RA Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA Shauleky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA Chisholm R.L., Gibbs R., Loomis W.F., Platzner M., Kay R.R.,
RA Williams J., Dear P.H., Noegel A.A., Barrall B., Kuspa A.;
RT "The genome of the social amoeba Dictyostelium discoideum."
RL Nature 0:0-0(2005).
CC -i- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAP10100151; EAL63792.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 300 AA; 34482 MW; 9D863B38B2007E61 CRC64;

Query Match 22.4%; Score 63.5; DB 2; Length 300;
Best Local Similarity 31.4%; Pred. No. 15;
Matches 16; Conservative 8; Mismatches 22; Indels 5; Gaps 2;

QY 1 LMQMAGCQNEYFDSLHACIP-CQLRCSN-TPPLTCORYGNASVT 46
DB 90 LIQSMRCNQPSVFKLCSVLFPCCLYTNKVAVPLTCYEECTQSV 140

RESULT 45
Q9G045 GIALA
ID Q9G045 GIALA PRELIMINARY; PRT; 548 AA.
AC Q9G045
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Variant-specific surface protein M21-1 (Fragment).
GN Names=M21-1;
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mansouri M., Ey P.L.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF298862; AAC37862.1; -; Genomic_DNA.
DR HSPB; O16119; IEZG.
DR InterPro; IPR006058; 2Fe2S_fd_BS.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR006210; IEGF_.
DR InterPro; IPR002350; Prot_inh_Kazal.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00261; FU; 4.
DR PROSITE; PS00197; 2Fe2S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00282; KAZAL; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 548
FT NON_TER 548
SQ SEQUENCE 548 AA; 56557 MW; 578FE4FDA0A2CF0E CRC64;

Query Match 22.4%; Score 63.5; DB 2; Length 548;
Best Local Similarity 30.4%; Pred. No. 28;
Matches 17; Conservative 4; Mismatches 20; Indels 15; Gaps 2;

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QY 5 AGCQSQNEYFDSLHACIP-CQLRCSNTPPLTCQ-----RVCNASVTNSVK 50
DB 209 AGCCDQGTADPTTGCKPCGI-----TDCATCEYNATISQPKCTCTSSNNWK 259

RESULT 46
Q68FG9 MOUSE
ID Q68FG9_MOUSE PRELIMINARY; PRT; 827 AA.
AC Q68FG9
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Scube3 protein (Fragment).
DR Name=Scube3;
GN Name=Scube3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore J., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC079849; AAH79849.1; -; mRNA.
DR MGI; MGI:3045253; Scube3.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011641; GCC2_GCC3.
DR InterPro; IPR006210; IEGF_.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF07699; GCC2_GCC3; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 9.
DR SMART; SM00179; EGF_CA; 7.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00266; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 4.
DR EGF-like domain.
FT NON_TER 1
FT NON_TER 827 AA; 90870 MW; DF6BB3337B4CE91D CRC64;
SQ SEQUENCE 827 AA; 90870 MW; DF6BB3337B4CE91D CRC64;

```



RESULT 48  
Q4UE95 THEAN  
ID Q4UE95 THEAN PRELIMINARY; PRT; 1563 AA.  
AC Q4UE95;

RN NUCLEOTIDE SEQUENCE (ISOFORM 1), AND DISEASE.  
 RC STRAIN=AJY; 75520; PubMed=11591325; DOI=10.1016/S0960-9822(01)00481-X;  
 RX MEDLINE=21475520;  
 RA Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Hartless S.M.,  
 RA Cancro M.P., Grewal I.S., Dixit V.M.;  
 RA "Identification of a novel receptor for B lymphocyte stimulator that  
 RT is mutated in a mouse strain with severe B cell deficiency.";  
 RT



RL Curr. Biol. 11:1547-1552(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RC STRAIN=57BL/6J; TISSUE=Small intestine;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanpin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer J.S.,

RA Gaasterland T., Gariboldi M., Giessi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierzki R.M., King P.A.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wyszaw-Boris A., Yanagisawa M., Yang L., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RP FUNCTION

RX MEDLINE=21614654; PubMed=11747827; DOI=10.1016/S0960-9822(01)00598-X;

RA Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,

RA Hilbert D.M., Hayes C.E., Cancro M.P.;

RT "Competition for BlyS-mediated signaling through Bcnd/BR3 regulates

RT peripheral B lymphocyte numbers.";

RL Curr. Biol. 11:1986-1989(2001).

CC -I- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BlyS.

CC Promotes the survival of mature B-cells and the B-cell response.

CC -I- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC -I- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q9BD0-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q9BD0-2; Sequence=VSP\_006506;

CC -I- TISSUE SPECIFICITY: Highly expressed in spleen and testis;

CC detected at lower levels in lung and thymus.

CC -I- DISEASE: Defects in Tnfrsf13c are a cause of severe B-cell

CC deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion

CC in the BAFF gene leading to an altered C-terminus. The mutant RNA

CC is not detectable. B-cell lymphopoiesis is normal, but the life

CC span of peripheral B-cells is much reduced.

CC -I- SIMILARITY: Contains 1 TNFR-Cys repeat.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

DR ENBL; AF373847; AAK91827.1; -; mRNA.

DR ENBL; AK008142; BAB25490.1; -; mRNA.

DR HSSP; Q96RJ3; 10QE.

DR MGI; MGI:1919299; Tnfrsf13c.

DR GO; GO:0009897; C:external side of plasma membrane; IDA.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR GO; GO:0031296; P:B cell costimulation; IDA.

DR GO; GO:0001782; P:B cell homeostasis; IMP.

DR GO; GO:0030890; P:positive regulation of B cell proliferation; IDA.

DR GO; GO:0045078; P:positive regulation of interferon-gamma bio. .; IMP.

DR GO; GO:0042102; P:positive regulation of T cell proliferation; IDA.

DR GO; GO:0050776; P:regulation of immune response; IMP.

DR GO; GO:0031295; P:T cell costimulation; IDA.

DR InterPro; IPR001368; TNFR\_c6.

DR PROSITE; PS00552; TNFR\_NGFR\_1; FALSE\_NEG.

DR PROSITE; PS00500; TNFR\_NGFR\_2; FALSE\_NEG.

DR Alternative splicing; Glycoprotein; Immune response; Receptor;

KW Signal-anchor; Transmembrane.

FT TOPO\_DOM 1 71 Extracellular (Potential).

FT TRANSMEM 72 92 Signal-anchor for type III membrane protein (Potential).

FT TOPO\_DOM 93 175 Cytoplasmic (Potential).

FT REPEAT 21 38 TNFR-Cys (incomplete).

FT CARBOHYD 23 23 N-linked (GlcNAc . .) (Potential).

FT DISULFID 22 35 By similarity.

FT DISULFID 27 38 By similarity.

FT VARSPLIC 133 143 Missing (in isoform 2).

FT /FTID=VSP\_006506.

SQ SEQUENCE 175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;

Query Match 22.3%; Score 63; DB 1; Length 175;

Best Local Similarity 50.0%; Pred. No. 9.8; Indels 0; Gaps 0;

Matches 10; Conservative 4; Mismatches 6;

QY 7 QCSQNEYFDSLHLHACIPCOL 26

DB 21 QCNQTECFDPLVRNCVSCSEL 40

RESULT 50

Q8R4W8 MOUSE PRELIMINARY; PRT; 175 AA.

AC Q8R4W8

DT 01-JUN-2002 (TRENBLrel. 21, Created)

DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE TRAF3 binding protein.

GN Name=Tnfrsf13c.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxId=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Mizuno K., Irie S., Sato T.-A.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR ENBL; AF350257; AAL83914.1; -; mRNA.

DR HSSP; Q96RJ3; 10QE.

DR MGI; MGI:1919299; Tnfrsf13c.

DR GO; GO:0009897; C:external side of plasma membrane; IDA.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR GO; GO:0001782; P:B-cell homeostasis; IMP.

DR GO; GO:0030890; P:positive regulation of B-cell proliferation; IDA.

DR GO; GO:0045078; P:positive regulation of interferon-gamma bio. .; IMP.

DR GO; GO:0042102; P:positive regulation of T-cell proliferation; IDA.

DR GO; GO:0050776; P:regulation of immune response; IMP.

SQ SEQUENCE 175 AA; 18846 MW; B64EFP4B52EE93B1 CRC64;

Query Match 22.3%; Score 63; DB 2; Length 175;

Best Local Similarity 50.0%; Pred. No. 9.8; Indels 0; Gaps 0;

Matches 10; Conservative 4; Mismatches 6;

QY 7 QCSQNEYFDSLHLHACIPCOL 26

DB 21 QCNQTECFDPLVRNCVSCSEL 40

RESULT 51

Q678B7\_9VIRU



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ID Q678B7_9VIRU PRELIMINARY; PRT; 289 AA.
AC Q678B7_2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
DE Lymphocystis disease virus - isolate China.
OS Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.
OX NCBI_TaxID=256729;
[1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
RX Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;
RA "Complete Genome Sequence of Lymphocystis Disease Virus Isolated from
RT China.";
RL J. Virol. 78:6982-6994 (2004).
DR EMBL; AY380826; AAU10940.1; -; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Hypothetical protein.
SQ SEQUENCE 289 AA; 32691 MW; 26B6114D4D5D6C3F CRC64;

Query Match 22.3%; Score 63; DB 2; Length 289;
Best Local Similarity 39.4%; Pred. No. 16;
Matches 13; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Oy 7 QCSQNEYPDSLHACIPQLRCSSNTPPLTCOR 39
Db 79 QCRQYYDPSESCFPCSCNESSKVKVTCNR 111

RESULT 52
O8CFA7_MOUSE
ID Q8CFA7_MOUSE PRELIMINARY; PRT; 341 AA.
AC Q8CFA7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Germ cell specific zinc finger protein.
GN Name=zfp393; Synonyms=Gzf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=129/SV x C57BL; TISSUE=Testis;
RX MEDLINE=22239718; PubMed=12351194; DOI=10.1016/S0925-4773(02)00258-7;
RA Yan W., Burns K.H., Ma L., Matzuk M.W.;
RT "Identification of zfp393, a germ cell-specific gene encoding a novel
RT zinc finger protein.";
RL Mech. Dev. 118:233-239 (2002).
DR EMBL; AF508984; RAN31656.1; -; mRNA.
DR HSPF; P08047; ISPL.
DR Ensembl; ENSMUSG00000048626; Mus musculus.
DR MGI; MGI:2181068; zfp393.
DR GO; GO:0007276; P:gametogenesis; IDA.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 3.
DR ProDom; PD0000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
KW Metal-binding; Nuclear_protein; Zinc; Zinc-finger.
SQ SEQUENCE 341 AA; 38074 MW; AC82D4C0472B054C CRC64;

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Query Match 22.3%; Score 63; DB 2; Length 341;
Best Local Similarity 28.2%; Pred. No. 19;
Matches 11; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

Oy 7 QCSQNEYPDSLHACIPQLRCSSNTPPLTCORYNASV 45
Db 59 RCNREWSQLRSUPEHGVRCPQLAPIPFQNYCORSI 97

RESULT 53
Q9D351_MOUSE
ID Q9D351_MOUSE PRELIMINARY; PRT; 341 AA.
AC Q9D351;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Mus musculus in vitro fertilized eggs cDNA, RIKEN full-length enriched
DE library, clone:7420700M05 product:weakly similar to DJ67558.1 (NOVEL
DE ZINC FINGER PROTEIN).
GN Name=zfp393;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gibbs C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bargh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).

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RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK018361; BAB31177.1; -; mRNA.
DR HSP; P08047; ISP1.
DR Ensembl; ENSMUSG00000048626; Mus musculus.
DR MGI; MGI:2181068; Zfp393.
DR GO; GO:0007276; P:gametogenesis; IDA.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF000096; zf-C2H2; 2.
DR ProDom; PD000003; Znf_C2H2; 3.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
DR Metal-binding; Nuclear protein; Zinc; Zinc-finger.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 341 AA; 38094 MW; A332DB7FE231AF6C CRC64;

Query Match 22.3%; Score 63; DB 2; Length 341;
Best Local Similarity 28.2%; Pred. No. 19;
Matches 11; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 7 QCSQNEVFDLLHACIPQLRCSSNTPPLTCQRYCNASV 45
Db 59 RCNEREWESQLRSLPEHGVRCPSQLAPFPQNYCORSI 97

RESULT 54
Q6P233 MOUSE
ID Q6P233_MOUSE PRELIMINARY; PRT; 341 AA.
AC Q6P233
DT 03-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Zinc finger protein 393.
GN Name=Zfp393;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Maman A., Rodriguez S., Sanchez A.,
RA Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
RG NIH MGC Project;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064748; RAH64748.1; -; mRNA.
DR Ensembl; ENSMUSG00000048626; Mus musculus.
DR MGI; MGI:2181068; Zfp393.
DR GO; GO:0007276; P:gametogenesis; IDA.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF000096; zf-C2H2; 3.
DR ProDom; PD000003; Znf_C2H2; 2.
DR SMART; SM00355; Znf_C2H2; 3.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 3.
KW Metal-binding; Nuclear protein; Zinc; Zinc-finger.
SQ SEQUENCE 341 AA; 38046 MW; 62BB8F5059125A2B CRC64;

Query Match 22.3%; Score 63; DB 2; Length 341;
Best Local Similarity 28.2%; Pred. No. 19;
Matches 11; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 7 QCSQNEVFDLLHACIPQLRCSSNTPPLTCQRYCNASV 45
Db 59 RCNEREWESQLRSLPEHGVRCPSQLAPFPQNYCORSI 97

RESULT 55
Q5JSG7_HUMAN
ID Q5JSG7_HUMAN PRELIMINARY; PRT; 1560 AA.
AC Q5JSG7
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Protease inhibitor 1, last annotation update)
GN Name=PCSK5; ORFName=RP11-422N19.4-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mashreghi-Mohammadi M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pelan S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Peck A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL391868; CA140675.1; -; Genomic_DNA.
DR EMBL; AL589653; CA140809.1; -; Genomic_DNA.
DR EMBL; AL353607; CA141234.1; -; Genomic_DNA.

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RESULT 57  
Q81Z06 HUMAN  
ID Q81Z06\_HUMAN PRELIMINARY; PRT; 985 AA.  
AC Q81Z06;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OC NCBI\_TaxID=9606;  
[1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung.  
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse J.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
PA















Chen E., Maiffa M.A., Marciussen K., McCombie W.K.;  
"Sequence and analysis of chromosome 4 of the plant Arabidopsis  
RA  
RT



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RA  Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA  George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA  Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA  Patel S., Phouanavong S., Wan K., Wu C., Lewis S.E., Rubin G.M.,
RA  Celniker S.;
RL  Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AY071103; AAU48725.1; -; mRNA.
DR  Ensembl: CG7348; Drosophila melanogaster.
DR  FlyBase: FBgn0036940; CG7348.
DR  GO: GO:0005576; C:extracellular region; IEA.
DR  GO: GO:0008061; F:chitin binding; IEA.
DR  GO: GO:0006030; P:chitin metabolism; IEA.
DR  InterPro: IPR002557; Chitin_bind_Pera.
DR  Pfam: PF01607; CBM_14; 4.
DR  SMART: SM00494; ChitBD2; 3.
DR  PROSITE: PS0940; CHIT BIND II; 4.
SQ  SEQUENCE 353 AA; 39712 MW; F5AB27B9A6FF9921 CRC64;

Query Match      21.7%; Score 61.5; DB 2; Length 353;
Best Local Similarity 28.1%; Pred. No. 31;
Matches 16; Conservative 8; Mismatches 20; Indels 13; Gaps 3;

QY  7 QCSQNEYFDSLHACIPCOL-----RCSSNTP-----PLTCQRY--CNASVTNSVK 50
Db  118 KCSVGNVYDFPARRACLPVAISAHAQCSVLDPNATLANPSCDCTYFRCHSGQAEVLQ 174
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 67
Q9VW81 DROME
ID  Q9VW81 DROME PRELIMINARY; PRT; 353 AA.
AC  Q9VW81.
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  CG7348-PA.
GN  Names=CG7348; ORFNames=CG7348;
OS  Drosophila melanogaster (fruit fly)
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC  Ephydroidea; Drosophilidae; Drosophila.
OX  NCBI_TaxID=7227;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA  Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA  Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA  Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA  Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA  Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA  Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA  Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA  Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA  Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA  Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA  de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA  Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA  Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA  Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasse K.,
RA  Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA  Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA  Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA  Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA  Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA  Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA  Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA  Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA  Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA  Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA  Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA  Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA  Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA  Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA  Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA  Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA  Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA  Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA  Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA  Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT  "The genome sequence of Drosophila melanogaster.";
RL  Science 287:2185-2195(2000).
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22426065; PubMed=12537568;
RA  Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA  Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA  George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA  Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA  Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA  Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT  "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT  melanogaster euchromatic genome sequence.";
RL  Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN  [3]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22426070; PubMed=12537573;
RA  Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirkas R.,
RA  Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA  Ashburner M., Celniker S.E.;
RT  "The transposable elements of the Drosophila melanogaster euchromatin:
RT  a genomics perspective.";
RL  Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN  [4]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=22426069; PubMed=12537572;
RA  Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA  Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA  Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA  Betencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA  Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA  Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA  Lewis S.E.;
RT  "Annotation of the Drosophila melanogaster euchromatic genome: a
RT  systematic review.";
RL  Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN  [5]
RP  NUCLEOTIDE SEQUENCE.
RG  Berkeley Drosophila Genome Project;
RA  Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA  Hoskins R., Stapleton M., Pacleb J., Park S., Svirkas R., Smith E.,
RA  Yu C., Rubin G.;
RT  "Drosophila melanogaster release 4 sequence.";
RL  Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN  [6]
RP  NUCLEOTIDE SEQUENCE.
RG  FlyBase;
RL  Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AE003514; AAF49068.1; -; Genomic DNA.
DR  Ensembl: CG7348; Drosophila melanogaster.
DR  FlyBase: FBgn0036940; CG7348.
DR  GO: GO:0005576; C:extracellular region; IEA.
DR  GO: GO:0008061; F:chitin binding; IEA.
DR  GO: GO:0006030; P:chitin metabolism; IEA.
DR  InterPro: IPR002557; Chitin_bind_Pera.
DR  Pfam: PF01607; CBM_14; 4.
DR  SMART: SM00494; ChitBD2; 3.
DR  PROSITE: PS0940; CHIT BIND II; 4.
SQ  SEQUENCE 353 AA; 39713 MW; 1C66916504FD130B CRC64;

Query Match      21.7%; Score 61.5; DB 2; Length 353;
Best Local Similarity 28.1%; Pred. No. 31;
Matches 16; Conservative 8; Mismatches 20; Indels 13; Gaps 3;

QY  7 QCSQNEYFDSLHACIPCOL-----RCSSNTP-----PLTCQRY--CNASVTNSVK 50
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 118 KCSVNFDPPARRACLPVAISAHQCSVLDPDNATLANPSCDCTFYRCHSGQAEVLQ 174
RESULT 68
ID Q61LZ9 CAEBR PRELIMINARY; PRT; 432 AA.
AC Q61LZ9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG08690.
GN Name=CBG08690;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium.
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; CAAC0100037; CAB54085.1; -; Genomic_DNA.
DR InterPro; IPR009475; DUF1096.
DR InterPro; IPR003341; DUF139_Cys-rich.
DR Pfam; PF02363; C triplex; 10.
DR Pfam; PF06493; DUF1096; 1.
KW Hypothetical protein.
SQ SEQUENCE 432 AA; 46913 MW; CIDBALE739E9B5F6 CRC64;
Query Match 21.7%; Score 61.5; DB 2; Length 432;
Best Local Similarity 31.9%; Pred. No. 38;
Matches 15; Conservative 4; Mismatches 15; Indels 13; Gaps 2;
Qy 3 QMAGQCSQNEYFDSLHACIPQLRC-SSNTPPLTCORYCNASVTNS 48
Db 361 QCASQCEQS-----CQOCVQQQPPAAQCQTACQSCSNS 395
RESULT 69
ID Q22423 CAEBL PRELIMINARY; PRT; 483 AA.
AC Q22423;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T12A7.2.
GN ORFNames=T12A7.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; Z73911; CAA98142.2; -; Genomic_DNA.
DR PIR; G88846; G88846.
DR PIR; T24856; T24856.
DR HSP; P00750; ITPG.
DR Ensembl; T12A7.2; Caenorhabditis elegans.
DR WormBase; WBGene00011723; T12A7.2.
DR WormPep; T12A7.2; CE23979.
DR InterPro; IPR00742; EGF.
DR InterPro; IPR006209; EGF-like.
DR Smart; SM00181; EGF; 1.
DR PROSITE; PS00022; EGF_1; 3.
```







Db	132	CNSTQLFDSTWNNNGSNNTBEGNDTIILPCRKIQIINNWKVKAMVTPPTSGQIRCSSNI	191
Qy	46	TNSV 49	
Db	192	TGLI 195	
RESULT 73			
Q4NR8	TETNG		
ID	Q4NR8	TETNG PRELIMINARY;	PRT; 354 AA.
AC	Q4NR8		
DT	13-SEP-2005	(TrEMBLrel. 31, Last sequence update)	
DT	13-SEP-2005	(TrEMBLrel. 31, Last annotation update)	
DE	Chromosome 2	SCAF15010, whole genome shotgun sequence.	
DE	(Fragment).		
GN	ORFNames=GSTENG00031440001;		
OS	Tetraodon nigroviridis (Green puffer).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes;		
OC	Tetraodontidae; Tetraodontidae; Tetraodon.		
OX	NCBI_TaxID=99883;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE		
RA	Jailion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,		
RA	Maucci E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,		
RA	Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,		
RA	Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,		
RA	Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,		
RA	Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,		
RA	Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,		
RA	Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,		
RA	Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,		
RA	Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,		
RA	Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,		
RA	Winkler P., Lander E.S., Weissenbach J., Roest Colluis H.,		
RT	"Genome duplication in the teleost fish Tetraodon nigroviridis reveals		
RT	the early vertebrate proto-karyotype."		
RL	Nature 431:946-957(2004).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE		
RG	Genoscope; Whitehead Institute Centre for Genome Research;		
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.		
CC	!- CAUTION: The sequence shown here is derived from an		
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is		
CC	preliminary data.		
DR	EMBL; CAAE01015010; CAG09964.1; -; Genomic_DNA.		
FT	NON_TER 1 354		
FT	NON_TER 354 354		
SQ	SEQUENCE 354 AA; 39608 MW; CBEB4C670F2BDC03 CRC64;		
Query Match 21.6%; Score 61; DB 2; Length 354;			
Best Local Similarity 30.6%; Pred. No. 36;			
Matches 15; Conservative 7; Mismatches 21; Indels 6; Gaps 2;			
Qy	3	QMACGCSQNEYFDSLLHACIPQLRCSSNTPTLTQRYCNASVTNSVKG 51	
Db	279	QFCGCLNRYGEEVDRALLDPENRC----PP--CRGICNGCFRCARDG 321	
RESULT 74			
Q4ZLE4	PSESY		
ID	Q4ZLE4	PSESY PRELIMINARY;	PRT; 815 AA.
AC	Q4ZLE4		
DT	13-SEP-2005	(TrEMBLrel. 31, Created)	
DT	13-SEP-2005	(TrEMBLrel. 31, Last sequence update)	
DE	Hypothetical protein.		
GN	ORFNames=Peysr 5001;		
OS	Pseudomonas syringae pv. syringae B728a.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		
OC	Pseudomonadaceae; Pseudomonas.		
Query Match 21.4%; Score 60.5; DB 2; Length 339;			
Best Local Similarity 31.8%; Pred. No. 39;			
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;			
Qy	8	CSQNEYFDSLLHACIPQLRCSSNTPTLTQRYCNASVTNSVKG 51	
Db	108	CMNDGYNFTLGRGV-----CTSNVGEHCIFRCNSGVNKTSG 146	
Search completed: December 21, 2005, 16:10:48			

OX	NCBI_TaxID=205918;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE		
RC	STRAIN=B728a;		
RG	DOS Joint Genome Institute;		
RA	Chain P., Larimer F., Dibartolo G., Copeland A., Lykidis A., Trong S.,		
RA	Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Dettler J.C.,		
RA	Land M., Richardson P.M., Kyripides N.C., Ivanova N.;		
RT	"Comparison of two complete genome sequences of Pseudomonas syringae		
RT	pv. syringae B728a and pv. tomato DC3000."		
RL	Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE		
RC	STRAIN=B728a;		
RA	Loper J.;		
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE		
RC	STRAIN=B728a;		
RA	Feil H., Feil W.S., Lindow S.E.;		
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; CP000075; AAY40028.1; -; Genomic_DNA.		
KW	Hypothetical protein.		
SQ	SEQUENCE 815 AA; 90781 MW; 8A638679CAF477D6 CRC64;		
Query Match 21.6%; Score 61; DB 2; Length 815;			
Best Local Similarity 30.4%; Pred. No. 85;			
Matches 17; Conservative 9; Mismatches 22; Indels 8; Gaps 2;			
Qy	4	MAGCSQNEYFDSLL-----HACIPQLRCSSNTPTLTQCO---RYCNASVTNSVKG 51	
Db	10	LAGNGSSAEWDDALPHFQHQHVPLELPGFGNPPQPCEDLASAYADALLATVKG 65	
RESULT 75			
Q61S18	CAEBR		
ID	Q61S18	CAEBR PRELIMINARY;	PRT; 339 AA.
AC	Q61S18;		
DT	25-OCT-2004	(TrEMBLrel. 28, Created)	
DT	25-OCT-2004	(TrEMBLrel. 28, Last sequence update)	
DT	25-OCT-2004	(TrEMBLrel. 28, Last annotation update)	
DE	Hypothetical protein CBG06165 (Fragment).		
GN	Names=CBG06165;		
OS	Caenorhabditis briggsae.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6238;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE		
RG	The C. briggsae Sequencing Consortium;		
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; CAAC01000028; CAE62124.1; -; Genomic_DNA.		
DR	InterPro; IPR000742; EGF_2.		
DR	InterPro; IPR006209; EGF-like.		
DR	InterPro; IPR006210; IEGF.		
DR	SMART; SM00181; EGF_2.		
DR	PROSITE; PS00022; EGF_1; 3.		
DR	PROSITE; PS01186; EGF_2; 1.		
DR	PROSITE; PS00026; EGF_3; 1.		
KW	EGF-like domain; Hypothetical protein.		
FT	NON_TER 339		
SQ	SEQUENCE 339 AA; 37704 MW; 2469B38E5B995B43 CRC64;		
Query Match 21.4%; Score 60.5; DB 2; Length 339;			
Best Local Similarity 31.8%; Pred. No. 39;			
Matches 14; Conservative 5; Mismatches 20; Indels 5; Gaps 1;			
Qy	8	CSQNEYFDSLLHACIPQLRCSSNTPTLTQRYCNASVTNSVKG 51	
Db	108	CMNDGYNFTLGRGV-----CTSNVGEHCIFRCNSGVNKTSG 146	



Job time : 191.8 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 21, 2005, 16:11:46 ; Search time 5.6 Seconds

(without alignments)

43.302 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_8\_41

Perfect score: 201

Sequence: 1 CSQNEVFDLSLLHACIPQLRCSNTPPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New:

1: /cgn2\_6/ptodata/2/pubaa/US08 NEW PUB.pcp.\*  
2: /cgn2\_6/ptodata/2/pubaa/US06 NEW PUB.pcp.\*  
3: /cgn2\_6/ptodata/2/pubaa/US07 NEW PUB.pcp.\*  
4: /cgn2\_6/ptodata/2/pubaa/PCT NEW PUB.pcp.\*  
5: /cgn2\_6/ptodata/2/pubaa/US09 NEW PUB.pcp.\*  
6: /cgn2\_6/ptodata/2/pubaa/US10 NEW PUB.pcp.\*  
7: /cgn2\_6/ptodata/2/pubaa/US11 NEW PUB.pcp.\*  
8: /cgn2\_6/ptodata/2/pubaa/US60 NEW PUB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	40	US-10-967-527A-9	Sequence 9, Appli
2	201	100.0	184	US-10-742-634-9	Sequence 9, Appli
3	201	100.0	184	US-10-967-527A-8	Sequence 8, Appli
4	136	67.7	185	US-10-967-527A-10	Sequence 10, Appli
5	71.5	35.6	249	US-10-967-527A-21	Sequence 21, Appli
6	66.5	33.1	48	US-10-967-527A-20	Sequence 20, Appli
7	66.5	33.1	292	US-10-967-527A-19	Sequence 19, Appli
8	66.5	33.1	293	US-10-742-634-7	Sequence 7, Appli
9	59.5	29.6	897	US-11-137-465-35	Sequence 35, Appli
10	59.5	29.6	993	US-11-137-465-36	Sequence 36, Appli
11	58	28.9	175	US-10-967-527A-7	Sequence 7, Appli
12	53.5	26.6	5405	US-11-108-172-1116	Sequence 1116, Ap
13	50	24.9	161	US-11-126-126-2	Sequence 2, Appli
14	50	24.9	455	US-11-182-946-3	Sequence 3, Appli
15	50	24.9	909	US-11-076-187-4	Sequence 4, Appli
16	49.5	24.6	997	US-11-113-424-37	Sequence 37, Appli
17	49	24.4	42	US-10-967-527A-18	Sequence 18, Appli
18	49	24.4	231	US-11-132-285-61	Sequence 61, Appli
19	49	24.4	297	US-10-967-527A-17	Sequence 17, Appli
20	48	23.9	49	US-10-967-527A-15	Sequence 15, Appli
21	48	23.9	447	US-10-967-527A-14	Sequence 14, Appli
22	47.5	23.6	1798	US-10-995-561-1033	Sequence 1033, Ap
23	47.5	23.6	1798	US-10-995-561-1034	Sequence 1034, Ap
24	47	23.4	349	US-11-182-946-13	Sequence 13, Appli
25	47	23.4	3690	US-10-995-561-1016	Sequence 1016, Ap

26	47	23.4	3714	6	US-10-995-561-1015	Sequence 1015, Ap
27	47	23.4	3717	6	US-10-821-234-1076	Sequence 1076, Ap
28	46.5	23.1	350	7	US-11-153-880-4	Sequence 4, Appli
29	46.5	23.1	419	7	US-11-064-769-2	Sequence 2, Appli
30	46.5	23.1	419	7	US-11-153-880-2	Sequence 2, Appli
31	46.5	23.1	419	7	US-11-064-774A-22	Sequence 22, Appli
32	46.5	23.1	487	7	US-11-147-047-50	Sequence 50, Appli
33	46.5	23.1	883	6	US-10-770-726-57	Sequence 57, Appli
34	46.5	23.1	961	7	US-11-113-424-35	Sequence 35, Appli
35	46.5	23.1	964	7	US-11-137-465-58	Sequence 58, Appli
36	46.5	23.1	965	7	US-11-113-424-2	Sequence 2, Appli
37	46.5	23.1	965	7	US-11-147-047-51	Sequence 51, Appli
38	46.5	23.1	997	7	US-11-080-991-50	Sequence 50, Appli
39	46.5	23.1	999	7	US-11-113-424-36	Sequence 36, Appli
40	46	22.9	63	7	US-11-078-735-12	Sequence 12, Appli
41	46	22.9	63	7	US-11-078-735-13	Sequence 13, Appli
42	46	22.9	63	7	US-11-078-735-14	Sequence 14, Appli
43	46	22.9	63	7	US-11-078-735-15	Sequence 15, Appli
44	46	22.9	350	7	US-11-132-285-41	Sequence 41, Appli
45	46	22.9	355	7	US-11-182-946-14	Sequence 14, Appli
46	46	22.9	1062	7	US-11-137-465-43	Sequence 43, Appli
47	46	22.9	1238	7	US-11-078-735-21	Sequence 21, Appli
48	45.5	22.6	272	6	US-10-986-501-120	Sequence 120, App
49	45	22.4	448	6	US-10-967-527A-16	Sequence 16, Appli
50	45	22.4	450	6	US-10-763-712A-76	Sequence 76, Appli
51	45	22.4	468	7	US-11-054-385-12	Sequence 12, Appli
52	44.5	22.1	320	6	US-10-689-742-186	Sequence 186, App
53	44.5	22.1	323	6	US-10-131-826A-272	Sequence 272, App
54	44.5	22.1	332	6	US-10-821-234-937	Sequence 937, App
55	44	21.9	304	6	US-10-821-234-1540	Sequence 1540, Ap
56	44	21.9	437	6	US-10-131-826A-466	Sequence 466, App
57	44	21.9	514	7	US-11-186-284-228	Sequence 228, App
58	44	21.9	703	6	US-10-821-234-1412	Sequence 1412, Ap
59	44	21.9	1028	7	US-11-067-121-7	Sequence 7, Appli
60	44	21.9	1036	6	US-10-131-826A-142	Sequence 142, App
61	44	21.9	1255	6	US-10-770-726-62	Sequence 62, Appli
62	44	21.9	1255	7	US-11-022-562-213	Sequence 213, App
63	44	21.9	1255	7	US-11-113-202-10	Sequence 10, Appli
64	44	21.9	2107	6	US-10-995-561-827	Sequence 827, App
65	44	21.9	2480	6	US-10-995-561-825	Sequence 825, App
66	44	21.9	3116	6	US-10-995-561-826	Sequence 826, App
67	43.5	21.6	347	6	US-10-821-234-1081	Sequence 1081, Ap
68	43.5	21.6	757	7	US-11-067-121-16	Sequence 16, Appli
69	43.5	21.6	757	7	US-11-186-284-41	Sequence 41, Appli
70	43	21.4	224	6	US-10-131-826A-86	Sequence 86, Appli
71	43	21.4	2214	7	US-11-080-991-94	Sequence 94, Appli
72	43	21.4	4655	6	US-10-995-561-556	Sequence 556, App
73	42.5	21.1	126	7	US-11-113-424-184	Sequence 184, App
74	42.5	21.1	160	6	US-10-846-172A-10	Sequence 10, Appli
75	42.5	21.1	419	6	US-10-821-234-1504	Sequence 1504, Ap
76	42.5	21.1	504	6	US-10-763-712A-78	Sequence 78, Appli
77	42.5	21.1	755	7	US-11-067-121-6	Sequence 6, Appli
78	42.5	21.1	886	6	US-10-821-234-1390	Sequence 1390, Ap
79	42.5	21.1	1018	7	US-11-067-121-17	Sequence 17, Appli
80	42	20.9	26	6	US-10-967-527A-6	Sequence 6, Appli
81	42	20.9	148	6	US-10-467-657-5478	Sequence 5478, Ap
82	42	20.9	184	6	US-10-742-634-5	Sequence 5, Appli
83	42	20.9	184	6	US-10-967-527A-5	Sequence 5, Appli
84	42	20.9	235	7	US-11-126-126-16	Sequence 16, Appli
85	42	20.9	444	7	US-11-029-003-16	Sequence 16, Appli
86	42	20.9	461	7	US-11-132-285-6	Sequence 6, Appli
87	42	20.9	461	7	US-11-182-946-4	Sequence 4, Appli
88	42	20.9	854	7	US-11-022-562-219	Sequence 219, App
89	42	20.9	2764	6	US-10-995-561-691	Sequence 691, App
90	42	20.9	2813	6	US-10-995-561-688	Sequence 688, App
91	42	20.9	2919	6	US-10-821-234-1133	Sequence 1133, Ap
92	41.5	20.6	842	6	US-10-645-441-2	Sequence 2, Appli
93	41	20.4	146	6	US-10-131-826A-408	Sequence 408, App
94	41	20.4	215	7	US-11-116-144-297	Sequence 297, App
95	41	20.4	276	6	US-10-972-587-30	Sequence 30, Appli
96	41	20.4	495	6	US-10-873-528-99	Sequence 99, Appli
97	41	20.4	859	7	US-11-000-463-423	Sequence 423, App
98	41	20.4	859	7	US-11-000-463-895	Sequence 895, App



99	41	20.4	1042	7	US-11-067-811-1	Sequence 1, Appl	172	39	19.4	659	6	US-10-661-966-14	Sequence 14, Appl
100	41	20.4	2725	7	US-11-113-424-52	Sequence 52, Appl	173	39	19.4	871	7	US-11-109-157A-10	Sequence 10, Appl
101	40.5	20.1	110	6	US-10-648-816-1	Sequence 2, Appl	174	39	19.4	1001	7	US-11-132-285-40	Sequence 40, Appl
102	40.5	20.1	110	6	US-10-648-816-2	Sequence 2, Appl	175	39	19.4	1013	6	US-10-131-826A-38	Sequence 38, Appl
103	40.5	20.1	110	6	US-10-648-816-3	Sequence 3, Appl	176	39	19.4	1103	7	US-11-109-157A-9	Sequence 9, Appl
104	40.5	20.1	110	6	US-10-648-816-4	Sequence 4, Appl	177	39	19.4	1367	6	US-10-995-561-538	Sequence 538, Appl
105	40.5	20.1	110	6	US-10-648-816-5	Sequence 5, Appl	178	39	19.4	1367	7	US-11-113-202-18	Sequence 18, Appl
106	40.5	20.1	110	6	US-10-648-816-6	Sequence 6, Appl	179	39	19.4	1368	6	US-10-995-561-539	Sequence 539, Appl
107	40.5	20.1	110	6	US-10-648-816-7	Sequence 7, Appl	180	39	19.4	1614	7	US-11-108-528-80	Sequence 82, Appl
108	40.5	20.1	110	6	US-10-648-816-8	Sequence 8, Appl	181	39	19.4	1615	7	US-11-108-528-80	Sequence 80, Appl
109	40.5	20.1	354	7	US-11-064-769-4	Sequence 4, Appl	182	38.5	19.2	72	6	US-10-467-657-4880	Sequence 4880, Ap
110	40.5	20.1	354	7	US-11-064-774A-119	Sequence 119, App	183	38.5	19.2	339	6	US-10-878-556A-18	Sequence 18, Appl
111	40.5	20.1	354	7	US-11-090-439-60	Sequence 60, Appl	184	38.5	19.2	339	6	US-10-995-561-681	Sequence 681, App
112	40.5	20.1	354	7	US-11-090-439-62	Sequence 62, Appl	185	38.5	19.2	339	6	US-10-995-561-682	Sequence 682, App
113	40.5	20.1	426	6	US-10-467-657-4808	Sequence 4808, Ap	186	38.5	19.2	339	6	US-10-995-561-685	Sequence 684, App
114	40.5	20.1	459	6	US-10-990-276-3	Sequence 3, Appl	187	38.5	19.2	339	6	US-10-995-561-685	Sequence 685, App
115	40.5	20.1	500	7	US-11-067-573-2	Sequence 2, Appl	188	38.5	19.2	339	6	US-10-995-561-686	Sequence 686, App
116	40.5	20.1	638	6	US-10-995-561-536	Sequence 536, App	189	38.5	19.2	339	6	US-10-995-561-687	Sequence 687, App
117	40.5	20.1	1122	7	US-11-191-374-3	Sequence 3, Appl	190	38.5	19.2	339	7	US-11-186-284-43	Sequence 43, Appl
118	40.5	20.1	1122	7	US-11-191-375-3	Sequence 3, Appl	191	38.5	19.2	344	6	US-10-821-234-923	Sequence 923, App
119	40.5	20.1	1148	7	US-11-110-082-29	Sequence 29, Appl	192	38.5	19.2	393	7	US-11-077-712-4	Sequence 4, Appl
120	40.5	20.1	1149	7	US-11-110-082-30	Sequence 30, Appl	193	38.5	19.2	724	6	US-10-131-826A-60	Sequence 60, Appl
121	40.5	20.1	3588	6	US-10-995-561-672	Sequence 672, App	194	38	18.9	18	6	US-10-532-480-43	Sequence 43, Appl
122	40.5	20.1	4346	6	US-10-995-561-671	Sequence 671, App	195	38	18.9	143	6	US-10-821-234-1216	Sequence 1216, Ap
123	40.5	20.1	4347	6	US-10-995-561-670	Sequence 670, App	196	38	18.9	161	7	US-11-113-424-38	Sequence 38, Appl
124	40.5	20.1	4419	6	US-10-821-234-1155	Sequence 1155, Ap	197	38	18.9	176	6	US-10-995-561-820	Sequence 820, App
125	40	19.9	47	7	US-11-000-463-408	Sequence 408, App	198	38	18.9	181	6	US-10-980-388-100	Sequence 100, App
126	40	19.9	304	7	US-11-087-177-4	Sequence 4, Appl	199	38	18.9	201	6	US-10-793-626-1514	Sequence 1514, Ap
127	40	19.9	305	7	US-11-080-091-2	Sequence 2, Appl	200	38	18.9	282	7	US-11-186-284-85	Sequence 85, Appl
128	40	19.9	305	7	US-11-087-177-7	Sequence 7, Appl	201	38	18.9	282	7	US-10-995-561-822	Sequence 822, App
129	40	19.9	379	6	US-10-763-712A-40	Sequence 40, Appl	202	38	18.9	342	6	US-10-980-388-118	Sequence 118, App
130	40	19.9	335	7	US-11-075-185-13	Sequence 13, Appl	203	38	18.9	476	7	US-11-143-980-44	Sequence 44, Appl
131	40	19.9	414	6	US-10-131-826A-418	Sequence 418, App	204	38	18.9	700	6	US-10-995-561-922	Sequence 922, App
132	40	19.9	418	6	US-10-312-954-4	Sequence 4, Appl	205	38	18.9	793	6	US-10-995-561-924	Sequence 924, App
133	40	19.9	421	6	US-10-763-712A-13	Sequence 13, Appl	206	38	18.9	793	6	US-10-995-561-925	Sequence 925, App
134	40	19.9	421	6	US-10-763-712A-41	Sequence 41, Appl	207	38	18.9	820	6	US-10-821-234-1176	Sequence 1176, Ap
135	40	19.9	427	7	US-11-182-946-5	Sequence 5, Appl	208	38	18.9	963	6	US-10-995-561-923	Sequence 923, App
136	40	19.9	488	6	US-10-995-561-860	Sequence 860, App	209	38	18.9	1076	6	US-10-467-657-5708	Sequence 5708, Ap
137	40	19.9	526	6	US-10-606-302-5	Sequence 5, Appl	210	37.5	18.7	32	7	US-11-121-301-27	Sequence 27, Appl
138	40	19.9	526	6	US-10-606-302-7	Sequence 7, Appl	211	37.5	18.7	160	6	US-10-995-561-819	Sequence 819, App
139	40	19.9	727	6	US-10-995-561-864	Sequence 864, App	212	37.5	18.7	245	7	US-11-046-456-69	Sequence 69, Appl
140	40	19.9	782	6	US-10-995-561-861	Sequence 861, App	213	37.5	18.7	245	7	US-11-046-644-69	Sequence 69, Appl
141	40	19.9	847	6	US-10-995-561-863	Sequence 863, App	214	37.5	18.7	303	6	US-10-967-671-17	Sequence 17, Appl
142	40	19.9	847	6	US-10-995-561-865	Sequence 865, App	215	37.5	18.7	397	6	US-10-878-556A-189	Sequence 189, App
143	40	19.9	2644	6	US-10-770-726-45	Sequence 45, Appl	216	37.5	18.7	397	6	US-10-995-561-928	Sequence 928, App
144	39.5	19.7	353	6	US-10-131-826A-296	Sequence 296, App	217	37.5	18.7	397	6	US-10-995-561-929	Sequence 929, App
145	39.5	19.7	379	6	US-10-131-826A-308	Sequence 308, App	218	37.5	18.7	849	6	US-10-467-962B-53	Sequence 53, Appl
146	39.5	19.7	618	7	US-11-078-735-18	Sequence 18, Appl	219	37.5	18.7	1121	7	US-11-113-735-24	Sequence 24, Appl
147	39.5	19.7	719	7	US-11-057-047-2	Sequence 2, Appl	220	37.5	18.7	1142	7	US-11-044-051-73	Sequence 73, Appl
148	39.5	19.7	784	7	US-11-057-047-1	Sequence 1, Appl	221	37.5	18.7	1159	7	US-11-113-751-27	Sequence 27, Appl
149	39.5	19.7	798	6	US-10-821-234-1034	Sequence 1034, Ap	222	37.5	18.7	2101	6	US-10-857-780-23	Sequence 23, Appl
150	39.5	19.7	1113	7	US-11-067-811-4	Sequence 4, Appl	223	37	18.4	34	7	US-11-121-301-82	Sequence 82, Appl
151	39.5	19.7	3011	6	US-10-985-205-3	Sequence 3, Appl	224	37	18.4	41	7	US-11-107-364-34	Sequence 34, Appl
152	39	19.4	41	7	US-11-027-111-15	Sequence 15, Appl	225	37	18.4	63	7	US-11-078-735-5	Sequence 5, Appl
153	39	19.4	136	7	US-11-051-267-29	Sequence 29, Appl	226	37	18.4	129	6	US-11-116-144-145	Sequence 145, App
154	39	19.4	157	7	US-11-051-267-27	Sequence 27, Appl	227	37	18.4	189	6	US-10-131-826A-240	Sequence 240, App
155	39	19.4	217	6	US-10-467-657-4018	Sequence 4018, Ap	228	37	18.4	281	7	US-11-087-177-3	Sequence 3, Appl
156	39	19.4	239	7	US-11-192-374-5	Sequence 5, Appl	229	37	18.4	282	6	US-10-131-826A-312	Sequence 312, App
157	39	19.4	317	7	US-11-000-463-428	Sequence 428, App	230	37	18.4	282	7	US-11-080-991-34	Sequence 34, Appl
158	39	19.4	318	6	US-10-821-234-1117	Sequence 1117, Ap	231	37	18.4	282	7	US-11-087-177-9	Sequence 9, Appl
159	39	19.4	333	6	US-10-131-826A-132	Sequence 132, App	232	37	18.4	295	7	US-11-192-374-4	Sequence 4, Appl
160	39	19.4	339	7	US-11-077-386-18	Sequence 18, Appl	233	37	18.4	295	7	US-11-192-374-24	Sequence 24, Appl
161	39	19.4	406	6	US-10-131-826A-82	Sequence 82, Appl	234	37	18.4	306	6	US-10-518-341-2	Sequence 2, Appl
162	39	19.4	410	6	US-10-821-234-952	Sequence 952, App	235	37	18.4	310	6	US-10-994-820A-10	Sequence 10, Appl
163	39	19.4	435	7	US-11-077-386-19	Sequence 19, Appl	236	37	18.4	320	7	US-11-112-882-76	Sequence 76, Appl
164	39	19.4	449	6	US-10-763-712A-21	Sequence 21, Appl	237	37	18.4	384	7	US-11-074-176-78	Sequence 78, Appl
165	39	19.4	449	6	US-10-763-712A-104	Sequence 104, App	238	37	18.4	421	6	US-10-467-657-2312	Sequence 2312, Ap
166	39	19.4	450	7	US-11-077-386-20	Sequence 20, Appl	239	37	18.4	421	6	US-10-763-712A-7	Sequence 7, Appl
167	39	19.4	451	6	US-10-770-726-79	Sequence 79, Appl	240	37	18.4	485	6	US-10-821-234-934	Sequence 934, App
168	39	19.4	460	6	US-10-990-276-1	Sequence 1, Appl	241	37	18.4	492	6	US-10-821-234-1108	Sequence 1108, Ap
169	39	19.4	567	7	US-11-167-856-30	Sequence 30, Appl	242	37	18.4	516	7	US-11-045-802-36	Sequence 36, Appl
170	39	19.4	631	6	US-10-995-561-546	Sequence 546, App	243	37	18.4	519	6	US-10-523-477-8	Sequence 8, Appl
171	39	19.4	637	7	US-11-154-324-4	Sequence 4, Appl	244	37	18.4	542	7	US-11-075-185-14	Sequence 14, Appl



Thu Dec 22 14:13:30 2005

Sequence 34, Appl1  
Sequence 460, App  
Sequence 702, App  
Sequence 659, App  
Sequence 14, Appl1  
Sequence 2, Appli  
Sequence 8, Appli  
Sequence 13, Appl  
Sequence 100, App  
Sequence 46, Appl  
Sequence 46, Appl  
Sequence 48, Appl  
Sequence 203, App  
Sequence 6, Appli  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 86, Appl  
Sequence 84, Appl  
Sequence 1, Appli  
Sequence 26, Appl  
Sequence 484, App  
Sequence 1403, Ap  
Sequence 3, Appli  
Sequence 69, Appl  
Sequence 76, Appl  
Sequence 37, Appl  
Sequence 113, App  
Sequence 115, App  
Sequence 6, Appli  
Sequence 318, App  
Sequence 120, App  
Sequence 122, App  
Sequence 123, App  
Sequence 131, App  
Sequence 133, App  
Sequence 134, App  
Sequence 69, Appl  
Sequence 122, App  
Sequence 112, App  
Sequence 1636, Ap  
Sequence 150, App  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 1016, Ap  
Sequence 6, Appli  
Sequence 18, Appl  
Sequence 18, Appl  
Sequence 46, Appl  
Sequence 46, Appl  
Sequence 75, Appl  
Sequence 5, Appli  
Sequence 1045, Ap  
Sequence 8638, Ap  
Sequence 1495, Ap  
Sequence 944, App  
Sequence 2799, App  
Sequence 2799, App

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; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 40
;

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; IIFB: FBI
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(40)
; OTHER INFORMATION: cys
US-10-967-527A-9

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Query Match 100.0%; Score 201; DB 6; Length 40;  
Best Local Similarity 100.0%; Pred. No. 3e-20;  
Matches 34; Conservative 0; Mismatches 0; Indels

QY	1	CSQNEYD	SL	HACIP	COL	RCSS	NT	PL	TC	QRYC	34
QY	1	CSQNEYD	SL	HACIP	COL	RCSS	NT <td>PL</td> <td>TC</td> <td>QRYC</td> <td>34</td>	PL	TC	QRYC	34

## RESULT 2

US-10-742-634-9  
: Sequence 9, Application US/10742634

```

; Publication No. US20050249671A9
;
; GENERAL INFORMATION:
;
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
;
; TITLE OF INVENTION: Neurokine-alpha Conj
; FILE REFERENCE: 1498.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 9
;
; LENGTH: 184
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
; US-10-742-634-9

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Query Match 100.0%; Score 201; DB 6; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.1e-19;  
Matches 34: Conservative 0; Mismatches 0; Indels

Qy	1	CSQNEVFDLLHACIPQLRCSSNPPLTCQRYC	34
pb	8	CSQNEVFDLLHACIPQLRCSSNPPLTCQRYC	41

### RESULT 3

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US-10-967-527A-8
; Sequence 8, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Znftr14, A Tumor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/9
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,691

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## ALIGNMENTS

RESULT 1  
US-10-967-527A-9  
; Sequence 9, Application US/10967527A  
; Publication NO. US20050256041A1  
; GENERAL INFORMATION:  
; APPLICANT: FOX, Brian A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: Znfx14, A Tumor Necrosis Factor  
; TITLE OF INVENTION: Receptor  
; FILE REFERENCE: 03-17  
; CURRENT APPLICATION NUMBER: US/10/967, 527A



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; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-8

Query Match
Best Local Similarity 100.0%; Score 201; DB 6; Length 184;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 4
US-10-967-527A-10
; Sequence 10, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 185
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-10

Query Match
Best Local Similarity 67.7%; Score 136; DB 6; Length 185;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 5
US-10-967-527A-21
; Sequence 21, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 249
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-21

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Query Match
Best Local Similarity 35.6%; Score 71.5; DB 6; Length 249;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 6 CFPKQYWDSSRKSCVSCALTCQRS-QRTCTDFC 38

RESULT 6
US-10-967-527A-20
; Sequence 20, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 48
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(48)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-20

Query Match
Best Local Similarity 33.1%; Score 66.5; DB 6; Length 48;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
Db 13 CPREQYDPDLGTCTCMSCIKCNHQS-QRTCAAFC 45

RESULT 7
US-10-967-527A-19
; Sequence 19, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 292
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-19

Query Match
Best Local Similarity 33.1%; Score 66.5; DB 6; Length 292;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34

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Query Match 28.9%; Score 58; DB 6; Length 175;  
Best Local Similarity 47.4%; Pred. No. 0.35;  
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CSQNEFYDSLHACIPCOL 19  
DB 22 CNGTECFDPLVRNCVSEL 40

## RESULT 12

US-11-108-172-1116  
; Sequence 1116, Application US/11108172  
; Publication No. US20050260177A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Lodes, Michael J.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Benson, Darin R.  
; APPLICANT: Meagher, Madeleine Joy  
; APPLICANT: Stolk, John A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Smith, Carole L.  
; APPLICANT: King, Gordon E.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Clapper, Jonathan D.  
; APPLICANT: Skeiky, Yasir A. W.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick Thomas S.  
; APPLICANT: Carter, Darrick  
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
; FILE REFERENCE: 21021.471C15  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 10/025,380  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: US 09/922,217  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 09/833,263  
; PRIOR FILING DATE: 2001-04-10  
; PRIOR APPLICATION NUMBER: US 09/649,811  
; PRIOR FILING DATE: 2000-08-28  
; PRIOR APPLICATION NUMBER: US 09/609,448  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 09/575,251  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: US 09/519,444  
; PRIOR FILING DATE: 2000-03-06  
; PRIOR APPLICATION NUMBER: US 09/504,629  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: US 09/480,321  
; PRIOR FILING DATE: 2000-01-10  
; PRIOR APPLICATION NUMBER: US 09/476,296  
; PRIOR FILING DATE: 1999-12-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1130  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1116  
; LENGTH: 5405  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-108-172-1116  
Query Match 26.6%; Score 53.5; DB 7; Length 5405;  
Best Local Similarity 34.3%; Pred. No. 26;  
Matches 12; Conservative 5; Mismatches 13; Indels 5; Gaps 2;

QY 1 CSQNEFYDSLHACI-PCQLRCSSTPPLTCQRYC 34  
DB 2733 CPQNSHYE-----LCADTCSLGSALSAPLQCPDGC 2763

## RESULT 13

US-11-126-126-2  
; Sequence 2, Application US/11126126  
; Publication No. US20050250696A1  
; GENERAL INFORMATION:  
; APPLICANT: Fisher F., Eric  
; APPLICANT: Edwards K., Carl  
; APPLICANT: Kieft L., Gary  
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and  
; TITLE OF INVENTION: Type-II Receptors  
; FILE REFERENCE: 02-006-A  
; CURRENT FILING DATE: 2005-05-10  
; PRIOR APPLICATION NUMBER: US/11/126,126  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 09/882,735  
; PRIOR FILING DATE: 1997-07-09  
; PRIOR APPLICATION NUMBER: 09/214,613  
; PRIOR FILING DATE: 1997-07-09  
; PRIOR APPLICATION NUMBER: PCT/US97/12244  
; PRIOR FILING DATE: 1997-07-09  
; PRIOR APPLICATION NUMBER: 60/039,792  
; PRIOR FILING DATE: 1997-03-04  
; PRIOR APPLICATION NUMBER: 60/039,314  
; PRIOR FILING DATE: 1997-02-07  
; PRIOR APPLICATION NUMBER: 60/037,737  
; PRIOR FILING DATE: 1997-01-23  
; PRIOR APPLICATION NUMBER: 60/032,534  
; PRIOR FILING DATE: 1996-12-06  
; PRIOR APPLICATION NUMBER: 60/021,443  
; PRIOR FILING DATE: 1996-07-09  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-126-126-2  
Query Match 24.9%; Score 50; DB 7; Length 161;  
Best Local Similarity 35.3%; Pred. No. 3.5;  
Matches 12; Conservative 5; Mismatches 13; Indels 4; Gaps 2;

QY 1 CSQNE---YFDSLHACIPCOLRCSSTPPLTCQ 31  
DB 87 CRKNQRYHWSENLPQCFNCSL-CLNGTWHLSQ 119

## RESULT 14

US-11-182-946-3  
; Sequence 3, Application US/11182946  
; Publication No. US20050255100A1  
; GENERAL INFORMATION:  
; APPLICANT: Wei, Ying-Fei  
; APPLICANT: Ni, Jian  
; APPLICANT: Gentz, Reiner  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5  
; FILE REFERENCE: 1486.1280004  
; CURRENT FILING DATE: 2005-07-18  
; PRIOR APPLICATION NUMBER: US/11/182,946  
; PRIOR FILING DATE: 2005-07-18  
; PRIOR APPLICATION NUMBER: US/10/186,643  
; PRIOR FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: US/09/573,986  
; PRIOR FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-11-182-946-3  
Query Match 24.9%; Score 50; DB 7; Length 455;  
Best Local Similarity 35.3%; Pred. No. 8.6;







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; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-285-61

Query Match      24.4%; Score 49; DB 7; Length 231;
Best Local Similarity 47.6%; Pred. No. 6.5;
Matches 10; Conservative 3; Mismatches 6; Indels 2; Gaps 2;

QY      1 CSONEYFDSLHACIPQCLRC 21
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Db      3 CQENEYWDQ-WGRCVTCQ-RC 21

RESULT 19
US-10-967-527A-17
; Sequence 17, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 297
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-17

Query Match      24.4%; Score 49; DB 6; Length 297;
Best Local Similarity 47.6%; Pred. No. 8.1;
Matches 10; Conservative 3; Mismatches 6; Indels 2; Gaps 2;

QY      1 CSONEYFDSLHACIPQCLRC 21
      | :|||:| | :|||
Db      3 CQENEYWDQ-WGRCVTCQ-RC 21

RESULT 20
US-10-967-527A-15
; Sequence 15, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 297
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-15

Query Match      24.4%; Score 49; DB 6; Length 297;
Best Local Similarity 47.6%; Pred. No. 8.1;
Matches 10; Conservative 3; Mismatches 6; Indels 2; Gaps 2;

QY      1 CSONEYFDSLHACIPQCLRC 21
      | :|||:| | :|||
Db      3 CQENEYWDQ-WGRCVTCQ-RC 21

RESULT 21
US-10-967-527A-14
; Sequence 14, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 447
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-14

Query Match      23.9%; Score 48; DB 6; Length 447;
Best Local Similarity 30.0%; Pred. No. 15;
Matches 9; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY      1 CSONEYFDSLHACIPQCLRCSSNTPTPLTC 30
      | :|||:| | :|||
Db      7 CGENEYNYQTTGLCQCPCPGGEPYLSLSC 36

RESULT 22
US-10-995-561-1033
; Sequence 1033, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1033
; LENGTH: 1798
```



```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1033

Query Match      23.6%; Score 47.5; DB 6; Length 1798;
Best Local Similarity 26.4%; Pred. No. 60;
Matches 14; Conservative 4; Mismatches 10; Indels 25; Gaps 3;

Qy 1 CSQNEYFDSL-----HACIP-----COL-RCSSNTPPL 28
Db 943 CHODEYSQQIVCHCRAGYTLGRCEACAPGHGDFSPRPGRCQLCECSGNIDPM 995

RESULT 23
US-10-995-561-1034
; Sequence 1034, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1034
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1034

Query Match      23.6%; Score 47.5; DB 6; Length 1798;
Best Local Similarity 26.4%; Pred. No. 60;
Matches 14; Conservative 4; Mismatches 10; Indels 25; Gaps 3;

Qy 1 CSQNEYFDSL-----HACIP-----COL-RCSSNTPPL 28
Db 943 CHODEYSQQIVCHCRAGYTLGRCEACAPGHGDFSPRPGRCQLCECSGNIDPM 995

RESULT 24
US-11-182-946-13
; Sequence 13, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Pei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-13

Query Match      23.4%; Score 47; DB 7; Length 349;
Best Local Similarity 43.5%; Pred. No. 17;
Matches 10; Conservative 4; Mismatches 5; Indels 4; Gaps 1;

Qy 2 SQNEYFDSLHACIPQLRCSSN 24
Db 1 CSQNEYFDSLHACIPQLRCSSN 24
```

```
Db 75 SRNNH-----LPACLSCNCRCSN 93

RESULT 25
US-10-995-561-1016
; Sequence 1016, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1016
; LENGTH: 3690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1016

Query Match      23.4%; Score 47; DB 6; Length 3690;
Best Local Similarity 26.0%; Pred. No. 1.3e+02;
Matches 13; Conservative 4; Mismatches 15; Indels 18; Gaps 2;

Qy 1 CSQNEYFD---SLHACIPCO-----LRCSSNTPPLTCOR 32
Db 1845 CAPGFYRDVKGLFLGRCPQCQCHGHSRDLCPGSGVCDQHNTEGAHCR 1894

RESULT 26
US-10-995-561-1015
; Sequence 1015, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1015
; LENGTH: 3714
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1015

Query Match      23.4%; Score 47; DB 6; Length 3714;
Best Local Similarity 26.0%; Pred. No. 1.3e+02;
Matches 13; Conservative 4; Mismatches 15; Indels 18; Gaps 2;

Qy 1 CSQNEYFD---SLHACIPCO-----LRCSSNTPPLTCOR 32
Db 1846 CAPGFYRDVKGLFLGRCPQCQCHGHSRDLCPGSGVCDQHNTEGAHCR 1895

RESULT 27
US-10-821-234-1076
; Sequence 1076, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
```



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; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1076
; LENGTH: 3717
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1076

```

Query Match 23.4%; Score 47; DB 6; Length 3717;  
Best Local Similarity 26.0%; Pred. No. 1.3e+02;  
Matches 13; Conservative 4; Mismatches 15; Indels 18; Gaps 2;

**Qy** 1 CSQNEYFD---SLHACIPCQ-----LRCSNTPPLTCOR 32  
| : | | | : | : | : | : |  
**D6** 1867 CAPGFYRDVKGLFGRVCPGCOCHGHSDRCLPGSGVCVDCONTEGAHCER 1916

RESULT 28  
US-11-153-880-4  
; Sequence 4, Application US/11153880  
; Publication No. US20050256050A1  
; GENERAL INFORMATION:  
; APPLICANT: HU, JING-SHAN  
; APPLICANT: ROSEN, CRAIG A.  
; APPLICANT: CAO, LIANG  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
; STREET: 1100 NEW YORK AVENUE

Query Match	23.1%	Score 46.5;	DB 7;	Length 350;
Best Local Similarity	33.3%	Pred. No. 20;		

	Matches	12;	Conservative	2;	Mismatches	19;	Indels	3;	Gaps	2;
Qy	1	CSQNEYFDSLHLHACIPQLRCCSNTP--PLTCQRYC	34							
Db	259	CGANREEDENTCCV--CKRTCPNPNPLNPKGKACEC	293							

```

RESULT 29
US-11-064-769-2
; Sequence 2, Application US/11064769
; Publication No. US20050256075A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Yi-Herttuaia, Seppo
; APPLICANT: Hiltunen, Mikko O
; APPLICANT: Jeltsch, Markku M
; APPLICANT: Achen, Marc G
; TITLE OF INVENTION: Use of VEGF-C or VEGF-D Gene or Protein to Prevent Restenosis
; FILE REFERENCE: 28967/35601A
; CURRENT APPLICATION NUMBER: US/11/064,769
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: US/09/427,657
; PRIOR FILING DATE: 1999-10-26
; PRIOR APPLICATION NUMBER: US 60/105,587
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-064-769-2

```

Query Match 23.1%; Score 46.5; DB 7; Length 419;  
Best Local Similarity 33.3%; Pred. No. 23;  
Matches 12; Conservative 2; Mismatches 19; Indels

Qy 1 CSQNEYFDLSLHACIPQQLRCSSTNP--PLTCQRYC 34  
Dd 328 CSANREFDENTCQCV-CKRTCPRNQPLNPGKACCEC 362

RESULT 30  
US-11-153-880-2  
Sequence 2, Application US/11153880  
Publication No. US20050256050A1  
GENERAL INFORMATION:  
APPLICANT: HU, JING-SHAN  
APPLICANT: ROSEN, CRAIG A.  
APPLICANT: CAO, LIANG  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 NEW YORK AVENUE  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/153,880  
FILING DATE: 16-jun-2005  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/219,442  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:



```
; APPLICATION NUMBER: 08/999,811
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MARKOWICZ, KAREN R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 1488.1000004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-11-153-880-2

Query Match      23.1%; Score 46.5; DB 7; Length 419;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 12; Conservative 2; Mismatches 19; Indels 3; Gaps 2;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTP--PLTCQRYC 34
Db 328 CGANREFDNTCCQV-CRRTCPRNQPLNPGKACAC 362

RESULT 31
US-11-064-774A-22
; Sequence 22, Application US/11064774A
; Publication No. US20050267024A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWTH
; FILE REFERENCE: 28967/35977B2
; CURRENT FILING DATE: 2005-02-24
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/795,006
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 1212
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-064-774A-22

Query Match      23.1%; Score 46.5; DB 7; Length 419;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 12; Conservative 2; Mismatches 19; Indels 3; Gaps 2;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTP--PLTCQRYC 34
Db 328 CGANREFDNTCCQV-CRRTCPRNQPLNPGKACAC 362

RESULT 32
US-11-147-047-50
; Sequence 50, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoqing
```

```
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-50

Query Match      23.1%; Score 46.5; DB 7; Length 487;
Best Local Similarity 23.7%; Pred. No. 26;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCO-----LRCSNT 25
Db 242 CSPGHYNTTTHRCIRCPVGTQPEFGQNHCTCPGNT 279

RESULT 33
US-10-770-726-57
; Sequence 57, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-57

Query Match      23.1%; Score 46.5; DB 6; Length 883;
Best Local Similarity 30.3%; Pred. No. 44;
Matches 10; Conservative 3; Mismatches 17; Indels 3; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOLRC---SSNTPPLTC 30
Db 235 CLDTVHFGRQASKCLEQVMCHPKCSTCLPATC 267

RESULT 34
US-11-113-424-35
; Sequence 35, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
```



```
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-113-424-35

Query Match      23.1%; Score 46.5; DB 7; Length 961;
Best Local Similarity 23.7%; Pred. No. 47;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

QY 1 CSQNEFYDSLHACIPQ-----LRCSNT 25
Db 743 CSPGHYNTTTHRCIRCPVGTQYQPEFGQNHCTCPGNT 780

RESULT 35
US-11-137-465-58
; Sequence 58, Application US/11137465
; Publication No. US2005025558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-58

Query Match      23.1%; Score 46.5; DB 7; Length 964;
Best Local Similarity 23.7%; Pred. No. 47;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

QY 1 CSQNEFYDSLHACIPQ-----LRCSNT 25
Db 743 CSPGHYNTTTHRCIRCPVGTQYQPEFGQNHCTCPGNT 780

RESULT 36
US-11-113-424-2
; Sequence 2, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-2

Query Match      23.1%; Score 46.5; DB 7; Length 965;
Best Local Similarity 23.7%; Pred. No. 47;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

QY 1 CSQNEFYDSLHACIPQ-----LRCSNT 25
Db 744 CSPGHYNTTTHRCIRCPVGTQYQPEFGQNHCTCPGNT 781

RESULT 37
US-11-147-047-51
; Sequence 51, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
```



```
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-51

Query Match      23.1%; Score 46.5; DB 7; Length 965;
Best Local Similarity 23.7%; Pred. No. 47;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

Qy      1 CSQNEYFDSLHACIPQ-----LRCSSNT 25
Db      743 CSPGHYNTTTHRCIRCPVGTQPEFGKNCVSCPGNT 780

RESULT 38
US-11-080-991-50
; Sequence 50, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-50

Query Match      23.1%; Score 46.5; DB 7; Length 997;
Best Local Similarity 23.7%; Pred. No. 48;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

Qy      1 CSQNEYFDSLHACIPQ-----LRCSSNT 25
Db      752 CSPGHYNTTTHRCIRCPVGTQPEFGKNCVSCPGNT 789

RESULT 39
US-11-113-424-36
; Sequence 36, Application US/1113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
```

```
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 999
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-36

Query Match      23.1%; Score 46.5; DB 7; Length 999;
Best Local Similarity 23.7%; Pred. No. 48;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

Qy      1 CSQNEYFDSLHACIPQ-----LRCSSNT 25
Db      754 CSPGHYNTTTHRCIRCPVGTQPEFGKNCVSCPGNT 791

RESULT 40
US-11-078-735-12
; Sequence 12, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAM JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-078-735-12

Query Match      22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 5.2;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy      12 HACIPCOLRCSNTPPLTCQRYC 34
Db      12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 41
US-11-078-735-13
; Sequence 13, Application US/11078735
; Publication No. US20050261477A1
```



```
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-13

Query Match      22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 5.2;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      12 HACIPQLRCSSNTPLTCQRYC 34
      | : : | | | | | | | | | |
DB      12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 42
US-11-078-735-14
; Sequence 14, Application US/11/078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-13

Query Match      22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 5.2;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      12 HACIPQLRCSSNTPLTCQRYC 34
      | : : | | | | | | | | | |
DB      12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 43
US-11-078-735-15
; Sequence 15, Application US/11/078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 15
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-15

Query Match      22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 5.2;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      12 HACIPQLRCSSNTPLTCQRYC 34
      | : : | | | | | | | | | |
DB      12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 44
US-11-132-285-41
; Sequence 41, Application US/11/132285
; Publication No. US20050244876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
; FILE REFERENCE: PFS11P1
; CURRENT APPLICATION NUMBER: US/11/132,285
```

```
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 15
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-15

Query Match      22.9%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 5.2;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      12 HACIPQLRCSSNTPLTCQRYC 34
      | : : | | | | | | | | | |
DB      12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 44
US-11-132-285-41
; Sequence 41, Application US/11/132285
; Publication No. US20050244876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
; FILE REFERENCE: PFS11P1
; CURRENT APPLICATION NUMBER: US/11/132,285
```



```

; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, ZhaoYing
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 1062
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-43

Query Match 22.9%; Score 46; DB 7; Length 1062;
Best Local Similarity 36.4%; Pred.No. 59;
Matches 8; Conservative 3; Mismatches 7; Indels 4; Gaps

QY 17 COLRC---SSNTPLPLTCQRYC 34
      |||||      :|||:|:|
Db 954 CNLCRLMWGCSIPFSCEDLC 975

RESULT 47
US-11-078-735-21
; Sequence 21, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 21
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-21

```



Query Match 22.9%; Score 46; DB 7; Length 1238;  
Best Local Similarity 30.4%; Pred. No. 68;  
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 12 HACIPQLRCSSNTPLTCQRYC 34  
DB 189 HLELQIRVRCDENYSATCNKFC 211

RESULT 48  
US-10-986-501-120  
; Sequence 120, Application US/10986501  
; Publication No. US20050244845A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 90 Human Secreted Proteins  
; FILE REFERENCE: P2013P2C1  
; CURRENT APPLICATION NUMBER: US/10/986,501  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: US/10/621,363  
; PRIOR FILING DATE: 2003-07-18  
; PRIOR APPLICATION NUMBER: 09/969,730  
; PRIOR FILING DATE: 2001-10-06  
; PRIOR APPLICATION NUMBER: 09/774,639  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: 60/238,291  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 09/244,112  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: PCT/US98/16235  
; PRIOR FILING DATE: 1998-08-04  
; PRIOR APPLICATION NUMBER: 60/056,371  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,732  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,366  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,364  
; PRIOR FILING DATE: 1997-08-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 373  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 120  
; LENGTH: 272  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: MISC FEATURE  
; LOCATION: (120)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (162)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (175)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (176)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (180)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-986-501-120

Query Match 22.6%; Score 45.5; DB 6; Length 272;  
Best Local Similarity 52.4%; Pred. No. 21;  
Matches 11; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

. QY 6 YFDSLHACIPQLRCSSNTP 26

DB 125 YSDQLLHR-IPSTYRSSGNSP 144

RESULT 49  
US-10-967-527A-16  
; Sequence 16, Application US/10967527A  
; Publication No. US20050256041A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Brian A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: Znftr14, A Tumor Necrosis Factor  
; TITLE OF INVENTION: Receptor  
; FILE REFERENCE: 03-17  
; CURRENT APPLICATION NUMBER: US/10/967,527A  
; CURRENT FILING DATE: 2004-10-18  
; PRIOR APPLICATION NUMBER: 60/511,698  
; PRIOR FILING DATE: 2003-10-16  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 448  
; TYPE: PRT  
; ORGANISM: mus musculus  
US-10-967-527A-16

Query Match 22.4%; Score 45; DB 6; Length 448;  
Best Local Similarity 30.3%; Pred. No. 38;  
Matches 10; Conservative 5; Mismatches 12; Indels 6; Gaps 2;

QY 1 CSQNEYFD---SLHACIPQLRCSSNTPPLTC 30  
DB 31 CGENEYHNQTTGLCCQCCPPCR---PGEEPYMSC 60

RESULT 50  
US-10-763-712A-76  
; Sequence 76, Application US/10763712A  
; Publication No. US20050266541A1  
; GENERAL INFORMATION:  
; APPLICANT: Solazyme, Inc.  
; APPLICANT: Dillon, Harrison F.  
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen  
; TITLE OF INVENTION: Production  
; FILE REFERENCE: H2042101-CIP  
; CURRENT APPLICATION NUMBER: US/10/763,712A  
; CURRENT FILING DATE: 2004-01-21  
; PRIOR APPLICATION NUMBER: US 10/287,750  
; PRIOR FILING DATE: 2002-11-04  
; PRIOR APPLICATION NUMBER: US 10/411,910  
; PRIOR FILING DATE: 2003-04-12  
; PRIOR APPLICATION NUMBER: US 60/500,032  
; PRIOR FILING DATE: 2003-09-03  
; NUMBER OF SEQ ID NOS: 184  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 76  
; LENGTH: 450  
; TYPE: PRT  
; ORGANISM: Clostridium acetobutylicum  
US-10-763-712A-76

Query Match 22.4%; Score 45; DB 6; Length 450;  
Best Local Similarity 29.6%; Pred. No. 38;  
Matches 8; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

QY 8 DSLHACIPQLRCSSNTPPLTCQRYC 34  
DB 74 DNIVEKIECDSSCHSNEGTPCQKSC 100

RESULT 51  
US-11-054-385-12



```

/ Sequence 12, Application US/11054395
/ Publication No. US20050257291A1
/ GENERAL INFORMATION:
/ APPLICANT: MIZUTANI, Maaako
/ APPLICANT: TANAKA, Yoshiakazu
/ APPLICANT: KUSUMI, Takaaki
/ APPLICANT: SAITO, Kazuki
/ APPLICANT: YAMAZAKI, Mani
/ APPLICANT: ZHIZHONG, Gong
/ TITLE OF INVENTION: GENES ENCODING
/ TITLE OF INVENTION: ACTIVITY
/ FILE REFERENCE: 001560-350
/ CURRENT APPLICATION NUMBER: US/11/0
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: US/09/147
/ PRIOR FILING DATE: 1999-03-24
/ PRIOR APPLICATION NUMBER: PCT/JP98/
/ PRIOR FILING DATE: 1998-07-16
/ PRIOR APPLICATION NUMBER: JP 9-200505
/ PRIOR FILING DATE: 1997-07-25
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 12
/ LENGTH: 468
/ TYPE: PRT
/ ORGANISM: Petunia hybrida
/ US-11-054-385-12

```

```

Query Match      22.4%; Score 45; DB 7; Length 468;
Best Local Similarity 53.3%; Pred.No. 39;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      19 LRCSSSTPPLTCQRY 33
      ||| ||| |
Db      97 LTCSENGOPITCLLY 111

```

```

RESULT 52
US-10-689-742-186
; Sequence 186, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: Lavallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 186
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-186

```

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Query Match      22.1% Score 44.5; DB 6; Length 320;
Best Local Similarity 33.3%; Pred. No. 33;
Matches 13; Conservative 1; Mismatches 16; Indels 9; Gaps 1;

QY 5 EYFDSLHACIFPCQLRCSSNTPPLT-----CORYC 34
      |||||
DB 36 EAFQSVLGDTSACHRCALTPLYPLTYKKEELYACORG 74
      |||||

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RESULT 53
US-10-131-826A-272
; Sequence 272, Application US/10131826A
; Publication No. US20050245730A1
;
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
;
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;
; FILE REFERENCE: F3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
;
; PRIORITY APPLICATION NUMBER: 60/049911
; PRIORITY FILING DATE: 1997-06-18
;
; PRIORITY APPLICATION NUMBER: 60/056974
; PRIORITY FILING DATE: 1997-08-26
;
; PRIORITY APPLICATION NUMBER: 60/059113
; PRIORITY FILING DATE: 1997-09-17
;
; PRIORITY APPLICATION NUMBER: 60/059115
; PRIORITY FILING DATE: 1997-09-17
;
; PRIORITY APPLICATION NUMBER: 60/059117
; PRIORITY FILING DATE: 1997-09-17
;
; PRIORITY APPLICATION NUMBER: 60/059122
; PRIORITY FILING DATE: 1997-09-17
;
; PRIORITY APPLICATION NUMBER: 60/059184
; PRIORITY FILING DATE: 1997-09-17
;
; PRIORITY APPLICATION NUMBER: 60/059263
; PRIORITY FILING DATE: 1997-09-18
;
; PRIORITY APPLICATION NUMBER: 60/059352
; PRIORITY FILING DATE: 1997-09-19
;
; PRIORITY APPLICATION NUMBER: 60/059588
; PRIORITY FILING DATE: 1997-09-19
;
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
;
; SEQ ID NO 272
;
; LENGTH: 323
;
; TYPE: PRT
;
; ORGANISM: Homo Sapien
US-10-131-826A-272

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Query Match 22.1%; Score 44.5; DB 6; Length 323;  
Best Local Similarity 33.3%; Pred. No. 33;  
Matches 13; Conservative 1; Mismatches 16; Indels 9; Gaps 1;

RESULT 54  
US-10-821-234-937  
; Sequence 337, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom



```
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 937
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-937

Query Match      22.1%; Score 44.5; DB 6; Length 332;
Best Local Similarity 33.3%; Pred. No. 34;
Matches 13; Conservative 1; Mismatches 16; Indels 9; Gaps 1;

QY      5 EYFDSLHACIPQLRCSSNTPLT-----CORYC 34
Db      44 EAFDSVLGDTASCHRAQLTYPLHTPKBEELYACQRC 82

RESULT 55
US-10-821-234-1540
; Sequence 1540, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1540
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1540

Query Match      21.9%; Score 44; DB 6; Length 304;
Best Local Similarity 28.9%; Pred. No. 37;
Matches 11; Conservative 7; Mismatches 16; Indels 4; Gaps 2;

QY      1 CSQNE---YFDSLHACIPQLR-CSSNTPLTTCQRYC 34
Db      226 CRANENRYNSVIGKCRPKPGKCGGNENNTSKQEC 263

RESULT 56
US-10-131-826A-466
; Sequence 466, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
```

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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 466
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-466

Query Match      21.9%; Score 44; DB 6; Length 437;
Best Local Similarity 42.1%; Pred. No. 50;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY      14 CIPQLRCSSNTPLTTCOR 32
Db      328 CVQPLGTCSSGSPRMTCPR 346

RESULT 57
US-11-186-284-228
; Sequence 228, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
```



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; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-228

Query Match      21.9%; Score 44; DB 7; Length 514;
Best Local Similarity 42.1%; Pred. No. 57;
Matches 8; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

Qy 12 HACIPCOL--RCSNTPPL 28
Db 262 HACIACRIIYRSDHEHPPI 280

RESULT 58
US-10-821-234-1412
; Sequence 1412, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1412
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1412

Query Match      21.9%; Score 44; DB 6; Length 703;
Best Local Similarity 27.3%; Pred. No. 75;
Matches 9; Conservative 2; Mismatches 12; Indels 10; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOLRCSNTPPLTCORY 33
Db 384 CKTYGYFDGISMVCDVN-----ECQRY 406

RESULT 59
US-11-067-121-7
; Sequence 7, Application US/11067121
; Publication No. US20050261185A1
; GENERAL INFORMATION:
; APPLICANT: Martijn, Cecile
; APPLICANT: Kondahl, Lena
; TITLE OF INVENTION: THERAPEUTIC PROTEINS
; FILE REFERENCE: 18909-002001
; CURRENT APPLICATION NUMBER: US/11/067,121
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/576,445
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: SE 0400489-1
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1028
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-067-121-7

Query Match      21.9%; Score 44; DB 7; Length 1028;

; NUMBER OF SEQ ID NOS: 859
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 859
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-131-826A-142

Query Match      21.9%; Score 44; DB 6; Length 1036;
Best Local Similarity 44.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 3; Mismatches 9; Indels 2; Gaps 2;

Qy 8 DSSLHA-CIPCOLRCSN-NTPLP 30
Db 826 DSCTHCYCLQQTLCSTVSCPP 850

RESULT 60
US-10-131-826A-142
; Sequence 142, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 142
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-142

Query Match      21.9%; Score 44; DB 6; Length 1036;
Best Local Similarity 44.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 3; Mismatches 9; Indels 2; Gaps 2;

Qy 8 DSSLHA-CIPCOLRCSN-NTPLP 30
Db 835 DSCTHCYCLQQTLCSTVSCPP 859

RESULT 61
```







```
Matches 13; Conservative 4; Mismatches 9; Indels 14; Gaps 2;

Qy 1 CSQNEYF-----DSLHACIPQLRCSSNTPPLTCQRYC 34
   | | | | | | | | | | | | | | | | | | | |
Db 867 CNDNLDIFSIPGCDLSGLSCLICK-----PGTTGRYC 898

RESULT 66
US-10-995-561-826
; Sequence 826, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 826
; LENGTH: 3116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-826

Query Match 21.9%; Score 44; DB 6; Length 3116;
Best Local Similarity 32.5%; Pred. No. 2.7e+02;
Matches 13; Conservative 4; Mismatches 9; Indels 14; Gaps 2;

Qy 1 CSQNEYF-----DSLHACIPQLRCSSNTPPLTCQRYC 34
   | | | | | | | | | | | | | | | | | | | |
Db 867 CNDNLDIFSIPGCDLSGLSCLICK-----PGTTGRYC 898

RESULT 67
US-10-821-234-1081
; Sequence 1081, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 1081
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1081

Query Match 21.6%; Score 43.5; DB 6; Length 347;
Best Local Similarity 30.2%; Pred. No. 48;
Matches 13; Conservative 4; Mismatches 11; Indels 15; Gaps 3;

Qy 6 YFDSLHACIP-----COLRCSS--NTPPLTCQRYC 34
   | | | | | | | | | | | | | | | | | | | |
Db 139 YLDRYL-SCVPRKAQLQLGAVCMVLASKLRTTFLTKLC 180

RESULT 68
US-11-067-121-16
; Sequence 16, Application US/11067121
; Publication No. US20050261185A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Martijn, Cecile
; APPLICANT: Rondahl, Lena
; TITLE OF INVENTION: THERAPEUTIC PROTEINS
; FILE REFERENCE: 18909-002001
; CURRENT APPLICATION NUMBER: US/11/067,121
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/576,445
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: SE 0400489-1
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 757
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-121-16

Query Match 21.6%; Score 43.5; DB 7; Length 757;
Best Local Similarity 35.0%; Pred. No. 93;
Matches 7; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Qy 12 HACIPQLRCSSNTPPLTCQ 31
   | | | | | | | | | | | | | |
Db 134 HPCFP-RVRCINTSPGFRCE 152

RESULT 69
US-11-186-284-41
; Sequence 41, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 757
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-41

Query Match 21.6%; Score 43.5; DB 7; Length 757;
Best Local Similarity 35.0%; Pred. No. 93;
Matches 7; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Qy 12 HACIPQLRCSSNTPPLTCQ 31
   | | | | | | | | | | | | | |
Db 134 HPCFP-RVRCINTSPGFRCE 152

RESULT 70
US-10-131-826A-86
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```
; Sequence 86, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deenoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 86
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-131-826A-86

Query Match 21.4%; Score 43; DB 6; Length 224;
Best Local Similarity 36.0%; Pred. No. 38;
Matches 9; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 10 LLHACIPQLCRSSNTPEPLTCQRYC 34
Db 42 LLPAC--CPVRAQNDTEPIVLEGKC 64

RESULT 71
US-11-080-991-94
; Sequence 94, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Perter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
```

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; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 2214
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-080-991-94

Query Match 21.4%; Score 43; DB 7; Length 2214;
Best Local Similarity 27.6%; Pred. No. 2.7e+02;
Matches 8; Conservative 5; Mismatches 8; Indels 8; Gaps 1;

QY 14 CIPQCLRCSSNT-----PPLTCQRYC 34
Db 1211 CIPQWACDGDTCDCQSGDEDFVNCCKC 1239

RESULT 72
US-10-995-561-556
; Sequence 556, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 556
; LENGTH: 4655
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-995-561-556

Query Match 21.4%; Score 43; DB 6; Length 4655;
Best Local Similarity 26.2%; Pred. No. 5.2e+02;
Matches 11; Conservative 6; Mismatches 17; Indels 8; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRC-----SSNTPEPLTCQRYC 34
Db 3512 CSSTQFLCANNEKCIPIWVKCDGQKDCSDGDELALCPQRF 3553

RESULT 73
US-11-113-424-184
; Sequence 184, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
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; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 184
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
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RESULT 74
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; Publication No. US20050257285A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; APPLICANT: Gupta, Goutam
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Pierce's Disease
; FILE REFERENCE: S-102,340
; CURRENT APPLICATION NUMBER: US/10/846.172A
; CURRENT FILING DATE: 2004-05-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein
US-10-846-172A-10

Query Match      21.1%; Score 42.5; DB 6; Length 160;
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Matches 8; Conservative 2; Mismatches 6; Indels 5; Gaps 1;

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; Sequence 1504, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 21, 2005, 16:11:05 ; Search time 88.4 Seconds  
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Perfect score: 201

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Scoring table: BLOSUM62

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA Main:\*

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- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	201	100.0	58	3	US-09-854-864-21
6	201	100.0	81	3	US-09-855-158-21
7	201	100.0	81	3	US-09-854-864-13
8	201	100.0	81	3	US-09-855-158-13
9	201	100.0	181	3	US-09-854-864-5
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18	201	100.0	184	4	US-10-008-063-7
19	201	100.0	184	4	US-10-152-363A-27
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23	201	100.0	184	5	US-10-626-914-6
24	201	100.0	184	5	US-10-485-489-6
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36	136	67.7	281	3	US-09-854-864-10	Sequence 10, Appl
37	136	67.7	281	3	US-09-855-158-10	Sequence 10, Appl
38	124	61.7	42	4	US-10-145-206-197	Sequence 197, App
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112	59.5	29.6	897	4	US-10-470-390A-12	Sequence 12, Appl1	185	53	26.4	70	4	US-10-380-703-28	Sequence 28, Appl1
113	59.5	29.6	897	5	US-10-450-763-36668	Sequence 36668, A	186	53	26.4	70	6	US-11-021-874-161	Sequence 161, App
114	59.5	29.6	914	4	US-10-406-073-6	Sequence 6, Appl1	187	53	26.4	78	4	US-10-424-599-131220	Sequence 191220, App
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116	59.5	29.6	974	3	US-09-998-570-14	Sequence 14, Appl1	189	53	26.4	111	4	US-10-425-115-296079	Sequence 296079, App
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135	58	28.9	65	4	US-10-380-703-14	Sequence 14, Appl1	208	52	25.9	70	6	US-11-021-874-154	Sequence 154, App
136	58	28.9	175	4	US-10-008-063-13	Sequence 13, Appl1	209	52	25.9	115	3	US-09-950-933A-65	Sequence 65, Appl1
137	58	28.9	175	4	US-10-380-703-9	Sequence 9, Appl1	210	52	25.9	118	4	US-10-425-115-330491	Sequence 330491, App
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145	57.5	28.6	138	4	US-10-767-701-62860	Sequence 62860, A	218	52	25.9	547	6	US-11-128-073-26	Sequence 26, Appl1
146	57.5	28.6	1679	6	US-11-097-143-8286	Sequence 8286, Ap	219	52	25.9	624	4	US-10-231-353-24	Sequence 24, Appl1
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163	54.5	27.1	5985	4	US-10-296-734-810	Sequence 810, App	236	51.5	25.6	77	3	US-09-498-272-40	Sequence 40, Appl1
164	54	26.9	70	4	US-10-380-703-19	Sequence 19, Appl1	237	51.5	25.6	77	3	US-10-825-692-54	Sequence 54, Appl1
165	54	26.9	70	6	US-11-021-874-152	Sequence 152, App	238	51.5	25.6	77	6	US-11-092-336-4	Sequence 4, Appl1
166	54	26.9	71	6	US-11-021-874-150	Sequence 150, App	239	51.5	25.6	77	6	US-11-092-336-40	Sequence 40, Appl1
167	54	26.9	71	6	US-11-021-874-151	Sequence 151, App	240	51.5	25.6	81	3	US-09-498-272-7	Sequence 7, Appl1
168	54	26.9	73	4	US-10-380-703-17	Sequence 17, Appl1	241	51.5	25.6	81	6	US-11-092-336-7	Sequence 7, Appl1
169	54	26.9	73	4	US-10-380-703-18	Sequence 18, Appl1	242	51.5	25.6	84	4	US-10-425-115-273719	Sequence 273719, App
170	54	26.9	98	5	US-10-926-683-1590	Sequence 1590, Ap	243	51.5	25.6	100	3	US-09-498-272-20	Sequence 20, Appl1
171	54	26.9	121	3	US-09-764-891-4135	Sequence 4135, Ap	244	51.5	25.6	100	6	US-11-092-336-20	Sequence 20, Appl1
172	54	26.9	333	4	US-10-425-114-63535	Sequence 63535, A	245	51.5	25.6	136	3	US-09-893-737-302	Sequence 302, App
173	54	26.9	986	5	US-10-450-763-38119	Sequence 38119, A	246	51.5	25.6	136	4	US-10-424-599-255239	Sequence 255239, App







```
; ORGANISM: Homo sapiens
US-09-854-864-6

Query Match      100.0%; Score 201; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYC 34
DB 5 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYC 38

RESULT 4
US-09-855-158-6
; Sequence 6, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-6

Query Match      100.0%; Score 201; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.1e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYC 34
DB 5 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYC 38

RESULT 5
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match      100.0%; Score 201; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYC 34
DB 1 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYC 34

RESULT 6
US-09-855-158-21
; Sequence 21, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

Query Match      100.0%; Score 201; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYC 34
DB 1 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYC 34

RESULT 7
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match      100.0%; Score 201; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYC 34
DB 1 CSONEYFDSLHACIPCOLRCSSNTPLTCQRYC 34

RESULT 8
US-09-855-158-13
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; Sequence 13, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BU
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
; US-09-855-158-13

Query Match      100.0%; Score 201; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
Db      1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34

RESULT 9
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-5

Query Match      100.0%; Score 201; DB 3; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
Db      5 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 38

RESULT 10
US-09-855-158-5
; Sequence 5, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BU
; TITLE OF INVENTION: 3, AND TACI
```

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; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-855-158-5

Query Match      100.0%; Score 201; DB 3; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
Db      5 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 38

RESULT 11
US-10-077-438-1
; Sequence 1, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Techopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
; US-10-077-438-1

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
Db      8 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 41

RESULT 12
US-10-077-438-7
; Sequence 7, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
```



```

; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-7

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   |||||
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 41
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RESULT 13
US-10-077-137-1
; Sequence 1, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-1

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   |||||
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 41
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RESULT 14
US-10-077-137-7
; Sequence 7, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: Mackay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc. S.A.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-137-7

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   |||||
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 41
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RESULT 15
US-10-068-725-2
; Sequence 2, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-2

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   |||||
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPTLTQRYC 41
```



```

RESULT 16
US-10-151-882-47
; Sequence 47, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-47

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 17
US-10-115-192-8
; Sequence 8, Application US/10115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Apotech R & D S.A.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 18
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 19
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34
Db      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 20
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; TITLE OF INVENTION: METHODS OF USE THEREOF
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11
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US-10-216-074-11
Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
    |||||
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 21
US-10-087-080-39
; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; APPLICANT: Case Western Reserve University
; TITLE OF INVENTION: No. US20030235820A1 Methods of Diagnosis of Metastatic Colorectal Cancer
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
; FILE REFERENCE: 018501-000840US
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
US-10-087-080-39

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
    |||||
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 22
US-10-742-634-9
; Sequence 9, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neurokine-alpha Conjugate, Neurokine-alpha Complex, and Uses Thereof
; FILE REFERENCE: 1488.181002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
```

```
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-9

Query Match      100.0%; Score 201; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
    |||||
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 23
US-10-626-914-6
; Sequence 6, Application US/10626914
; Publication No. US20050043516A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: CHUNTHARAPAI, ANAN
; APPLICANT: GREWAL, Iqbal
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: YAN, MINHONG
; TITLE OF INVENTION: TAC1 Antibodies and Uses Thereof
; FILE REFERENCE: P1942R1
; CURRENT APPLICATION NUMBER: US/10/626,914
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,530
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-626-914-6

Query Match      100.0%; Score 201; DB 5; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
    |||||
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 24
US-10-485-489-6
; Sequence 6, Application US/10485489
; Publication No. US20050070689A1
; GENERAL INFORMATION:
; APPLICANT: Dixit, Vishva
; APPLICANT: Grewal, Iqbal
; APPLICANT: Ridgway, John
; APPLICANT: Van, Minhong
; TITLE OF INVENTION: TAC1s and BR3 Polypeptides and Uses Thereof
; FILE REFERENCE: 11669.175USWO
; CURRENT APPLICATION NUMBER: US/10/485,489
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/US02/23487
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/310,114
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/377,171
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 6
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-489-6

Query Match      100.0%; Score 201; DB 5; Length 184;
```



Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CSQNEYFDSL	LLHACIPCOL	RCSSTPPL	TCQRYC	34
Qy						
Db	8	CSQNEYFDSL <td>LLHACIPCOL <td>RCSSTPPL <td>TCQRYC</td> <td>41</td> </td></td>	LLHACIPCOL <td>RCSSTPPL <td>TCQRYC</td> <td>41</td> </td>	RCSSTPPL <td>TCQRYC</td> <td>41</td>	TCQRYC	41

```

RESULT 25
US-10-861-049-27
; Sequence 27, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: "Qian Gong"
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040RIUS
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-049-27

```

Query Match 100.0%; Score 201; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.1e-16;  
Matches 14: Conservative 0; Mismatches 0; Indels

QY	1	CSQNEYFDSL	HACIPCOL	RCSSTNP	PLTCQRYC	34
dh	8	CSQNEYFDSL <td>HACIPCOL <td>RCSSTNP <td>PLTCQRYC <td>41</td> </td></td></td>	HACIPCOL <td>RCSSTNP <td>PLTCQRYC <td>41</td> </td></td>	RCSSTNP <td>PLTCQRYC <td>41</td> </td>	PLTCQRYC <td>41</td>	41

RESULT 26  
US-10-989-826-46  
; Sequence 46, Application US/10989826  
; Publication No. US20050238650A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Crowley, Craig  
; APPLICANT: De Sauvage, Frederic J.  
; APPLICANT: Eaton, Daniel L.  
; APPLICANT: Ebens, Allen  
; APPLICANT: Polson, Andrew  
; APPLICANT: Smith, Victoria  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Tumor of  
; TITLE OF INVENTION: Hematopoietic Origin  
; FILE REFERENCE: P510SR1US  
; CURRENT APPLICATION NUMBER: US/10/989,826  
; CURRENT FILING DATE: 2004-11-16  
; PRIOR APPLICATION NUMBER: US 60/520,842  
; PRIOR FILING DATE: 2003-11-17  
; PRIOR APPLICATION NUMBER: US 60/532,426  
; PRIOR FILING DATE: 2003-12-24  
; NUMBER OF SEQ ID NOS: 75  
; SEQ ID NO 46  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-989-826-46

Query Match	100.0%;	Score 201;	DB 5;	Length 184;
Best Local Similarity	100.0%;	Pred. No. 1.1e-16;		
Matches 34:	Conservative	0;	Mismatches 0;	Indels 0;
	Gaps	0;		

QY	1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 34
pB	8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYC 41

RESULT 27  
US-11-021-874-27  
; Sequence 27, Application US/11021874  
; Publication No. US20050163775A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew Chan  
; APPLICANT: Qian Gong  
; APPLICANT: Flavius Martin  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040R1P1  
; CURRENT APPLICATION NUMBER: US/11/021,874  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 10/861,049  
; PRIOR FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 27  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-874-27

Query Match	100.0%	Score 201;	DB 6;	Length 184;
Best Local Similarity	100.0%;	Pred. No. 1.1e-16;		
Matches 34:	Conservative	0;	Mismatches 0;	Indels 0;
	Conservative	0;	Mismatches 0;	Indels 0;
	Conservative	0;	Mismatches 0;	Indels 0;

QY	1	CSQNEYFDSL	LLHACIPCOL	RCSSTNPPL	TCQRYC	34
pb	8	CSQNEYFDSL <td>LLHACIPCOL <th>8</th> <th>RCSSTNPPL</th> <th>TCQRYC</th> </td>	LLHACIPCOL <th>8</th> <th>RCSSTNPPL</th> <th>TCQRYC</th>	8	RCSSTNPPL	TCQRYC

RESULT 28  
US-09-854-864-9  
; Sequence 9, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION: LARS EYDE  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 283  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-9

Query Match	100.0%	Score 201;	DB 3;	Length 283;
Best Local Similarity	100.0%	Pred. No. 1.6e-16;		
Matches 14: Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	CSQNEYFDSLHLHACIPQLRCSSNPPLTCQRYC	34
nb	5	CSQNEYFDSLHLHACIPQLRCSSNPPLTCQRYC	38



```

; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
; US-10-077-438-3

Query Match          90.0%; Score 181; DB 4; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.3e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 1 CSQNEVFDSLHACIPQCLRCSSTPPLTCQRYC 34
Db 5 CSQNEVFDSLHACIPQCLRCSSTPPLTCQRYC 38

RESULT 30
US-10-115-192-12
; Sequence 12, Application US/10/115192
; Publication No. US20030082175A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R & D S.A.
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
; FILE REFERENCE: A083PCT
; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/215688
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/181807
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/157933
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-115-192-12

Query Match          100.0%; Score 201; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDSLHACIPQCLRCSSTPPLTCQRYC 34
Db 31 CSQNEVFDSLHACIPQCLRCSSTPPLTCQRYC 64

RESULT 31
US-10-077-438-3
; Sequence 3, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschoopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; APPLICANT: Apotech R&D S.A.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/183,536
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
; US-10-077-137-3

Query Match          90.0%; Score 181; DB 4; Length 207;
Best Local Similarity 63.0%; Pred. No. 3.3e-14;
Matches 34; Conservative 0; Mismatches 0; Indels 20; Gaps 1;
```



```

Qy      1  CSONEYFDSL-----LHACIPQCLRCSSNTPPLTTCQRYC 3
      |||||
Db      46 CSONEYFDSLHACIPQCLRCSSNTPPLTCLHACIPQCLRCSSNTPPLTTCQRYC 99

RESULT 33
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING AP
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11

```

```

; Sequence 17, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-03-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-216-074-17

```

Query Match 67.7%; Score 136; DB 3; Length 185;  
Best Local Similarity 70.6%; Pred. No. 9.5e-09;  
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPPLTCQRYC 34  
| : ||||| ||||| : |||||  
DB 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 34  
US-09-855-158-11  
; Sequence 11, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BU  
; TITLE OF INVENTION: 3, AND TACI  
; FILE REFERENCE: A-68GA  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Murine  
US-09-855-158-11

Query Match 67.7%; Score 136; DB 3; Length 185;  
Best Local Similarity 70.6%; Pred. No. 9.5e-09;  
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNTPPLTCQRYC 34  
| : ||||| ||||| : |||||  
DB 5 CFHSEYFDSLHACKPCHLRCSN--PPATCQPYC 36

RESULT 35  
US-10-216-074-17



```
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-158-10

Query Match          67.7%; Score 136; DB 3; Length 281;
Best Local Similarity 70.6%; Pred. No. 1.4e-08;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSONEYFDSLHACIPCQLRCSNTPTLCQRYC 34
   :|||||||||:|||||:|||||
Db 5 CFHSEYFDSLHACKCHLRCSN--PPATCQPYC 36
   :|||||||||:|||||:|||||

RESULT 38
US-10-145-206-197
; Sequence 197, Application US/10145206
; Publication No. US20030195156A1
; GENERAL INFORMATION:
; APPLICANT: MIN, HOSUNG
; APPLICANT: HSU, HAILING
; APPLICANT: ZHONG, FEI
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
; FILE REFERENCE: A-743
; CURRENT APPLICATION NUMBER: US/10/145,206
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,196
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 197
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Human
US-10-145-206-197

Query Match          61.7%; Score 124; DB 4; Length 42;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHACIPCQLRC 21
   :|||||||||:|||||:|||||
Db 22 CSONEYFDSLHACIPCQLRC 42
   :|||||||||:|||||:|||||

RESULT 39
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match          46.5%; Score 93.5; DB 3; Length 117;
Best Local Similarity 69.7%; Pred. No. 0.00096;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

QY 2 SONEYFDSLHACIPCQLRCSNTPTLCQRYC 34
   :|||||||||:|||||:|||||
Db 2 AQCEYFDSLHAC-PC-LRCS----PPTCQ-YC 27
   :|||||||||:|||||:|||||

RESULT 40
US-09-855-158-12
; Sequence 12, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-855-158-12

Query Match          46.5%; Score 93.5; DB 3; Length 117;
Best Local Similarity 69.7%; Pred. No. 0.00096;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

QY 2 SONEYFDSLHACIPCQLRCSNTPTLCQRYC 34
   :|||||||||:|||||:|||||
Db 2 AQCEYFDSLHAC-PC-LRCS----PPTCQ-YC 27
   :|||||||||:|||||:|||||

RESULT 41
US-10-087-192-1647
; Sequence 1647, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1647
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-1647
```







```

; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-16

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Query Match 33.1%; Score 66.5; DB 3; Length 67;  
Best Local Similarity 32.4%; Pred. No. 1.1;  
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

**Qy**

1 CSQNEYDLSLLHACIPQLRCSSNTPPLTCQRVC 34  
| : | : | : | : | : | : | :

**Dd**

1 CPPEOYDPDLGTCWSCKTICNHOS-RTCAAFc 33

RESULT 47  
US-09-855-158-16

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; Sequence 16, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS
; TITLE OF INVENTION: 3. AND TAC1
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-855-158-16

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Query Match 33.1%; Score 66.5; DB 3; Length 67;  
Best Local Similarity 32.4%; Pred. No. 1.1;  
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy	1	CSQNEYDLSLLHACIPQLRCSSNTPPLTCQRYC	34
		: :       : : :   : :   :   :	
Db	1	CPEQYVDPPLGLTGCWSCKTINHOS-GETCAAFEC	33

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RESULT 48
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITI
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27

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; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-854-864-15

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Query Match 33.1%; Score 66.5; DB 3; Length 166;  
Best Local Similarity 32.4%; Pred. No. 2.7;  
Matches 11; Conservative 8; Mismatches 14; Indels

**Qy** 1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34  
| : | : | : | : | : | : | : | : | :  
**Dd** 34 CPPEOYDPLLGTWCSCKTIINHOS-ORTCAAFc 66

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RESULT 49
US-09-855-158-15
: Sequence 15, Application US/09855158
: Publication No. US2002086018A1
: GENERAL INFORMATION:
: APPLICANT: THEILL, LARS EYDE
: APPLICANT: YU, GANG
: TITLE OF INVENTION: METHODS AND COMPOSITIONS
: TITLE OF INVENTION: 3, AND TACI
: FILE REFERENCE: A-686A
: CURRENT APPLICATION NUMBER: US/09/855,158
: CURRENT FILING DATE: 2001-09-11
: PRIOR APPLICATION NUMBER: US 60/214,591
: PRIOR FILING DATE: 2000-06-27
: PRIOR APPLICATION NUMBER: US 60/204,039
: PRIOR FILING DATE: 2000-05-12
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 15
: LENGTH: 166
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-855-158-15

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Query Match	33.1%;	Score 66.5;	DB 3;	Length 166;
Best Local Similarity	32.4%;	Pred. No. 2.7;		
Matches 11: Conservative	8;	Mismatches 14;	Indels 1;	Gaps 1;

<b>QY</b>	1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34   :   :   :   :   :   :   :
<b>D6</b>	34 CPREEYNDFLLGTGMSCKTICNHOS-RTCAAF 66   :   :   :   :   :   :   :

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RESULT 50
US-10-293-816-6
; Sequence 6, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCTE SURFACE
; TITLE OF INVENTION: CAML AND METHODS OF
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT

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; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
; FILE REFERENCE: PFS24PI
; CURRENT APPLICATION NUMBER: US/09/961,376
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-961-376-2

Query Match 33.1%; Score 66.5; DB 3; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYPDSLHACIPQCLRCSSNTPTLTQRCYC 34
Db 34 CPEQYWDPLLGTCMSCKTICNHQS-ORTCAAF 66

RESULT 62
US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-779-050A-42

Query Match 33.1%; Score 66.5; DB 3; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYPDSLHACIPQCLRCSSNTPTLTQRCYC 34
Db 34 CPEQYWDPLLGTCMSCKTICNHQS-ORTCAAF 66

RESULT 63
US-09-302-863-2
; Sequence 2, Application US/09302863
; Publication No. US2003002233A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wanwan S
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

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; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-46

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSNTPTLTQRYC 34
Db 34 CPEQYWDPLLTGTCMSCKTICNHQS-QRTCAAF 66

RESULT 69
US-10-293-816-2
; Sequence 2, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-2

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSNTPTLTQRYC 34
Db 34 CPEQYWDPLLTGTCMSCKTICNHQS-QRTCAAF 66

RESULT 70
US-10-008-063-8
; Sequence 8, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis, J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-8

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSNTPTLTQRYC 34
Db 34 CPEQYWDPLLTGTCMSCKTICNHQS-QRTCAAF 66

RESULT 71
US-10-152-363A-2
; Sequence 2, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-2

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLRCSNTPTLTQRYC 34
Db 34 CPEQYWDPLLTGTCMSCKTICNHQS-QRTCAAF 66

RESULT 72
US-10-268-951-22
; Sequence 22, Application US/10268951
; Publication No. US2003016864A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P2
; CURRENT APPLICATION NUMBER: US/10/268,951
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 10/082,260
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/879,919
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/328,401
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/293,812
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
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; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-951-22

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY      1 CSQNEYFDSLHACIPCOLRCSSNTPLTTCQRYC 34
Db      34 CPEEQYWDPLLTGTCMCKTICNHQS-QRTCAAF 66

RESULT 73
US-10-258-368-1
; Sequence 1, Application US/10258368
; Publication No. US20040013674A1
; GENERAL INFORMATION:
; APPLICANT: Ambrose, Christine
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Schneider, Pascal
; APPLICANT: Rennert, Paul
; TITLE OF INVENTION: Taci As Anti-Tumor Agent
; FILE REFERENCE: BIOG0130 NP of PCT/US01/40626
; CURRENT APPLICATION NUMBER: US/10/258,368
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: USSN 60/199,946
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-368-1

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY      1 CSQNEYFDSLHACIPCOLRCSSNTPLTTCQRYC 34
Db      34 CPEEQYWDPLLTGTCMCKTICNHQS-QRTCAAF 66

RESULT 74
US-10-618-797-4
; Sequence 4, Application US/10618797
; Publication No. US20040048296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based Thereon
; FILE REFERENCE: PF527D1
; CURRENT APPLICATION NUMBER: US/10/618,797
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 09/848, 295
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
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; ORGANISM: human
US-10-618-797-4

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY      1 CSQNEYFDSLHACIPCOLRCSSNTPLTTCQRYC 34
Db      34 CPEEQYWDPLLTGTCMCKTICNHQS-QRTCAAF 66

RESULT 75
US-10-742-634-7
; Sequence 7, Application US/10742634
; Publication No. US20040208824A1
; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neurokine-alpha Conjugate, Neurokine-alpha Complex, and Uses Thereof
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-7

Query Match      33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 4.6;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY      1 CSQNEYFDSLHACIPCOLRCSSNTPLTTCQRYC 34
Db      34 CPEEQYWDPLLTGTCMCKTICNHQS-QRTCAAF 66

Search completed: December 21, 2005, 16:30:38
Job time : 90.4 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 16:00:55 ; Search time 26 Seconds  
(without alignments)

108.114 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_8\_41

Perfect score: 201

Sequence: 1 CSQNEVFDLSLHACIPQLRCSNTPTLCQRYC 34

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/6 COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCFUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	201	100.0	51	2	US-09-854-864-6
3	201	100.0	58	2	US-09-854-864-21
4	201	100.0	81	2	US-09-854-864-13
5	201	100.0	181	2	US-09-854-864-5
6	201	100.0	184	2	US-09-565-423-11
7	201	100.0	192	2	US-09-949-016-11115
8	201	100.0	283	2	US-09-854-864-9
9	136	67.7	185	2	US-09-565-423-17
10	136	67.7	185	2	US-09-854-864-11
11	136	67.7	281	2	US-09-854-864-10
12	93.5	46.5	117	2	US-09-854-864-12
13	66.5	33.1	59	2	US-09-854-864-20
14	66.5	33.1	67	2	US-09-854-864-16
15	66.5	33.1	166	1	US-08-810-572A-6
16	66.5	33.1	166	2	US-09-290-333-6
17	66.5	33.1	166	2	US-09-782-857A-6
18	66.5	33.1	166	2	US-09-854-864-15
19	66.5	33.1	293	1	US-08-810-572A-2
20	66.5	33.1	293	2	US-09-290-333-2
21	66.5	33.1	293	2	US-09-782-857A-2
22	66.5	33.1	293	2	US-09-873-919-22
23	66.5	33.1	293	2	US-09-848-295-4
24	66.5	33.1	293	2	US-09-854-864-14
25	66.5	33.1	397	2	US-09-854-864-18
26	61	30.3	1106	2	US-09-949-016-9626
27	59.5	23.6	581	2	US-10-104-047-2804

28	59.5	29.6	880	2	US-10-104-047-2834	Sequence 2834, Ap
29	56	27.9	2476	1	US-08-276-967-2	Sequence 2, Appli
30	54	26.9	98	2	US-09-621-976-6330	Sequence 6330, Ap
31	54	26.9	98	2	US-09-471-276-1590	Sequence 1590, Ap
32	54	26.9	431	2	US-09-252-991A-25721	Sequence 25721, A
33	53.5	26.6	381	2	US-09-257-580-2	Sequence 2, Appli
34	53.5	26.6	5405	2	US-08-718-388-9	Sequence 9, Appli
35	53	26.4	108	2	US-09-950-933A-61	Sequence 61, Appl
36	52.5	26.1	142	2	US-09-848-295-2	Sequence 2, Appli
37	52	25.9	115	2	US-09-950-933A-65	Sequence 65, Appl
38	52	25.9	547	2	US-09-877-730-26	Sequence 26, Appl
39	52	25.9	624	2	US-09-877-730-24	Sequence 24, Appl
40	52	25.9	712	2	US-09-877-730-22	Sequence 22, Appl
41	52	25.9	826	2	US-09-877-730-16	Sequence 16, Appl
42	52	25.9	904	2	US-09-877-730-6	Sequence 6, Appli
43	52	25.9	991	2	US-09-877-730-12	Sequence 12, Appl
44	52	25.9	1069	2	US-09-877-730-2	Sequence 2, Appli
45	51.5	25.6	63	1	US-08-117-080-12	Sequence 12, Appl
46	51.5	25.6	63	1	US-08-471-329-12	Sequence 12, Appl
47	51.5	25.6	63	1	US-08-915-142-12	Sequence 12, Appl
48	51.5	25.6	77	1	US-08-465-380-4	Sequence 4, Appli
49	51.5	25.6	77	1	US-08-465-380-40	Sequence 40, Appl
50	51.5	25.6	77	1	US-08-480-478-33	Sequence 33, Appl
51	51.5	25.6	77	1	US-08-486-397-4	Sequence 4, Appli
52	51.5	25.6	77	1	US-08-486-397-40	Sequence 40, Appl
53	51.5	25.6	77	1	US-08-486-399-4	Sequence 4, Appli
54	51.5	25.6	77	1	US-08-486-399-40	Sequence 40, Appl
55	51.5	25.6	77	1	US-08-461-965-4	Sequence 4, Appli
56	51.5	25.6	77	1	US-08-461-965-40	Sequence 40, Appl
57	51.5	25.6	77	1	US-08-326-110A-33	Sequence 33, Appl
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59	51.5	25.6	77	1	US-08-634-641-40	Sequence 40, Appl
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113	51.5	25.6	282	2	US-09-544-618-19	Sequence 19, Appl	186	50	24.9	336	2	US-08-910-991-8	Sequence 8, Appl
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134	50	24.9	124	1	US-08-050-319B-4	Sequence 4, Appl	207	50	24.9	455	2	US-09-756-854-5	Sequence 5, Appl
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155	50	24.9	161	2	US-09-326-394-2	Sequence 2, Appl	228	49.5	24.6	487	2	US-09-004-838-101	Sequence 101, App
156	50	24.9	167	1	US-08-050-319B-2	Sequence 2, Appl	229	49.5	24.6	488	2	US-09-004-838-47	Sequence 47, Appl
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297	47	23.4	478	2	US-09-004-838-105	Sequence 105, App
298	47	23.4	480	2	US-09-004-838-49	Sequence 49, Appl
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Prior Application Number: US 60/214,591

Prior Filing Date: 2000-06-27

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Software: PatentIn version 3.1

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Type: PRT

Organism: Homo sapiens

US-09-854-864-7

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Prior Application Number: US 60/214,591

Prior Filing Date: 2000-06-27

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Software: PatentIn version 3.1

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Prior Application Number: US 60/214,591

Prior Filing Date: 2000-06-27

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Prior Application Number: US 60/214,591

Prior Filing Date: 2000-06-27

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US-09-854-864-21

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Db 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYC 34

RESULT 4
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-04,039
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match      100.0%; Score 201; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 7e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYC 34
Db 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYC 34

RESULT 5
US-09-854-864-5
; Sequence 5, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-04,039
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-5

Query Match      100.0%; Score 201; DB 2; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYC 34
Db 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYC 49

RESULT 6
US-09-565-423-11
; Sequence 11, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-423-11

Query Match      100.0%; Score 201; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYC 41

RESULT 7
US-09-949-016-11115
; Sequence 1115, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11115
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11115

Query Match      100.0%; Score 201; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYC 34
Db 16 CSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYC 49

RESULT 8
US-09-854-864-9
```



APPLICANT: BUREAU OF AERONAUTICS  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B



```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match          33.1%; Score 66.5; DB 2; Length 117;
Best Local Similarity 32.4%; Pred. No. 0.00052;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;

QY 2 SONEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   :|||:|||||:|||||:|||||:|||||:
Db 2 AQCEYWDPLLGTCMSCKTICNHQS-ORTCAAF 27
   :|||:|||||:|||||:|||||:|||||:

RESULT 13
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCNA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match          33.1%; Score 66.5; DB 2; Length 59;
Best Local Similarity 32.4%; Pred. No. 0.42;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   :|||:|||||:|||||:|||||:|||||:
Db 1 CPEEQYWDPLLGTCMSCKTICNHQS-ORTCAAF 33
   :|||:|||||:|||||:|||||:|||||:

RESULT 14
US-09-854-864-16
; Sequence 16, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCNA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-16

Query Match          33.1%; Score 66.5; DB 2; Length 166;
Best Local Similarity 32.4%; Pred. No. 1.1;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSONEYFDSLHACIPQCLRCSSNTPTLTQRYC 34
   :|||:|||||:|||||:|||||:|||||:
Db 34 CPEEQYWDPLLGTCMSCKTICNHQS-ORTCAAF 66
   :|||:|||||:|||||:|||||:|||||:

RESULT 16
US-09-290-333-6
; Sequence 6, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
```







```
US-08-810-572A-2
; Sequence 2, Application US/09810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
Query Match      33.1%; Score 66.5; DB 1; Length 293;
Best Local Similarity 32.4%; Pred. No. 2;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY       1 CSONEYFDLSLHACIPQLRCSSNTPPLTCORYC 34
          | : | : || | : | : | : | : | : | : |
DB       34 CPSEQWDPLLGTCMCKTICNHQS-QRTCAAF 66

RESULT 20
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
```







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; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-18

Query Match          33.1%; Score 66.5; DB 2; Length 397;
Best Local Similarity 32.4%; Pred. No. 2.7;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOLRCSNSTPPLTCORVC 34
Db 34 CPEQYWDPLLTGCMCKTICNHQS-ORTCAAPC 66

RESULT 26
US-09-949-016-9626
; Sequence 9626, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9626
; LENGTH: 1106
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-9626

Query Match          30.3%; Score 61; DB 2; Length 1106;
Best Local Similarity 28.0%; Pred. No. 32;
Matches 14; Conservative 6; Mismatches 14; Indels 16; Gaps 2;

QY 1 CSQNEYFDSLHACIPCOLRC-----SSTPPL-----TCORVC 34
Db 899 CSFSEYWDPAFCCKVCKFCMGPAPDQCQTCPNLSLLNTTCVKDC 948

RESULT 27
US-10-104-047-2804
; Sequence 2804, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2804
; LENGTH: 581
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-2804

Query Match          29.6%; Score 59.5; DB 2; Length 581;
Best Local Similarity 28.9%; Pred. No. 26;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOL-----RCSNST 25
Db 337 CSPGHYYNTSIHRCIRCAMGSYQDPFRQNFCSRCPGNT 374

RESULT 28
US-10-104-047-2834
; Sequence 2834, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2834
; LENGTH: 880
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-104-047-2834

Query Match          29.6%; Score 59.5; DB 2; Length 880;
Best Local Similarity 28.9%; Pred. No. 39;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEYFDSLHACIPCOL-----RCSNST 25
Db 636 CSPGHYYNTSIHRCIRCAMGSYQDPFRQNFCSRCPGNT 673

RESULT 29
US-08-276-967-2
; Sequence 2, Application US/08276967
; Patent No. 5851817
; GENERAL INFORMATION:
; APPLICANT: Hardy, Daniel M.
; APPLICANT: Garbers, David L.
; TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
; TITLE OF INVENTION: Sperm
; NUMBER OF INVENTIONS: 8
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/276,967
; FILING DATE: Submitted Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSD:418\KIT
; TELECOMMUNICATION INFORMATION:
```



```
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2476 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-276-967-2

Query Match 27.9%; Score 56; DB 1; Length 2476;
Best Local Similarity 31.6%; Pred. No. 2.7e+02;
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

QY 1 CSQNEYFDSLHACIP-CQ---LRCSSTNPPLTCQRYC 34
Db 1851 CSAHSVYTCVPSCLPSCQDPEGQCTGAGAPSTCEGC 1888

RESULT 30
US-09-621-976-6330
; Sequence 6330, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6330
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6330

Query Match 26.9%; Score 54; DB 2; Length 98;
Best Local Similarity 38.1%; Pred. No. 21;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 14 CIPCOLRCSSNTPLTCQRYC 34
Db 58 CLPCFSQSPSCPPQPCTKPC 78

RESULT 31
US-09-471-276-1590
; Sequence 1590, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSET.025CPI
; CURRENT APPLICATION NUMBER: US/09/471.276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057.719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069.047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: FCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1590
; LENGTH: 98
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```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-276-1590

Query Match 26.9%; Score 54; DB 2; Length 98;
Best Local Similarity 38.1%; Pred. No. 21;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 14 CIPCOLRCSSNTPLTCQRYC 34
Db 58 CLPCFSQSPSCPPQPCTKPC 78

RESULT 32
US-09-252-991A-25721
; Sequence 25721, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074.788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094.190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25721
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25721

Query Match 26.9%; Score 54; DB 2; Length 431;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 10; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

QY 13 ACIPCOLRCSSNTPLTCQRYC 32
Db 242 AC--CRARCSNAWPPTACRR 259

RESULT 33
US-09-257-580-2
; Sequence 2, Application US/09257580
; Patent No. 6307036
; GENERAL INFORMATION:
; APPLICANT: Yorkshire Cancer Research
; TITLE OF INVENTION: Tumour Suppressor Gene
; FILE REFERENCE: Canine p53
; CURRENT APPLICATION NUMBER: US/09/257.580
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 9804178.3
; PRIOR FILING DATE: 1998-02-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Canis
US-09-257-580-2

Query Match 26.6%; Score 53.5; DB 2; Length 381;
Best Local Similarity 48.3%; Pred. No. 89;
Matches 14; Conservative 1; Mismatches 13; Indels 1; Gaps 1;

QY 4 NEYFDSLHACIPCOLRCSSNTPLTCQRYC 32
Db 118 NKLFQCLAKTC-PVQLWVSSPPPTTCVR 145
```



```
RESULT 34
US-08-718-388-9
; Sequence 9, Application US/08718388
; Patent No. 6271362
; GENERAL INFORMATION:
; APPLICANT: MORIKAWA, MINORU
; APPLICANT: HARADA, NAOKI
; TITLE OF INVENTION: GENE ENCODING IGG Fc REGION-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,388
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-718-388-9

Query Match      26.6%; Score 53.5; DB 2; Length 5405;
Best Local Similarity 34.3%; Pred. No. 1.2e+03;
Matches 12; Conservative 5; Mismatches 13; Indels 5; Gaps 2;

QY      1 CSQNEYFDSLHACI-PCQLRCSNTPTPLTCQRYC 34
| | | | |
Db      2733 CPQNSHYE----LCADTCSLGCSALSAPLQCPDGC 2763

RESULT 35
US-09-950-933A-61
; Sequence 61, Application US/09950933A
; Patent No. 6875907
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro, Pedro
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/238472
; CURRENT APPLICATION NUMBER: US/09/950,933A
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Glycine max
; US-09-950-933A-61

Query Match      26.4%; Score 53; DB 2; Length 108;
US-09-950-933A-61
```

```
Best Local Similarity 44.4%; Pred. No. 30;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      17 COLRCSNTPTPLTCQRYC 34
| | | | |
Db      53 CKTRCSAHSRPNVCNRC 70

RESULT 36
US-09-848-295-2
; Sequence 2, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; TITLE OF INVENTION: Thereon
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-848-295-2

Query Match      26.1%; Score 52.5; DB 2; Length 142;
Best Local Similarity 29.4%; Pred. No. 45;
Matches 10; Conservative 8; Mismatches 15; Indels 1; Gaps 1;

QY      1 CSQNEYFDSLHACIPCOLRCSNTPTPLTCQRYC 34
| | | | |
Db      4 CPEEQYMAALLGTCTMFCFCAICNHQS-QRTCAASC 36

RESULT 37
US-09-950-933A-65
; Sequence 65, Application US/09950933A
; Patent No. 6875907
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro, Pedro
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/238472
; CURRENT APPLICATION NUMBER: US/09/950,933A
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Glycine max
; US-09-950-933A-65

Query Match      25.9%; Score 52; DB 2; Length 115;
Best Local Similarity 44.4%; Pred. No. 42;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      17 COLRCSNTPTPLTCQRYC 34
| | | | |
Db      60 CAVRCSLHSRPKICSRAC 77

RESULT 38
US-09-877-730-26
; Sequence 26, Application US/09877730
```



```
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 547
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-877-730-26

Query Match      25.9%; Score 52; DB 2; Length 547;
Best Local Similarity 33.3%; Pred. No. 1.9e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy      4 NEYFDSLHACIPQQLRCSNTPTLTCORY 33
      | : | : | : | : | : | : | : | : |
Db      503 NSPIDAKVLSCGICISRSSIPPPCVCKMY 532

RESULT 39
US-09-877-730-24
; Sequence 24, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 624
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-877-730-24

Query Match      25.9%; Score 52; DB 2; Length 624;
Best Local Similarity 33.3%; Pred. No. 2.2e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy      4 NEYFDSLHACIPQQLRCSNTPTLTCORY 33
      | : | : | : | : | : | : | : | : |
Db      580 NSPIDAKVLSCGICISRSSIPPPCVCKMY 609

RESULT 40
US-09-877-730-22
; Sequence 22, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
```

```
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 712
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-877-730-22

Query Match      25.9%; Score 52; DB 2; Length 712;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy      4 NEYFDSLHACIPQQLRCSNTPTLTCORY 33
      | : | : | : | : | : | : | : | : |
Db      668 NSPIDAKVLSCGICISRSSIPPPCVCKMY 697

RESULT 41
US-09-877-730-16
; Sequence 16, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 826
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-877-730-16

Query Match      25.9%; Score 52; DB 2; Length 826;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy      4 NEYFDSLHACIPQQLRCSNTPTLTCORY 33
      | : | : | : | : | : | : | : | : |
Db      782 NSPIDAKVLSCGICISRSSIPPPCVCKMY 811

RESULT 42
US-09-877-730-6
; Sequence 6, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
```



```
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 904
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-6

Query Match      25.9%; Score 52; DB 2; Length 904;
Best Local Similarity 33.3%; Pred. No. 3.1e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY      4 NEYFDSLLHACIPCOLRCSSNTPTPLTCQRY 33
| : | : | : | : | : | : | : | : | : |
Db      860 NSPIDAKVLSCGICCSRSISPPPCVCCKMY 889
| : | : | : | : | : | : | : | : | : |

RESULT 43
US-09-877-730-12
; Sequence 12, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 991
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-12

Query Match      25.9%; Score 52; DB 2; Length 991;
Best Local Similarity 33.3%; Pred. No. 3.4e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY      4 NEYFDSLLHACIPCOLRCSSNTPTPLTCQRY 33
| : | : | : | : | : | : | : | : | : |
Db      947 NSPIDAKVLSCGICCSRSISPPPCVCCKMY 976
| : | : | : | : | : | : | : | : | : |

RESULT 44
US-09-877-730-2
; Sequence 2, Application US/09877730
; Patent No. 6465632
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
```

```
; TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the
; FILE REFERENCE: LEX-0189-USA
; CURRENT APPLICATION NUMBER: US/09/877,730
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,607
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1069
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-877-730-2

Query Match      25.9%; Score 52; DB 2; Length 1069;
Best Local Similarity 33.3%; Pred. No. 3.6e+02;
Matches 10; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY      4 NEYFDSLLHACIPCOLRCSSNTPTPLTCQRY 33
| : | : | : | : | : | : | : | : | : |
Db      1025 NSPIDAKVLSCGICCSRSISPPPCVCCKMY 1054
| : | : | : | : | : | : | : | : | : |

RESULT 45
US-08-117-080-12
; Sequence 12, Application US/08117080
; Patent No. 5482928
; GENERAL INFORMATION:
; APPLICANT: DE BOLLE, MIGUEL
; APPLICANT: BROEKAERT, WILLEM F
; APPLICANT: CAMMUE, BRUNO PA
; APPLICANT: VANDERLEVDEN, JOZEF
; APPLICANT: REES, SARAH B
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
; STREET: TOWER
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,080
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00423
; FILING DATE: 10-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9105052.6
; FILING DATE: 11-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9105684.6
; FILING DATE: 19-MAR-1991
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861 3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
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ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2  
US-08-117-080-12

Query Match 25.6%; Score 51.5; DB 1; Length 63;  
Best Local Similarity 38.5%; Pred. No. 27;  
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy 10 LLHACIPQLRCSNT-PPLTCQRYC 34  
Db 24 MIEACIGNGRCNENVPYCCSGFC 49

RESULT 46

US-08-471-329-12  
; Sequence 12, Application US/08471329  
; Patent No. 5689048  
; GENERAL INFORMATION:  
; APPLICANT: DE BOLLE, MIGUEL  
; APPLICANT: BROEKAERT, WILLEM F  
; APPLICANT: CAMMUE, BRUNO PA  
; APPLICANT: VANDERLEYDEN, JOZEF  
; APPLICANT: REES, SARAH B  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST  
; STREET: TOWER  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471.329  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/117,080  
; FILING DATE: 20-DEC-1993  
; APPLICATION NUMBER: PCT/GB92/00423  
; FILING DATE: 10-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9105052.6  
; FILING DATE: 11-MAR-1991  
; APPLICATION NUMBER: US 08/117,080  
; FILING DATE: 20-DEC-1993  
; APPLICATION NUMBER: PCT/GB92/00423  
; FILING DATE: 10-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9105052.6  
; FILING DATE: 11-MAR-1991  
; APPLICATION NUMBER: GB 9105684.6  
; FILING DATE: 19-MAR-1991  
; APPLICATION NUMBER: PCT/GB92/00423  
; FILING DATE: 10-MAR-1992  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861 3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 63 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2  
US-08-471-329-12

Query Match 25.6%; Score 51.5; DB 1; Length 63;  
Best Local Similarity 38.5%; Pred. No. 27;  
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy 10 LLHACIPQLRCSNT-PPLTCQRYC 34  
Db 24 MIEACIGNGRCNENVPYCCSGFC 49

Db 24 MIEACIGNGRCNENVPYCCSGFC 49

RESULT 47

US-08-915-142-12  
; Sequence 12, Application US/08915142  
; Patent No. 5942663  
; GENERAL INFORMATION:  
; APPLICANT: DE BOLLE, MIGUEL  
; APPLICANT: BROEKAERT, WILLEM F  
; APPLICANT: CAMMUE, BRUNO PA  
; APPLICANT: VANDERLEYDEN, JOZEF  
; APPLICANT: REES, SARAH B  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST  
; STREET: TOWER  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/915.142  
; FILING DATE: 20-AUG-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,329  
; FILING DATE: 02-JUN-1995  
; APPLICATION NUMBER: US 08/117,080  
; FILING DATE: 20-DEC-1993  
; APPLICATION NUMBER: PCT/GB92/00423  
; FILING DATE: 10-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9105052.6  
; FILING DATE: 11-MAR-1991  
; APPLICATION NUMBER: GB 9105684.6  
; FILING DATE: 19-MAR-1991  
; APPLICATION NUMBER: PCT/GB92/00423  
; FILING DATE: 10-MAR-1992  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861 3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 63 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2  
US-08-915-142-12

Query Match 25.6%; Score 51.5; DB 1; Length 63;  
Best Local Similarity 38.5%; Pred. No. 27;  
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy 10 LLHACIPQLRCSNT-PPLTCQRYC 34  
Db 24 MIEACIGNGRCNENVPYCCSGFC 49

RESULT 48

US-08-465-380-4  
; Sequence 4, Application US/08465380  
; Patent No. 5863894



```

;
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,380
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-465-380-4

Query Match 25.6%; Score 51.5; DB 1; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEYFDSLHAC---IPCQLRCSNTP----PLTCQRYC 34
|:::| | | | | | | | | | | | | | | | | |
Db 6 CGENEWLDD---CGTQKPCAKCNEPPEEDPICRSRC 42

RESULT 49
US-08-465-380-40
; Sequence 40, Application US/08465380
; Patent No. 5863894
; GENERAL INFORMATION:
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,
; APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
; APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
;
;
;
;

```

```

;
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,380
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-465-380-40

Query Match 25.6%; Score 51.5; DB 1; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEYFDSLHAC---IPCQLRCSNTP----PLTCQRYC 34
|:::| | | | | | | | | | | | | | | | | |
Db 6 CGENEWLDD---CGTQKPCAKCNEPPEEDPICRSRC 42

RESULT 50
US-08-480-478-33
; Sequence 33, Application US/08480478
; Patent No. 5864009
; GENERAL INFORMATION:
; APPLICANT: GEORGE P. VLASUK; PATRICK ERIC
; APPLICANT: HUGO STANSENS; JORIS HILDA
; APPLICANT: LIEVEN MESSENS; MARC JOZEF
; APPLICANT: LAUWEREYS; YVES RENE LAROCHE;
; APPLICANT: LAURENT STEPHANE JESPERS; and
; APPLICANT: YANNICK GEORGES JOZEF
; APPLICANT: GANSEMAN
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
; TITLE OF INVENTION: COAGULANT PROTEIN
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
;
;
;
;

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Query Match 25.6%; Score 51.5; DB 1; Length 77;



Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy	1	CSQNEYFDSLHAC---	IPQLRCSNTP----	PLTCQRYC	34
		:    :	:   :	:	
Db	6	CGENEWLDD----	CGTQKPCEAKCNEEPP	EEEDPICRSRG	42

RESULT 53

US-08-486-399-4  
; Sequence 4, Application US/08486399  
; Patent No. 5866543  
; GENERAL INFORMATION:  
; APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
; APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
; APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
; APPLICANT: Yannick G.J. Gansmeant, Matthew Moyle,  
; APPLICANT: Peter W. Bergum  
; TITLE OF INVENTION: NENATODE-EXTRACTED ANTICOAGULANT  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.

RESULT 54

US-08-486-399-40  
; Sequence 40, Application US/08486399  
; Patent No. 5866543

1 GENERAL INFORMATION:  
2 APPLICANT: George P. Vlaauk, Patric H. Stanssens,  
3 APPLICANT: Joris H. L. Mengens, Marc J. Lauwereys,  
4 APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
5 APPLICANT: Yannick G. J. Gansemaans, Matthew Noyle,  
6 APPLICANT: Peter W. Barmum  
7 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
8 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
9

```

NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486.399

```

FILING DATE: June 5, 1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 213/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 40:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 77 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum  
 US-08-486-399-40

Query Match 25.6%; Score 51.5; DB 1; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels

[illegible]

RESULT 55

US-08-461-965-4  
; Sequence 4, Application US/08461965  
; Patent No. 5872098

? GENERAL INFORMATION:  
 ? APPLICANT: George P. Vlausk, Patric H. Stanssens,  
 ? APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
 ? APPLICANT: Yves R. Laroche, Laurent S. Jeepers,  
 ? APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
 ? APPLICANT: Peter W. Bergum  
 ? TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
 ? TITLE OF INVENTION: PROTEIN  
 ? NUMBER OF SEQUENCES: 356  
 ? CORRESPONDENCE ADDRESS:  
 ? ADDRESSEE: Lyon & Lyon  
 ? STREET: 633 West Fifth Street  
 ?

Query Match	25.6%	Score 51.5;	DB 1;	Length 77;
Best Local Similarity	29.3%	Pred. No. 33;		
Matches 12; Conservative	6;	Mismatches 12;	Indels	

**Qy** 1 CSQNEYFDSLHAC---IPCQLRCSSNTP----PLTCQRVC 34  
| : || | | ||| : | : | :  
**Db** 6 CGENEWLDD-----CGTKPCEAKCNPEEPDEEDPICRSRG 42

RESULT 54

US-08-486-399-40  
; Sequence 40, Application US/08486399  
; Patent No. 5866543



STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,965  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 210/243

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE: Ancylostoma caninum  
ORGANISM: Ancylostoma caninum

US-08-461-965-4

Query Match 25.6%; Score 51.5; DB 1; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEYFDSLHAC---IPQLRCSNTP-----PLTCQRYC 34  
DB 6 CGNEWLDD---CGTKPCEAKCNEPPEEDPICRSRGC 42

RESULT 56  
US-08-461-965-40  
Sequence 40, Application US/08461965  
Patent No. 5872098

GENERAL INFORMATION:  
APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Menssens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum  
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1







TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
US-08-634-641-40

Query Match 25.6%; Score 51.5; DB 1; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEVFDSLHAC---IPCQLRCSSNTP---PLTCQRYC 34  
Db 6 CGENWLDD---CGTQKPCAKCNEPPPEEDPICSRGCC 42

RESULT 60

US-09-249-471-4  
Sequence 4, Application US/09249471  
Patent No. 6040441  
GENERAL INFORMATION:  
APPLICANT: Vlaauk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwerys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganssemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Beigum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
FILING DATE: US/09/249,471  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
US-09-249-471-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEVFDSLHAC---IPCQLRCSSNTP---PLTCQRYC 34  
Db 6 CGENWLDD---CGTQKPCAKCNEPPPEEDPICSRGCC 42

RESULT 61

US-09-249-471-40  
Sequence 40, Application US/09249471  
Patent No. 6040441  
GENERAL INFORMATION:  
APPLICANT: Vlaauk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwerys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganssemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Beigum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
FILING DATE: US/09/249,471  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965



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; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,390
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-472-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSQNEVFDSLHAC---IPCQRCSSNTP-----PLTCQRYC 34
   |||:| | | | | | | | | | | | | | | | | |
Db 6 CGSENEWLDD---CGTKPCPEAKCNBEPPEEDPICRSRG 42

RESULT 63
US-09-249-472-40
; Sequence 40, Application US/09249472
; Patent No. 6046318
; GENERAL INFORMATION:
; APPLICANT: Vlausk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Ganssemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Berqum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,472
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231

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; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-472-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSQNEYFDSLHAC---IPCLRCSSNTP----PLTCORYC 34
Db 6 CGENEWLLDD---CGTQKPCAKNRPPEEDPICRSGC 42

RESULT 64
US-09-249-451-4
; Sequence 4, Application US/09249451
; Patent No. 6087487
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansemans, Yannick Georges Jozef
; APPLICANT: Moyle, Peter W.
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,451
; FILING DATE:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/465,380
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-451-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

Qy 1 CSQNEYFDSLHAC---IPCLRCSSNTP----PLTCORYC 34
Db 6 CGENEWLLDD---CGTQKPCAKNRPPEEDPICRSGC 42

RESULT 65
US-09-249-451-40
; Sequence 40, Application US/09249451
; Patent No. 6087487
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansemans, Yannick Georges Jozef
; APPLICANT: Moyle, Peter W.
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,451
; FILING DATE:
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; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,451
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-451-40

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSONEYFDSLHAC---IPCQLRCSNTP----PLTCQRYC 34
      |||:| | | | | | | | | | | | | | | | | |
Db 6 CGENELDD-----CGTQKCEAKCNEPPEEDPICSRGC 42

RESULT 66
US-08-809-455-4
; Sequence 4, Application US/08809455
; Patent No. 6090916
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,455
; FILING DATE: April 17, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/486,397
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-809-455-4

Query Match 25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

QY 1 CSONEYFDSLHAC---IPCQLRCSNTP----PLTCQRYC 34
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Db 6 CGENELDD-----CGTQKCEAKCNEPPEEDPICSRGC 42

RESULT 67
US-08-809-455-40
; Sequence 40, Application US/08809455
; Patent No. 6090916
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Laroche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansemans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Bergum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
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ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/809,455  
FILING DATE: April 17, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
US-08-809-455-40  
  
Query Match 25.6%; Score 51.5; DB 2; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;  
  
Qy 1 CSQNEYFDSLHAC---IPCQLRCSSNTP-----PLTCQRYC 34  
Db 6 CGENEWLLD-----CGTQKPCAKCNBPPBEEEDPICRSRG 42  
  
RESULT 68  
US-09-249-461-4  
Sequence 4, Application US/09249461  
Patent No. 6096877  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Gangsemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Beirgum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles

STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/249,461  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
US-09-249-461-4  
  
Query Match 25.6%; Score 51.5; DB 2; Length 77;  
Best Local Similarity 29.3%; Pred. No. 33;  
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;  
  
Qy 1 CSQNEYFDSLHAC---IPCQLRCSSNTP-----PLTCQRYC 34  
Db 6 CGENEWLLD-----CGTQKPCAKCNBPPBEEEDPICRSRG 42  
  
RESULT 69  
US-09-249-461-40  
Sequence 40, Application US/09249461  
Patent No. 6096877  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Gangsemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Beirgum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:



```

; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/249,461
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-461-40

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Query Match      25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

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QY 1 CSQNEYFDSLHAC---IPCQLRCSNTP-----PLTCQRYC 34
Db 6 CGENEWDD----CGTQKPCAKCNPEEPEDPICRSRG 42

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RESULT 70
US-09-249-448-4
; Sequence 4, Application US/09249448
; Patent No. 6121435
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Larocche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane
; APPLICANT: Gansmans, Yannick Georges Jozef
; APPLICANT: Moyle, Matthew
; APPLICANT: Berghum, Peter W.
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

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; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/249,448
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,455
; FILING DATE: April 17, 1997
; APPLICATION NUMBER: PCT/US95/13231
; FILING DATE: October 17, 1995
; APPLICATION NUMBER: 08/486,399
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/461,965
; FILING DATE: June 5, 1995
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 216/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-09-249-448-4

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Query Match      25.6%; Score 51.5; DB 2; Length 77;
Best Local Similarity 29.3%; Pred. No. 33;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps 3;

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QY 1 CSQNEYFDSLHAC---IPCQLRCSNTP-----PLTCQRYC 34
Db 6 CGENEWDD----CGTQKPCAKCNPEEPEDPICRSRG 42

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RESULT 71
US-09-249-448-40
; Sequence 40, Application US/09249448
; Patent No. 6121435
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; APPLICANT: Stanssens, Patrick Eric Hugo
; APPLICANT: Messens, Joris Hilda Lieven
; APPLICANT: Lauwereys, Marc Josef
; APPLICANT: Larocche, Yves Rene
; APPLICANT: Jespers, Laurent Stephane

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RESULT 72  
US-09-249-473-4  
; Sequence 4, Application US/09249473  
; Patent No. 6534629  
; GENERAL INFORMATION:  
; APPLICANT: Vlasuk, George Phillip  
; APPLICANT: Stanssena, Patrick Eric Hugo











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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 21, 2005, 15:43:09 ; Search time 106.4 Seconds  
(without alignments)  
140.403 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_8\_41

Perfect score: 201

Sequence: 1 CSQNEVFDLSLHACIFCQLRCSNTPTPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : A Geneseq\_21.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	201	100.0	34	6	ADA49366 Human BCM
3	201	100.0	40	9	ADZ67761 Human tum
4	201	100.0	51	5	AAE15485 Human B-C
5	201	100.0	52	9	AEC02032 Amino aci
6	201	100.0	58	5	AAE15501 Human B C
7	201	100.0	181	5	AAE15484 Human B-C
8	201	100.0	184	3	AAE08843 Amino aci
9	201	100.0	184	3	AAE094001 A human B
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19	201	100.0	184	6	ABR40082 Human tum
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25	201	100.0	184	8	ADQ94442	Adq94442 Neutrokin
26	201	100.0	184	8	ADP56014	Adp56014 Human PRO
27	201	100.0	184	9	ADW03432	Adw03432 Human BCM
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68	66.5	33.1	33	5	AAE15495	Aae15495 Human TAC
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104	66.5	33.1	233	8	ADQ76815	Human TAC	177	58	28.9	175	9	ADW21300	Mouse Bly
105	66.5	33.1	233	8	ADQ94440	Neutrokin	178	58	28.9	175	9	ADZ67759	Mouse tum
106	66.5	33.1	233	9	ADW03430	Human TAC	179	58	28.9	175	9	AEA01659	B-cell ac
107	66.5	33.1	233	9	ADK00765	hTACI sp1	180	58	28.9	175	9	ADW03396	Mouse BR3
108	66.5	33.1	234	8	ADW03443	Human TAC	181	58	28.9	316	9	AEA01660	Murine BA
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110	66.5	33.1	332	6	AAE35228	Human TAC	183	57.5	28.6	1679	4	ABE60502	Drosophil
111	66.5	33.1	334	6	AAO14133	Protein o	184	57.5	28.6	1680	8	ADS96568	Drosophil
112	66.5	33.1	344	6	AAE35224	Human TAC	185	56	27.9	268	8	ADT60022	Plant pol
113	66.5	33.1	348	6	AAE35225	Human TAC	186	56	27.9	2476	2	AAW67738	Pig p105
114	66.5	33.1	357	6	AAE35226	Human TAC	187	55.5	27.6	225	4	ABE71511	Drosophil
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116	66.5	33.1	382	6	AAE35223	Human TAC	189	55.5	27.6	558	8	ADQ82379	Novel hum
117	66.5	33.1	397	5	AAE15498	Human TAC	190	55.5	27.6	672	8	ADQ82385	Fibulin-1
118	66.5	33.1	404	5	AAO14136	Protein o	191	55.5	27.6	775	8	ADQ82382	Fibulin-1
119	65	32.3	1994	6	ADRI8912	Human muc	192	55.5	27.6	818	8	ADQ82380	Fibulin-1
120	61	30.3	1887	6	ABU12113	Human pro	193	55.5	27.6	818	8	ADQ82377	Novel hum
121	61	30.3	1897	7	ABE80242	Human sub	194	55.5	27.6	818	8	ADQ82383	Fibulin-1
122	61	30.3	1887	7	ADM92324	Human nov	195	55.5	27.6	934	8	ADH72262	Human pro
123	59.5	29.6	138	5	ABP69063	Human pol	196	55.5	27.6	955	6	ADA55084	Human pro
124	59.5	29.6	353	4	ABB71555	Drosophil	197	55.5	27.6	955	8	ADQ82381	Fibulin-1
125	59.5	29.6	418	5	ABB08238	Human 567	198	55.5	27.6	955	8	ADQ82384	Fibulin-1
126	59.5	29.6	418	9	ADY54276	Human 567	199	55.5	27.6	992	7	AAE38809	Human POL
127	59.5	29.6	581	7	ADB64650	Human pro	200	55.5	27.6	2820	4	ABE63296	Drosophil
128	59.5	29.6	735	5	AAE68258	Human POL	201	55.5	27.6	2820	8	ADQ01056	Fruit fly
129	59.5	29.6	735	6	ABU12091	Novel hum	202	55	27.4	477	7	ADC32665	Human nov
130	59.5	29.6	845	5	AAE68259	Human POL	203	55	27.4	477	9	AEA21141	Novel hum
131	59.5	29.6	845	6	ABU12092	Novel hum	204	55	27.4	739	9	AEA20333	Novel hum
132	59.5	29.6	845	7	AAE38807	Human POL	205	55	27.4	770	5	AAE23338	Human int
133	59.5	29.6	880	7	ADB64680	Human pro	206	55	27.4	824	6	ADC30933	Human nov
134	59.5	29.6	897	4	AAE58887	Amino aci	207	55	27.4	858	8	ADA55005	Human pro
135	59.5	29.6	897	4	ABG06309	Novel hum	208	55	27.4	858	8	ABM80296	Tumour-as
136	59.5	29.6	897	5	ABG91402	Primate L	209	55	27.1	955	4	ABG22836	Novel hum
137	59.5	29.6	897	7	ADE07852	Novel pro	210	54.5	27.1	45	8	ABO54007	Human gen
138	59.5	29.6	897	7	ADE08940	Novel pro	211	54.5	27.1	751	7	ADC31546	Human nov
139	59.5	29.6	914	8	ADI27628	Human SCU	212	54.5	27.1	1366	8	ADS98652	Protein f
140	59.5	29.6	939	6	AAE29932	Human LP2	213	54.5	27.1	1997	5	AAU84802	HCV HepC
141	59.5	29.6	973	5	AAE68260	Human POL	214	54.5	27.1	2198	8	ADU98030	Protein f
142	59.5	29.6	974	6	ABU12093	Novel hum	215	54.5	27.1	5985	5	AAU84799	HCV HepCI
143	59.5	29.6	974	7	AAE38808	Human POL	216	54	26.9	34	9	AEC02039	Formula 1
144	59.5	29.6	985	7	ADM04189	Human pro	217	54	26.9	70	5	AAE22252	Human BAF
145	59.5	29.6	989	6	AAE30306	Human LP2	218	54	26.9	73	5	AAE22251	Human BAF
146	59.5	29.6	991	6	AAO16645	Human ext	219	54	26.9	73	5	AAE22251	Human BAF
147	59.5	29.6	993	4	AAE58888	Amino aci	220	54	26.9	98	3	AAE5429	Human 5'
148	59.5	29.6	993	6	AAE29931	Human LP2	221	54	26.9	98	8	ADU72993	Non-signa
149	59.5	29.6	993	6	ADI27630	Human SCU	222	54	26.9	98	9	ADZ73984	Human com
150	59.5	29.6	993	8	ADI27637	SCUBE3-2	223	54	26.9	121	4	AAW95477	Human rep
151	59.5	29.6	1006	5	AAU79172	Human MEG	224	54	26.9	121	4	AAW95477	Human rep
152	59.5	29.6	1009	5	AAE58261	Human POL	225	54	26.9	182	4	ABE93696	Human tes
153	59.5	29.6	1009	6	AAE29930	Human LP2	226	54	26.9	185	5	AAE22266	Human pro
154	59.5	29.6	1009	6	ABU12094	Novel hum	227	54	26.9	333	8	ADY07720	Plant ful
155	59	29.4	34	5	AAE15496	Human TAC	228	54	26.9	431	7	ABO76975	Pseudomon
156	59	29.4	34	6	ADA49369	Human TAC	229	54	26.9	986	4	ABG07760	Novel hum
157	59	29.4	38	5	ADU10952	Human AGP	230	54	26.9	1240	6	ABR41659	Human DIT
158	59	29.4	175	9	ADM03418	Rat BR3 p	231	54	26.9	1966	8	ABM84359	Human dia
159	59	29.4	175	9	ADM21317	Rat Blys	232	54	26.9	1973	8	ABM84358	Human dia
160	59	29.4	246	6	ABP97720	Amino aci	233	54	26.9	1974	8	ABM84357	Human dia
161	59	29.4	246	6	ADK00762	Native hu	234	54	26.9	2022	7	ADJ68792	Human hea
162	59	29.4	246	9	ADM03438	Human TAC	235	54	26.9	2022	7	ADY18702	Human bet
163	59	29.4	247	3	AAE39998	Human BR4	236	54	26.9	2158	7	ADD18702	Human dis
164	59	29.4	247	7	ABR61797	Human RYZ	237	54	26.9	4072	4	ABE63614	Drosophil
165	59	29.4	266	8	ADO69971	Plasmodiu	238	53.5	26.6	76	8	ABO58965	Human gen
166	59	29.4	2459	8	ADO69969	Plasmodiu	239	53.5	26.6	109	5	ABP09548	Human ORF
167	58.5	29.1	428	8	ADQ97204	Mouse can	240	53.5	26.6	381	5	AAE14247	Canine p5
168	58	28.9	65	5	AAE22247	Mouse BAF	241	53.5	26.6	508	4	ABG22213	Novel hum
169	58	28.9	67	8	ADT94167	Murine BA	242	53.5	26.6	758	5	ABP35698	Fungal 2B
170	58	28.9	128	9	ADZ12994	Murine ca	243	53.5	26.6	2957	4	ABG22214	Novel hum



cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
rheumatoid arthritis; atherosclerosis.

Homo sapiens.  
WO200187979-A2.  
22-NOV-2001.  
14-MAY-2001; 2001WO-US015567.  
12-MAY-2000; 2000US-0204039P.  
27-JUN-2000; 2000US-0214591P.  
14-MAY-2001; 2001US-00214591.  
(AMGE-) AMGEN INC.  
Theill LE, Yu G;  
WPI; 2002-066686/09.  
Inhibiting activity of B cell maturation protein and/or transmembrane  
activator and intracellular cyclophilin ligand interactor, by  
administering a binding partner for APRIL, a tumor necrosis factor family  
ligand.  
Claim 1; Fig 10A; 94pp; English.  
The invention relates to a method for inhibiting TACI (transmembrane  
activator and intracellular CAML interactor) and/or B cell maturation  
protein (BCMA) activity in a mammal. The method comprises administering a  
specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
family ligand), having the consensus region of TACI, BCMA, or the TACI/  
BCMA extracellular consensus sequence, but not the extracellular region  
of TACI or BCMA. The method is useful for inhibiting activity of TACI  
and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
lymphoproliferative disorders, one or more solid tumours such as lung,  
gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
antagonists are useful for treating inflammation and immune function  
diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
disease), drug and insect sting allergy, inflammatory bowel disease  
(Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
with leucocyte infiltration of the skin or organs. The present sequence  
is human BCMA protein cysteine-rich consensus region

Sequence 34 AA;  
Query Match 100.0%; Score 201; DB 5; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.8e-18;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORVC 34  
Db 1 CSQNEYFDSLHACIPQLRCSSNTPLTCORVC 34

RESULT 2  
ADA49366  
ID ADA49366 standard; peptide; 34 AA.  
XX  
AC ADA49366;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human BCMA cysteine rich domain.

Aaw14749 IGG-Fc bi  
Abp55383 Human col  
Adl15023 Human Igg  
Adq18828 Human sof  
Adv70227 Tumour-ass  
Abg22216 Novel hum  
Aae22261 Human BAF  
Aao21306 Soybean K  
Aaw98909 Mouse IMC  
Aaw98908 Mouse IMC  
Ade25527 Mouse SLP  
Adf28912 Mouse SLP  
Adx02863 Murine an  
Adq59487 Human can  
Adz13856 Murine ca  
Aae22267 Human BAF  
Adj92151 Human hai  
Adn22513 Bacterial  
Abp34972 Human ORF  
Adf77377 Human tum  
Adj92512 Human TR2  
Aae23295 Human gen  
Aao13678 Human tra  
Aab11195 Human tra  
Aae22254 Human BAF  
Aao21310 Soybean K  
Adx88417 Plant ful  
Adv69654 Human sof  
Ade07963 Novel pro  
Adj92159 Human hai  
Abb62442 Drosophil  
Ady09383 Plant ful  
Abu54207 Human nov  
Abu54212 Human nov  
Abu10466 Novel hum  
Abu54211 Human nov  
Abu10465 Novel hum  
Abu54210 Human nov  
Abu10464 Novel hum  
Abu10464 Novel hum  
Abg07994 Novel hum  
Abu54207 Human nov  
Abu10461 Novel hum  
Abu54202 Human nov  
Abu10456 Novel hum  
Abu54205 Human nov  
Abu10459 Novel hum  
Abu54200 Human nov  
Abu10454 Novel hum  
Abb66271 Drosophil  
Aar27113 Mj-AMP2 p  
Aar57301 Antimicro  
Abg32139 Dendroasp  
Aay30383 Nematode  
Aay30413 Mature ne  
Aab15298 A. caninu  
Ady37282 Hookworm  
Aar91699 AcanNAPS.  
Aay30394 Nematode

53.5 26.6 5405 2 AAW14749  
53.5 26.6 5405 6 ABP55383  
53.5 26.6 5405 7 ADL15023  
53.5 26.6 5405 8 ADQ18828  
53.5 26.6 5405 9 ADV70227  
53.5 26.6 7337 4 ABG22216  
53 26.4 70 5 AAE22261  
53 26.4 108 5 AAO21306  
53 26.4 126 2 AAW98909  
53 26.4 131 2 AAW98908  
53 26.4 131 7 ADE25527  
53 26.4 131 9 ADF28912  
53 26.4 131 9 ADX02863  
53 26.4 146 8 ADQ59487  
53 26.4 146 9 ADZ13856  
53 26.4 185 5 AAE22267  
53 26.4 271 7 ADJ92151  
53 26.4 2824 8 ADN22513  
52.5 26.1 114 5 ABP34972  
52.5 26.1 142 7 ADF77377  
52.5 26.1 142 8 ADJ92512  
52.5 26.1 154 5 AAE23295  
52.5 26.1 166 4 AAO13678  
52.5 26.1 976 4 ABB11195  
52.5 26.1 70 5 AAE22254  
52 25.9 115 5 AAO21310  
52 25.9 133 8 ADX88417  
52 25.9 161 9 ADV69654  
52 25.9 281 7 ADE07963  
52 25.9 292 7 ADJ92159  
52 25.9 330 4 ABB62442  
52 25.9 384 8 ADY09383  
52 25.9 547 6 ABU54212  
52 25.9 547 6 ABU10466  
52 25.9 624 6 ABU54211  
52 25.9 624 6 ABU10465  
52 25.9 712 6 ABU54210  
52 25.9 712 6 ABU10464  
52 25.9 780 4 ABG07994  
52 25.9 826 6 ABU54207  
52 25.9 826 6 ABU10461  
52 25.9 904 6 ABU54202  
52 25.9 904 6 ABU10456  
52 25.9 991 6 ABU54205  
52 25.9 991 6 ABU10459  
52 25.9 1069 6 ABU54200  
52 25.9 1069 6 ABU10454  
51.5 25.6 45 4 ABB66271  
51.5 25.6 63 2 AAR27113  
51.5 25.6 63 2 AAR57301  
51.5 25.6 76 5 ABG32139  
51.5 25.6 77 2 AAY30383  
51.5 25.6 77 2 AAY30413  
51.5 25.6 77 3 AAB15298  
51.5 25.6 77 9 ADY37282  
51.5 25.6 100 2 AAR91699  
51.5 25.6 100 2 AAY30394

AW14749 IGG-Fc bi  
Abp55383 Human col  
Adl15023 Human Igg  
Adq18828 Human sof  
Adv70227 Tumour-ass  
Abg22216 Novel hum  
Aae22261 Human BAF  
Aao21306 Soybean K  
Aaw98909 Mouse IMC  
Aaw98908 Mouse IMC  
Ade25527 Mouse SLP  
Adf28912 Mouse SLP  
Adx02863 Murine an  
Adq59487 Human can  
Adz13856 Murine ca  
Aae22267 Human BAF  
Adj92151 Human hai  
Adn22513 Bacterial  
Abp34972 Human ORF  
Adf77377 Human tum  
Adj92512 Human TR2  
Aae23295 Human gen  
Aao13678 Human tra  
Aab11195 Human tra  
Aae22254 Human BAF  
Aao21310 Soybean K  
Adx88417 Plant ful  
Adv69654 Human sof  
Ade07963 Novel pro  
Adj92159 Human hai  
Abb62442 Drosophil  
Ady09383 Plant ful  
Abu54207 Human nov  
Abu54212 Human nov  
Abu10466 Novel hum  
Abu54211 Human nov  
Abu10465 Novel hum  
Abu54210 Human nov  
Abu10464 Novel hum  
Abu10464 Novel hum  
Abg07994 Novel hum  
Abu54207 Human nov  
Abu10461 Novel hum  
Abu54202 Human nov  
Abu10456 Novel hum  
Abu54205 Human nov  
Abu10459 Novel hum  
Abu54200 Human nov  
Abu10454 Novel hum  
Abb66271 Drosophil  
Aar27113 Mj-AMP2 p  
Aar57301 Antimicro  
Abg32139 Dendroasp  
Aay30383 Nematode  
Aay30413 Mature ne  
Aab15298 A. caninu  
Ady37282 Hookworm  
Aar91699 AcanNAPS.  
Aay30394 Nematode

RESULT 1  
AAE15486  
ID AAE15486 standard; peptide; 34 AA.  
XX  
AC AAE15486;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human B-cell maturation (BCMA) protein cysteine-rich consensus region.  
XX  
DE Human; transmembrane activator and intracellular CAML interactor; TACI;  
KW



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XX TALL-1; antagonist; immunosuppressive; antirheumatic; antihypertensive; antiinflammatory;
KW antiarthritic; dermatological; antidiabetic; vasotrophic; neuroprotective;
KW antichryoid; antipyrctic; nephrotropic; vasotrophic; vaccine;
KW autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;
KW insulin dependent diabetes mellitus; multiple sclerosis;
KW myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;
KW autoimmune thrombocytopenic purpura; Goodpasture's syndrome;
KW pemphigus vulgaris; acute rheumatic fever;
KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; CRD;
KW cysteine rich domain.
XX
XX Homo sapiens.
XX
XX WO2003035846-A2.
XX
XX 01-MAY-2003.
XX
XX 24-OCT-2002; 2002WO-US034376.
XX
XX 24-OCT-2001; 2001US-0345106P.
XX
XX 14-JAN-2002; 2002US-0348962P.
XX
XX 07-FEB-2002; 2002US-0354966P.
XX
XX 13-AUG-2002; 2002US-0403364P.
XX
XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
XX Zhang G, Shu H, Liu Y, Xu L;
XX
XX WPI; 2003-403345/38.
XX
XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological
XX activity in mammal, has a modification in the region connecting beta
XX strands D and E that reduces the biological activity of TALL-1
XX antagonist.
XX
XX Disclosure; Page 616; 618pp; English.
XX
XX The invention relates to a novel TALL-1 antagonist protein, comprising a
XX sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
XX NO:2, by at least one modification in the region connecting 6bgr; strands
XX D and E that reduces the biological activity of the TALL-1 antagonist as
XX compared to wild-type TALL-1. A protein of the invention has
XX immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
XX dermatological, antidiabetic, neuroprotective, antichryoid, antipyrctic,
XX nephrotropic, and vasotrophic activity. A TALL-1 antagonist may be used in
XX a vaccine. A protein of the invention is useful for inhibiting TALL-1
XX biological activity in a mammal. TC is useful for treating autoimmune
XX diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
XX dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
XX Grave's disease, autoimmune hemolytic anaemia, autoimmune
XX thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
XX acute rheumatic fever, post-streptococcal glomerulonephritis and
XX polyarteritis nodosa. The present sequence represents a cysteine rich
XX domain (CRD) module of human BCMA.
XX
XX Sequence 34 AA;
XX
XX Query Match 100.0%; Score 201; DB 6; Length 34;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-18;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CSQNEYFDSLLHACIPQCLRCSSNTPTPLTCQRYC 34
XX |||||
XX 1 CSQNEYFDSLLHACIPQCLRCSSNTPTPLTCQRYC 34
XX
XX RESULT 3
XX AD267761
XX ID AD267761 standard; protein; 40 AA.
XX
XX AC AD267761;
XX
XX

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DT 14-JUL-2005 (first entry)
XX
DE Human tumor necrosis factor receptor BCMA Cys-rich domain.
XX
XX Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;
KW cytostatic.
XX
XX Homo sapiens.
XX
XX WO2005037865-A2.
XX
XX 28-APR-2005.
XX
XX 18-OCT-2004; 2004WO-US034375.
XX
XX 16-OCT-2003; 2003US-0511698P.
XX
XX 18-OCT-2004; 2004US-0619552P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Fox BA, Holloway JL, Sheppard PO, Dillon SR;
XX
XX WPI; 2005-315682/32.
XX
XX New tumor necrosis factor receptor (TNFR) polypeptides, useful as
XX detecting ligands, and for modulating tumor growth, metastasis and
XX immunity, such as separating resting from stimulated immune cells.
XX
XX Disclosure; SEQ ID NO 9; 132pp; English.
XX
XX The invention provides novel tumor necrosis factor receptor ztnfr14
XX polynucleotides AD267753 and polypeptides AD267754, expression vectors
XX and antibodies. Ztnfr14 polynucleotides are used in claimed methods for
XX detecting a genetic abnormality in a patient and for detecting a cancer
XX in a patient. Recombinant ztnfr14 polypeptide, optionally conjugated to a
XX toxin, is used in a claimed method of killing cancer cells. Ztnfr14
XX polypeptides can be used to detect ligands, agonists and antagonists. The
XX polypeptides, polynucleotides and antibodies may also be used in methods
XX that modulate tumor growth, metastasis, and immunity such as separating
XX resting from stimulated immune cells. The present sequence is that of the
XX Cys-rich domain of human TNFR BCMA AD267760. This sequence was compared
XX with that of ztnfr14 in the identification of ztnfr14 as a member of the
XX TNFR family.
XX
XX Sequence 40 AA;
XX
XX Query Match 100.0%; Score 201; DB 9; Length 40;
XX Best Local Similarity 100.0%; Pred. No. 3.3e-18;
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CSQNEYFDSLLHACIPQCLRCSSNTPTPLTCQRYC 34
XX |||||
XX 3 CSQNEYFDSLLHACIPQCLRCSSNTPTPLTCQRYC 36
XX
XX Db
XX
XX RESULT 4
XX AAEE15485
XX ID AAEE15485 standard; peptide; 51 AA.
XX
XX AC AAEE15485;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human B-cell maturation (BCMA) protein extracellular domain.
XX
XX Human; transmembrane activator and intracellular CAML interactor; TAC1;
KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX

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XX OS Homo sapiens.  
 XX PN WO200187979-A2.  
 XX PD 22-NOV-2001.  
 XX PF 14-MAY-2001; 2001WO-US015567.  
 XX PR 12-MAY-2000; 2000US-0204039P.  
 XX PR 27-JUN-2000; 2000US-0214591P.  
 XX PR 14-MAY-2001; 2001US-00214591.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI Theill LE, Yu G;  
 XX DR WPI; 2002-066686/09.  
 XX PT Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactior, by administering a binding partner for APRIL, a tumor necrosis factor family ligand.  
 XX PS Claim 1; Fig 10A; 94pp; English.  
 XX CC The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactior) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, proctitis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein extracellular domain

XX SQ Sequence 51 AA;  
 Query Match 100.0%; Score 201; DB 5; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-18;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CSQNEFDSLHACIPQLRCSSTPPLTCQRYC 34  
 DB 5 CSQNEFDSLHACIPQLRCSSTPPLTCQRYC 38  
 RESULT 5  
 AEC02032  
 ID AEC02032 standard; peptide; 52 AA.  
 XX AC AEC02032;  
 XX DT 20-OCT-2005 (first entry)  
 XX DE Amino acid sequence of an extracellular domain of BCMA.  
 XX KW APRIL; BAPF; immune disorder; immunomodulator; antiinflammatory; cancer;  
 KW cytotatic; neoplasm; immunosuppressive; therapeutic;  
 KW B-cell maturation antigen; BCMA.  
 XX OS Synthetic.

PN WO2005075511-A1.  
 XX 18-AUG-2005.  
 XX PF 04-AUG-2004; 2004WO-US025247.  
 XX PR 29-JAN-2004; 2004US-0540271P.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Kelley RF, Patel D;  
 XX DR WPI; 2005-555932/56.  
 XX PT New polypeptides that inhibit APRIL and/or BAPF binding to BCMA, useful for treating immune-related disease, cancer or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation.  
 XX PS Disclosure; SEQ ID NO 21; 140pp; English.  
 XX CC The specification describes polypeptides that bind April or BAPF. The polypeptides inhibit APRIL or BAPF binding to B-cell maturation antigen (BCMA). APRIL and BAPF are tumor necrosis family (TNF) members. The polypeptides of the invention are useful for treating immune-related diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic lupus erythematosus; cancer such as leukemia, lymphoma, or multiple sclerosis, or T-cell mediated disease such as graft rejection, graft versus host disease (GVHD) and inflammation. The present sequence represents an extracellular domain of BCMA.  
 XX SQ Sequence 52 AA;  
 Query Match 100.0%; Score 201; DB 9; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-18;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CSQNEFDSLHACIPQLRCSSTPPLTCQRYC 34  
 DB 8 CSQNEFDSLHACIPQLRCSSTPPLTCQRYC 41  
 RESULT 6  
 AAE15501  
 ID AAE15501 standard; peptide; 58 AA.  
 XX AC AAE15501;  
 XX DT 12-MAR-2002 (first entry)  
 XX DE Human B cell maturation protein cysteine rich extracellular region.  
 XX KW Human; transmembrane activator and intracellular CAML interactior; TACI; cytotatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.  
 XX OS Homo sapiens.  
 XX PN WO200187979-A2.  
 XX PD 22-NOV-2001.  
 XX PF 14-MAY-2001; 2001WO-US015567.  
 XX PR 12-MAY-2000; 2000US-0204039P.  
 XX PR 27-JUN-2000; 2000US-0214591P.  
 XX PR 14-MAY-2001; 2001US-00214591.



PA (AMGE-) AMGEN INC.  
XX Theill LE, Yu G;  
XX WPI; 2002-066686/09.  
XX Inhibiting activity of B cell maturation protein and/or transmembrane  
XX activator and intracellular cyclophilin ligand interactor, by  
XX administering a binding partner for APRIL, a tumor necrosis factor family  
XX ligand.  
XX  
XX Disclosure; Fig 13; 94pp; English.  
XX  
XX The invention relates to a method for inhibiting TACI (transmembrane  
XX activator and intracellular CAML interactor) and/or B cell maturation  
XX protein (BCMA) activity in a mammal. The method comprises administering a  
XX specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/  
XX BCMA extracellular consensus sequence, but not the extracellular region  
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI  
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
XX lymphoproliferative disorders, one or more solid tumours such as lung,  
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
XX antagonists are useful for treating inflammation and immune function  
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
XX disease), drug and insect sting allergy, inflammatory bowel disease  
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
XX with leucocyte infiltration of the skin or organs. The present sequence  
XX is human BCMA cysteine-rich extracellular region  
XX  
XX Sequence 58 AA;  
XX  
XX Query Match 100.0%; Score 201; DB 5; Length 58;  
XX Best Local Similarity 100.0%; Pred. No. 4.8e-18;  
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34  
XX |||||  
XX Db 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34  
XX  
XX RESULT 7  
XX AAE15484  
XX ID AAE15484 standard; protein; 181 AA.  
XX AC AAE15484;  
XX XX 12-MAR-2002 (first entry)  
XX DE Human B-cell maturation (BCMA) protein.  
XX KW Human; transmembrane activator and intracellular CAML interactor; TACI;  
XX KW Cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
XX KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
XX KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
XX KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
XX KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
XX KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
XX KW rheumatoid arthritis; atherosclerosis.  
XX OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Region 5..38  
XX FT /note= "Cysteine-rich consensus region; This is region is  
XX FT specifically claimed as SEQ ID NO: 7 in claim 1 of the  
XX FT specification"  
XX FT 52..72  
XX FT /label= Transmembrane\_domain  
XX FT

PN WO200187979-A2.  
XX 22-NOV-2001.  
XX 14-MAY-2001; 2001WO-US015567.  
XX 12-MAY-2000; 2000US-0204039P.  
XX 27-JUN-2000; 2000US-0214591P.  
XX 14-MAY-2001; 2001US-00214591.  
XX (AMGE-) AMGEN INC.  
XX Theill LE, Yu G;  
XX WPI; 2002-066686/09.  
XX Inhibiting activity of B cell maturation protein and/or transmembrane  
XX activator and intracellular cyclophilin ligand interactor, by  
XX administering a binding partner for APRIL, a tumor necrosis factor family  
XX ligand.  
XX  
XX Disclosure; Fig 10A; 94pp; English.  
XX  
XX The invention relates to a method for inhibiting TACI (transmembrane  
XX activator and intracellular CAML interactor) and/or B cell maturation  
XX protein (BCMA) activity in a mammal. The method comprises administering a  
XX specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
XX family ligand), having the consensus region of TACI, BCMA, or the TACI/  
XX BCMA extracellular consensus sequence, but not the extracellular region  
XX of TACI or BCMA. The method is useful for inhibiting activity of TACI  
XX and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
XX lymphoproliferative disorders, one or more solid tumours such as lung,  
XX gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
XX antagonists are useful for treating inflammation and immune function  
XX diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
XX dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
XX disease), drug and insect sting allergy, inflammatory bowel disease  
XX (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
XX sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
XX bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
XX with leucocyte infiltration of the skin or organs. The present sequence  
XX is human BCMA protein  
XX  
XX Sequence 181 AA;  
XX  
XX Query Match 100.0%; Score 201; DB 5; Length 181;  
XX Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
XX Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34  
XX |||||  
XX Db 5 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 38  
XX  
XX RESULT 8  
XX AAB08843  
XX ID AAB08843 standard; peptide; 184 AA.  
XX AC AAB08843;  
XX XX 02-JAN-2001 (first entry)  
XX DE Amino acid sequence of human.  
XX KW BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;  
XX KW anti-cell death gene; apoptosis; viral infection; inflammatory response;  
XX KW rheumatoid arthritis; inflammatory bowel disease; septic shock.  
XX OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Domain 57..77  
XX FT /note= "putative transmembrane domain"  
XX FT



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XX PN WO200050633-A1.
XX PD 31-AUG-2000.
XX PF 24-FEB-2000; 2000WO-US004925.
XX PR 24-FEB-1999; 99US-0121485P.
XX PA (GEO ) GEN HOSPITAL CORP.
XX PI Seed B, Ting A;
XX PI WPI; 2000-558405/51.
XX DR
XX PT Identifying a modulator of gene expression for drug designing, by
XX PT contacting a compound library with a cell expressing an anti-cell death
XX PT gene and reporter gene, and determining alteration in reporter gene
XX PT expression.
XX PS
XX PS Claim 32; Fig 7A; 53pp; English.
XX CC
XX CC The present sequence represents a BCMA (not defined) polypeptide. BCMA is
XX CC a necrosis factor (NF)-kB activator. The method of the invention is used
XX CC to identify compounds which modulate BCMA activity (and thus NF-kB
XX CC activity). The specification describes a method of identifying a
XX CC polypeptide which increases gene expression from a promoter. The method
XX CC involves contacting a library of with a cell which expresses a
XX CC recombinant anti-cell death gene and a reporter gene operably linked to
XX CC the promoter, and then determining whether the expression of the reporter
XX CC gene is altered as a result of contact with library. The method is useful
XX CC for identifying polypeptides which increase or decrease gene expression
XX CC from a promoter. The BCMA polypeptide or nucleic acid are useful for
XX CC preparing a pharmaceutical composition for treating cancer, apoptosis,
XX CC viral infections, inflammatory response, such as rheumatoid arthritis,
XX CC inflammatory bowel disease or septic shock. BCMA is useful for
XX CC identifying compounds that modulate NF-kB expression and thus for drug
XX CC designing
XX CC
XX SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41
|||||
|||||

RESULT 9
AA94001
ID AA94001 standard; protein; 184 AA.
XX AC AA94001;
XX XX
XX DT 20-OCT-2000 (first entry)
XX DE
XX DE A human BCMA protein, a B cell protein related to TACI.
XX KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
XX KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
XX KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
XX KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
XX KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
XX KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
XX KW renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
XX KW immune response; immunosuppression; graft rejection; joint pain;
XX KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
XX KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
XX KW renal artery stenosis; occlusion; cholesterol; renal emboli.
XX OS Homo sapiens.

Query Match 100.0%; Score 201; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34
Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41
|||||
|||||

RESULT 10
AAE09241
ID AAE09241 standard; protein; 184 AA.
XX AC AAE09241;
XX XX
XX DT 19-NOV-2001 (first entry)
XX DE Human BCMA protein.
XX KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
XX KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
XX KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
XX OS Homo sapiens.
XX PN WO200160397-A1.

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WO200040716-A2.

13-JUL-2000.

07-JAN-2000; 2000WO-US000396.

07-JAN-1999; 99US-00226533.

(ZYMO ) ZYMOGENETICS INC.

Gross JA, Xu W, Madden K, Yee DP;

WPI; 2000-452538/39.

N-PSDB; AAA58559.

Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

Disclosure; Page 152; 175pp; English.

The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF) receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. ztnf4 is a TNF ligand. They may also be used for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, glomerulonephritis, vasculitis, lymphomas, light chain neuropathy, neoplasms, multiple myelomas, lymphomas, immunosuppression, graft rejection, moderating immune response, inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli

Sequence 184 AA;

Query Match 100.0%; Score 201; DB 3; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.5e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 34

Db 8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41

|||||

|||||

RESULT 10

AAE09241

ID AAE09241 standard; protein; 184 AA.

XX AC AAE09241;

XX XX

XX DT 19-NOV-2001 (first entry)

XX DE Human BCMA protein.

XX KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;

XX KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;

XX KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

XX OS Homo sapiens.

XX PN WO200160397-A1.







XX WO200112812-A2.  
XX 22-FEB-2001.  
XX 16-AUG-2000; 2000WO-US022507.  
XX 17-AUG-1999; 99US-0149378P.  
PR 11-FEB-2000; 2000US-0181684P.  
PR 18-FEB-2000; 2000US-0183536P.  
XX (BIOJ ) BIOGEN INC.  
PA (APOT-) APOTECH R & D SA.  
XX Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;  
PI Thompson J;  
XX WPI; 2001-202866/20.  
DR N-PSDB; AAF59998.  
XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell  
PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,  
PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.  
XX  
XX Claim 20; Fig 1; 59pp; English.  
XX The invention relates to the use of a BAFF receptor (BAFF-R, also known  
CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the  
CC treatment of a variety of immune-related disorders. BAFF-R is a member of  
CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory  
CC agent, and also plays a role in the development of hypertension and  
CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-  
CC specific antibodies can be used for inhibiting B-cell growth, dendritic  
CC cell-induced B-cell growth and maturation, and immunoglobulin production,  
CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative  
CC disorders, hypertension and renal disorders. The BAFF-R proteins may also  
CC be used in the treatment of immunosuppressive disorders and HIV  
CC infection, and in patients undergoing organ transplantation. The BAFF-R  
CC proteins or BAFF-R specific antibodies may be used for treating,  
CC suppressing or altering an immune response involving a signalling pathway  
CC between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R  
CC inhibits B-cell growth and maturation it is useful for treating diseases  
CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,  
CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly  
CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding  
CC human BAFF-R may be used in gene therapy to treat tumours, lymphomas,  
CC autoimmune disorders and inherited B-cell-associated disorders. The  
CC present sequence represents human BAFF-R  
XX  
XX Sequence 184 AA;  
Query Match 100.0%; Score 201; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 34  
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 41  
RESULT 13  
ID AAE00506  
XX AAE00506 standard; protein; 184 AA.  
XX  
AC AAE00506;  
XX  
DT 31-JUL-2001 (first entry)  
XX  
DE Human B cell maturation protein (BCMA).  
XX  
KW Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;  
KW gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;  
KW carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;

KW systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;  
KW B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;  
KW organ transplantation; HIV; human immunodeficiency virus; TNF;  
KW tumour necrosis factor; BCMA; B cell maturation protein.  
XX Homo sapiens.  
OS  
XX WO200124811-A1.  
PN  
XX 12-APR-2001.  
PD  
XX 05-OCT-2000; 2000WO-US027579.  
XX 06-OCT-1999; 99US-0157933P.  
PR 11-FEB-2000; 2000US-0181807P.  
PR 30-JUN-2000; 2000US-0215688P.  
XX (BIOJ ) BIOGEN INC.  
PA (APOT-) APOTECH R & D SA.  
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;  
PI WPI; 2001-266242/27.  
XX N-PSDB; AAD03844.  
DR  
XX Treating a mammal for a condition associated with undesired cell  
PT proliferation such as cancer or carcinoma, comprises administering a  
PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)  
PT antagonist.  
XX  
XX Claim 3; Fig 3A; 85pp; English.  
XX The invention relates to a method of treating a mammal for a condition  
CC associated with undesired cell proliferation such as cancer or carcinoma.  
CC The method involves administering a composition comprising A  
CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell  
CC maturation protein (BCM or BCMA) antagonist that antagonises the  
CC interaction between APRIL and its cognate receptor(s). This method is  
CC useful for treating undesired cell proliferation such as cancer or  
CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,  
CC prostate carcinoma, and other carcinomas whose proliferation is modulated  
CC by APRIL. It is also useful for treating autoimmune diseases (Grave's  
CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular  
CC diseases, renal disorders, B-cell lympho-proliferative disorders,  
CC immunosuppressive diseases, organ transplantation, inflammation and human  
CC immunodeficiency virus (HIV), and for treating, suppressing or altering  
CC an immune response involving a signalling pathway between APRIL-R and its  
CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence  
CC is human APRIL-R also referred as BCMA or BCM protein  
XX  
XX Sequence 184 AA;  
Query Match 100.0%; Score 201; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 34  
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 41  
RESULT 14  
ID ABB81487  
XX ABB81487 standard; protein; 184 AA.  
XX  
AC ABB81487;  
XX  
DT 02-SEP-2002 (first entry)  
XX  
DE Human BCMA receptor related protein SEQ ID NO:7.  
XX  
KW Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;  
KW immunosuppressive; dermatological; antinflammatory; antidiabetic;



KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;  
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;  
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;  
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;  
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;  
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;  
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;  
 KW light chain neuropathy; hypertension; large vessel disease;  
 KW graft-versus host disease; graft rejection; Crohn's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200238766-A2.  
 XX  
 PD 16-MAY-2002.  
 XX  
 PF 05-NOV-2001; 2001WO-US047018.  
 XX  
 PR 07-NOV-2000; 2000US-0246449P.  
 PR 20-DEC-2000; 2000US-0257131P.  
 PR 28-JUN-2001; 2001US-0301715P.  
 PR 29-AUG-2001; 2001US-0315565P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Gross JA, Xu W, Henne RM, Grant FJ;  
 XX  
 XX WPI; 2002-508212/54.  
 DR  
 XX  
 PT Novel isolated human tumor necrosis factor receptor polypeptide, termed  
 PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage  
 PT renal failure or renal disease and lymphoma.  
 XX  
 PS Disclosure; Page 135-136; 154pp; English.  
 XX  
 CC The present invention describes a human tumour necrosis factor receptor  
 CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,  
 CC dermatological, antiinflammatory, neuroprotective, antidiabetic,  
 CC antineumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive  
 CC activities, and can be used in gene therapy. (I) can be used for  
 CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12  
 CC (e.g. ZTNF4), for treating disorders and diseases associated with B  
 CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for  
 CC inhibiting the proliferation of tumour cells. (I) is useful for treating  
 CC autoimmune disorders such as systemic lupus erythematosus, myasthenia  
 CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,  
 CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure  
 CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid  
 CC leukaemia, nephritis, and pyelonephritis, and for treating renal  
 CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or  
 CC amyloidosis, hypertension, large vessel diseases, graft-versus host  
 CC disease, graft rejection and Crohn's disease. (I) is useful for  
 CC modulating the immune system, for regulating B cell responses and  
 CC development, for modulating development of other cells, antibody  
 CC production and cytokine production, and for modulating T and B cell  
 CC communication. The present sequence represents a protein which is given  
 CC in the exemplification of the present invention  
 XX  
 SQ Sequence 184 AA;  
 Query Match 100.0%; Score 201; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34  
 |||||  
 Db 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41  
 |||||  
 RESULT 15  
 ABP54694  
 ID ABP54694 standard; protein; 184 AA.  
 , XX

AC ABP54694;  
 XX  
 DT 30-DEC-2002 (first entry)  
 XX  
 DE Metastatic colorectal cancer-associated polypeptide.  
 XX  
 DE Colorectal cancer; metastasis; differential expression; cytostatic;  
 KW diagnosis; gene therapy; vaccine.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO200268677-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 27-FEB-2002; 2002WO-US006001.  
 XX  
 PR 27-FEB-2001; 2001US-0272206P.  
 PR 02-APR-2001; 2001US-0281149P.  
 PR 17-APR-2001; 2001US-0284555P.  
 XX  
 PA (EOSB-) EOS BIOTECHNOLOGY INC.  
 PA (UYCA-) UNIV CASE WESTERN RESERVE.  
 XX  
 PI Mack DH, Markowitz SD;  
 XX  
 XX WPI; 2002-698677/75.  
 DR N-PSDB; ABQ81560.  
 DR  
 XX  
 PT New genes that are up- or down-regulated in colorectal cancer, useful for  
 PT diagnosing colorectal cancer in a subject, or for identifying modulators  
 PT of colorectal cancer-associated proteins and genes for treating  
 PT colorectal cancer.  
 XX  
 PS Claim 8; Page 255; 260pp; English.  
 XX  
 CC The present sequence is the protein sequence of a human polypeptide  
 CC encoded by a gene that exhibits decreased expression in colon cancer-  
 CC derived metacases compared to normal colon tissue. It is an example of  
 CC claimed polypeptides that are encoded by genes which are differentially  
 CC expressed in metastatic colorectal cancer cells. Such polypeptides are  
 CC useful in diagnostic and prognostic assays, for raising antibodies useful  
 CC e.g. in immunotherapy, and in screening for modulator compounds of  
 CC therapeutic value  
 XX  
 SQ Sequence 184 AA;  
 Query Match 100.0%; Score 201; DB 5; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34  
 |||||  
 Db 8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41  
 |||||  
 RESULT 16  
 AAE28961  
 ID AAE28961 standard; protein; 184 AA.  
 XX  
 AC AAE28961;  
 XX  
 DT 27-JAN-2003 (first entry)  
 XX  
 DE Human B-cell maturation antigen (BCMA).  
 XX  
 KW Human; tumour; B-cell maturation antigen; transmembrane activator;  
 KW calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy;  
 KW neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease;  
 KW non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;  
 KW BCMA; multiple myeloma.  
 XX  
 OS Homo sapiens.



XX FH Key Location/Qualifiers  
FT Region 1..54  
FT /note= "Antigenic epitope"  
FT Domain 1..48  
FT /note= "Extracellular domain"  
FT Region 8..41  
FT /note= "Cysteine rich region"  
XX WO200266516-A2.  
XX 29-AUG-2002.  
XX 06-FEB-2002; 2002WO-US003500.  
XX 20-FEB-2001; 2001US-0270274P.  
XX 12-APR-2001; 2001US-0283447P.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Kindvogel W;  
XX WPI; 2002-723183/78.  
XX N-PSDB; AAD46410.  
XX B-cell maturation antigen and transmembrane activator and calcium-  
modulator and cyclophilin ligand-interactor, useful for treating  
disorders e.g. inflammation or lymphoma.  
XX Disclosure; Page 63; 67pp; English.  
XX The invention relates to the manufacture of a composition for inhibiting  
the proliferation of tumour cells. The method involves using an antibody  
component that binds both the B-cell maturation antigen (BCMA) and the  
transmembrane activator and calcium-modulator and cyclophilin ligand-  
interactor (TACI). BCMA and TACI binding antibody compositions are useful  
for inhibiting proliferation of tumour cells, particularly inhibiting  
TGF $\beta$  activity in a mammal associated with increased endogenous antibody  
production or a disorder consisting of neoplasia, chronic lymphocytic  
leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation  
lymphoproliferative disease or light chain gammopathy or inflammation  
e.g. asthma. The invention is also useful in gene therapy. The present is  
human BCMA protein  
XX Sequence 184 AA;  
Query Match 100.0%; Score 201; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 34  
Db 8 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 41  
RESULT 17  
AAE35216  
ID AAE35216 standard; protein; 184 AA.  
XX AAE35216;  
XX 28-MAY-2003 (first entry)  
XX Human B-cell maturation receptor (BCMA) protein.  
XX Transmembrane activator; calcium modulator; nephrotropic; antibacterial;  
TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;  
anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive;  
glomerulonephritis; asthma; bronchitis; graft rejection; septic shock;  
dermatological; neuroprotective; cyclophilin ligand-interactor; human;  
autoimmune disease; systemic lupus erythematosus; multiple sclerosis;  
diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;  
B-cell maturation receptor; BCMA; receptor.

XX OS Homo sapiens.  
XX WO200294852-A2.  
XX 28-NOV-2002.  
XX 20-MAY-2002; 2002WO-US015910.  
XX 24-MAY-2001; 2001US-0293343P.  
XX (ZYMO ) ZYMOGENETICS INC.  
XX Rixon MW, Gross JA;  
XX WPI; 2003-148455/14.  
XX N-PSDB; AAD53754.  
XX Transmembrane activator and calcium modulator and cyclophilin ligand-  
interactor (TACI)-immunoglobulin fusion protein, for treating cancer or  
diabetes, comprises a TACI receptor group and an immunoglobulin group.  
XX Disclosure; Col 100; 71pp; English.  
XX The invention relates to fusion proteins comprising transmembrane  
activator and calcium modulator and cyclophilin ligand-interactor (TACI)  
receptor group that binds tumour necrosis factor-like protein (ZTNF2) or  
ZTNF4; and an immunoglobulin group comprising a constant region of an  
immunoglobulin. The invention is used to manufacture a medicament for  
inhibiting the proliferation of tumour cells in a mammalian subject. The  
composition comprising the fusion protein may also be used in treating  
autoimmune diseases (e.g. systemic lupus erythematosus, multiple  
sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal  
diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft  
rejection, anaemia and septic shock. The fusion proteins are also used in  
gene therapy. The present sequence is human B-cell maturation receptor  
(BCMA) protein used in the invention  
XX Sequence 184 AA;  
Query Match 100.0%; Score 201; DB 6; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 34  
Db 8 CSQNEYFDSLHACIPCOLRCSNTPLTCQRYC 41  
RESULT 18  
ADA49361  
ID ADA49361 standard; protein; 184 AA.  
XX ADA49361;  
XX 20-NOV-2003 (first entry)  
XX Human BCMA protein.  
XX human; TALL-1; antagonist; immunosuppressive; antirheumatic;  
antiinflammatory; antiarthritic; dermatological; antidiabetic;  
neuroprotective; antithyroid; antipruritic; nephrotropic; vasotropic;  
vaccine; autoimmune diseases; rheumatoid arthritis;  
systemic lupus erythematosus; insulin dependent diabetes mellitus;  
multiple sclerosis; myasthenia gravis; Grave's disease;  
autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura;  
Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;  
post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.  
XX Homo sapiens.  
XX WO2003035846-A2.  
XX



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PD 01-MAY-2003.
XX
PF 24-OCT-2002; 2002WO-US034376.
XX
XX 24-OCT-2001; 2001US-0345106P.
PR 14-JAN-2002; 2002US-0348962P.
PR 07-FEB-2002; 2002US-0354966P.
PR 13-AUG-2002; 2002US-0403364P.
XX
XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
XX Zhang G, Shu H, Liu Y, Xu L;
XX
XX WPI; 2003-403345/38.
DR N-PSDB; ADA49360.
XX
XX Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological
PT activity in mammal, has a modification in the region connecting beta
PT strands D and E that reduces the biological activity of TALL-1
PT antagonist.
XX
XX Claim 62; Page 613; 618pp; English.
XX
XX The invention relates to a novel TALL-1 antagonist protein, comprising a
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID
CC NO:2, by at least one modification in the region connecting ebgrr; strands
CC D and E that reduces the biological activity of the TALL- 1 antagonist as
CC compared to wild-type TALL-1. A protein of the invention has
CC immunosuppressive, anti-rheumatic, neuroprotective, antiarthritic,
CC dermatological, anti-diabetic, neuroprotective, anti-inflammatory, antihypertic,
CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in
CC a vaccine. A protein of the invention is useful for inhibiting TALL-1
CC biological activity in a mammal. TC is useful for treating autoimmune
CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin
CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,
CC Grave's disease, autoimmune hemolytic anaemia, autoimmune
CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,
CC acute rheumatic fever, post-streptococcal glomerulonephritis and
CC polyarthritis nodosa. The present sequence represents human BCMA.
XX
XX SQ Sequence 184 AA;
Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDLSLLHACIPQLRCSSNTPTLTQRYC 34
|||
|||
Db 8 CSQNEVFDLSLLHACIPQLRCSSNTPTLTQRYC 41

RESULT 19
ABR40082
ID ABR40082 standard; protein; 184 AA.
XX
AC ABR40082;
XX
XX 27-JUN-2003 (first entry)
XX
XX Human Genoxit.
XX
XX Human; genoxit; anorectic; antilipaeamic; antiarteriosclerotic; cardiant;
KW antidiabetic; hypotensive; ophthalmological; neuroprotective;
KW nephrotropic; obesity; Tumour Necrosis Factor Receptor Super Family;
KW Type III transmembrane protein; insulin resistance; atherosclerosis;
KW atheromatous disease; heart disease; hypertension; stroke; syndrome X;
KW diabetes mellitus; hyperlipidaemia; hyperuricaemia.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 1. .54
FT Domain /label= Extracellular_domain
, FT

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FT Misc-difference 3
FT Domain /label= Gln, Lys
FT 55. .77
FT /label= Transmembrane domain
FT Domain 78. .184
FT /label= Intracellular_domain
XX
XX WO2003013582-A1.
XX
XX 20-FEB-2003.
XX
XX 05-AUG-2002; 2002WO-IB003498.
XX
XX 06-AUG-2001; 2001US-0310754P.
XX (GEST ) GENSET SA.
XX
XX Lucas J, Dialynas D, Briggs K;
XX
XX WPI; 2003-268160/26.
DR N-PSDB; ACC00340.
XX
XX New use of agonist or antagonist of Genoxit activity for preventing or
PT treating obesity-related diseases or disorders, e.g. hyperlipidemia and
PT atherosclerosis.
XX
XX Disclosure; Page 32; 35pp; English.
XX
XX The present invention relates to the use of an agonist or antagonist of
CC Genoxit activity for preventing or treating obesity. Genoxit is a member
CC of the Tumour Necrosis Factor Receptor Super Family and is a Type III
CC transmembrane protein. The agonists or antagonists of the invention are
CC useful for treating or preventing obesity-related diseases or disorders,
CC e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease,
CC heart disease (e.g. cardiac insufficiency, coronary insufficiency, high
CC blood pressure), hypertension, stroke, syndrome X, diabetes mellitus
CC (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic
CC complications, e.g. microangiopathic lesions, ocular lesions,
CC retinopathy, neuropathy and renal lesions
XX
XX SQ Sequence 184 AA;
Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDLSLLHACIPQLRCSSNTPTLTQRYC 34
|||
|||
Db 8 CSQNEVFDLSLLHACIPQLRCSSNTPTLTQRYC 41

RESULT 20
ABP60552
ID ABP60552 standard; protein; 184 AA.
XX
XX ABP60552;
AC
XX
XX 28-MAR-2003 (first entry)
XX
XX Human tumour necrosis factor BCMA.
XX
XX APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
KW dermatological; immunosuppressive; antiinflammatory; antirheumatic;
KW antiarthritic; cytostatic; antianaemic; antiallergic; antiaschmatic;
KW neuroprotective; ophthalmological; tuberculostatic; antidiabetic;
KW antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;
KW haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;
KW inflammatory disorder; proliferative disorder; single chain antibody;
KW antibody; human; BCMA; tumour necrosis factor.
XX
XX Homo sapiens.
OS
XX WO200294192-A2.
PN

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XX PD 28-NOV-2002.
XX PF
XX PF
XX PR 22-MAY-2002; 2002WO-US016106.
XX PR 24-MAY-2001; 2001US-0293100P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Ruben SM;
XX PI
XX DR WPI; 2003-156740/15.
XX DR
XX PT Novel isolated antibody that immunospecifically binds tumor necrosis
XX PT factor delta, useful for treating, preventing or ameliorating Non-
XX PT Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
XX PT syndrome.
XX PS Disclosure; Page 222; 225pp; English.
XX CC The invention relates to a novel antibody or its fragment, which
XX CC immunospecifically binds tumor necrosis factor Delta (TNF-delta/APRIL).
XX CC The antibody of the invention has dermatological, immunosuppressive,
XX CC antiinflammatory, antirheumatic, antiarthritic, cytostatic, antianaemic,
XX CC antiallergic, antiasthmatic, neuroprotective, ophthalmological,
XX CC tuberculostatic, antidiabetic, antipeoriatic, anti-HIV,
XX CC antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.
XX CC The antibody or its fragment are useful for treating, preventing or
XX CC ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
XX CC human, disease or disorder such as autoimmune disease, and graft versus
XX CC host disease (GVHD). The autoimmune disease is systemic lupus
XX CC erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody
XX CC is useful for detecting, diagnosing, prognosing, treating, preventing or
XX CC ameliorating a disease or disorder associated with aberrant APRIL or
XX CC APRIL receptor expression or aberrant function of APRIL or APRIL
XX CC receptor. The disease or disorders includes autoimmune and inflammatory
XX CC disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,
XX CC asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,
XX CC uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune
XX CC system, particularly B cell cancers, immune disorders such as myasthenia
XX CC gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,
XX CC infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and
XX CC proliferative disorders (e.g. leukemia). The present sequence represents
XX CC the tumour necrosis factor BCMA
XX SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPTLCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPTLCQRYC 41

RESULT 21
ABP97717
ID ABP97717 standard; protein; 184 AA.
XX AC ABP97717;
XX DT 28-MAY-2003 (first entry)
XX DE Amino acid sequence of human BCMA receptor.
XX KW Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
XX KW TALL-1; April; systemic lupus erythematosus; BCMA.
XX OS Homo sapiens.
XX PN WO2003014294-A2.

XX PD 20-FEB-2003.
XX PF 24-JUL-2002; 2002WO-US023487.
XX PR 03-AUG-2001; 2001US-0310114P.
XX PR 30-APR-2002; 2002US-0377171P.
XX PA (GETH ) GENENTECH INC.
XX PI Dixit V, Grewal I, Ridgway J, Yan M;
XX PI
XX DR WPI; 2003-256560/25.
XX DR N-PSDB; AB268871.
XX PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
XX PT preparing a composition for treating systemic lupus erythematosus.
XX PS Disclosure; Fig 2; 153pp; English.
XX CC The present sequence represents a human BCMA polypeptide. The
XX CC specification also describes TACI and BR3 polypeptides. TACI and BR3 are
XX CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
XX CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
XX CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
XX CC preparing a composition for treating systemic lupus erythematosus
XX SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPCOLRCSSNTPTLCQRYC 34
Db 8 CSQNEYFDSLHACIPCOLRCSSNTPTLCQRYC 41

RESULT 22
ADD67527
ID ADD67527 standard; protein; 184 AA.
XX AC ADD67527;
XX DT 15-JAN-2004 (first entry)
XX DE Human Ly1732P protein SEQ ID NO:4.
XX KW haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
XX KW vaccine; immunotherapy; cancer; multiple myeloma cell;
XX KW chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
XX KW human.
XX OS Homo sapiens.
XX PN WO2003062401-A2.
XX PD 31-JUL-2003.
XX PF 22-JAN-2003; 2003WO-US002353.
XX PR 22-JAN-2002; 2002US-00057475.
XX PA (CORI-) CORIYA CORP.
XX PI Gaiger A, Algate PA, Mannion J, Clapper JD, Wang A, Ordonez N;
XX PI Carter L, McNeill PD;
XX DR WPI; 2003-598749/56.
XX DR N-PSDB; ADD67526.
XX PT New hematological malignancy-related genes and polypeptides, useful for
XX PT screening anti-cancer agents, and generating antibodies or
XX PT immunoconjugates for treating e.g. multiple myeloma cell or chronic

```



PT Lymphocytic leukemia.

XX Claim 9; SEQ ID NO 4; 307pp; English.

XX The present invention describes an isolated polynucleotide (I), which is

CC overexpressed in haematological malignancies, and which encodes a

CC polypeptide or an immunogenic fragment of the polypeptide. Also

CC described: (1) an isolated polypeptide; (2) an expression vector

CC comprising (1) operably linked to an expression control sequence; (3) a

CC host cell comprising an expression vector; (4) an isolated antibody that

CC specifically binds to the polypeptide or its immunogenic fragment; and

CC (5) immunoconjugates comprising the antibody above, or an antibody that

CC specifically binds to a polypeptide, or its immunogenic fragment, encoded

CC by (1). (I) has cytostatic and immunostimulant activities, and can be

CC used in vaccines and immunotherapy. The immunoconjugates are useful in

CC the manufacture of a medicament, particularly as active ingredients in a

CC composition for treating cancer, e.g. multiple myeloma cell, chronic

CC lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep,

CC primates, goats, bovines, equines, porcines, lupines, canines or felines.

CC The polynucleotide (I) or polypeptide can be used for screening anti-

CC cancer agents, and generating antibodies or immunoconjugates for treating

CC or preventing the above-mentioned diseases. The polynucleotide,

CC polypeptide or antibody can be used for detecting, diagnosing or

CC prognosticating the haematological malignancies described above. The

CC present sequence is used in the exemplification of the present invention.

XX Sequence 184 AA;

SEQ Match 100.0%; Score 201; DB 7; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.5e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHLHACIPQLRCSSNTPLTCQRYC 34

DB 8 CSONEYFDSLHLHACIPQLRCSSNTPLTCQRYC 41

RESULT 23

ADG43715

ID ADG43715 standard; protein; 184 AA.

AC ADG43715;

AC ADG43715;

DT 26-FEB-2004 (first entry)

XX Human B-cell maturation antigen SEQ ID NO:1.

XX human; neurodegenerative immunological disorder; demyelination;

XX Central Nervous System; CNS; inflammation; B-cell maturation antigen;

XX BCMA; multiple sclerosis; neuroprotective; neurotropic; antiinflammatory;

XX gene therapy.

XX Homo sapiens.

XX WO2003072713-A2.

XX 04-SEP-2003.

XX 21-FEB-2003; 2003WO-US005147.

XX 21-FEB-2002; 2002US-0358427P.

XX (BIOJ ) BIOGEN INC.

XX Kalled SL, Reid H;

XX WPI: 2003-721758/68.

XX N-PSDB; ADG43716.

XX Treating a neurodegenerative immunological disorder, e.g. demyelination

XX or inflammation in a mammal comprises administering a B-cell maturation

XX antigen (BCMA), an antibody against BCMA or a BCMA ligand.

PS Claim 8; Page 68-69; 72pp; English.

XX The invention relates to a novel method for treating a neurodegenerative

CC immunological disorder, demyelination or Central Nervous System (CNS)

CC inflammation in a mammal. The method comprises administering B-cell

CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand

CC (the mammal has or is at risk of developing multiple sclerosis). The

CC method of the invention has neuroprotective, neurotropic, and

CC antiinflammatory activity, and may have a use in gene therapy. The

CC methods, BCMA, and antibodies are useful for treating a neurodegenerative

CC immunological disorder such as multiple sclerosis, demyelination or CNS

CC inflammation. The present sequence represents human BCMA.

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 7; Length 184;

Best Local Similarity 100.0%; Pred. No. 1.5e-17;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSONEYFDSLHLHACIPQLRCSSNTPLTCQRYC 34

DB 8 CSONEYFDSLHLHACIPQLRCSSNTPLTCQRYC 41

RESULT 24

ADK00756

ID ADK00756 standard; protein; 184 AA.

XX ADK00756;

XX ADK00756;

DT 06-MAY-2004 (first entry)

XX Native human BCMA.

XX CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;

XX Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;

XX Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;

XX Antibacterial; antiparasitic; systemic lupus erythematosus;

XX diabetes mellitus; AIDS; BCMA.

XX Homo sapiens.

XX WO2004011611-A2.

XX 05-FEB-2004.

XX 25-JUL-2003; 2003WO-US023421.

XX 25-JUL-2002; 2002US-0398530P.

XX (GETH ) GENENTECH INC.

XX Chuntharapai A, Grewal I, Kim KJ, Yan M;

XX WPI: 2004-143841/14.

XX N-PSDB; ADK00755.

XX New anti-TACI receptor monoclonal antibody, useful for diagnosing and

XX treating pathological conditions associated with tumor necrosis factor,

XX e.g. cancer or immune-related disease, such as rheumatoid arthritis or

XX psoriasis.

XX Disclosure; SEQ ID NO 6; 110pp; English.

XX The present invention relates to an isolated monoclonal antibody which

CC binds to a transmembrane activator of and CAML interactor (TACI)

CC receptor. The TACI antibodies are useful for modulating TALL-1 or TACI

CC polypeptide biological activity in mammalian cells, or for diagnosing and

CC treating pathological conditions associated with TNF and TNF receptor-

CC treating molecules, e.g. cancer or immune-related disease, such as

CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,

CC systemic vasculitis, diabetes mellitus, Crohn's disease,

CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or



CC infectious diseases including AIDS, hepatitis infection, bacterial  
 CC infection, fungal infection, protozoal infection and parasitic infection.  
 CC The present sequence represents native human BCMA.

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 8; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34  
 |||||  
 Db 8 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 41

RESULT 25  
 ADQ94442  
 ID ADQ94442 standard; protein; 184 AA.

XX AC ADQ94442;

XX DT 07-OCT-2004 (first entry)

XX DE Neurokine-alpha, BCMA.

XX KW neurokine-alpha; chelator; B-lymphocyte stimulator; BLYS; TALL-1; THANK;  
 KW BAPF; neurokine-alpha receptor; complex; metal ion; radiotherapy;  
 KW B-cell mediated disease; non-Hodgkin's lymphoma;  
 KW chronic lymphocytic leukaemia; multiple myeloma;  
 KW systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis;  
 KW Crohn's disease; diabetes; Wegener's granulomatosis; myasthenia gravis;  
 KW asthma; cancer; Sjogren's syndrome; diagnostic imaging; lymphocyte;  
 KW B cell; cancerous cell; metastasis; lymphatic system.

XX OS Homo sapiens.

XX PN WO2004058309-A1.

XX PD 15-JUL-2004.

XX PF 22-DEC-2003; 2003WO-US040979.

XX PR 23-DEC-2002; 2002US-0435262P.

XX PR 02-MAY-2003; 2003US-0467198P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Parmelee D, Yeh R, Galperina O, Hilbert D, Rosen CA;

XX DR WPI; 2004-553134/53.

XX DR N-PSDB; ADQ94441.

XX DR GENBANK; NM\_001192.

XX PT Neurokine-alpha conjugate useful for targeting complexed metal ion to  
 PT cells expressing receptor (predominantly lymphoid) for radiotherapy  
 PT treatment of, for example, non-Hodgkin's lymphoma comprises neurokine-  
 PT alpha protein and chelator.

XX PS Disclosure; SEQ ID NO 9; 228pp; English.

XX CC This sequence represents neurokine-alpha, BCMA, which may be used in the  
 CC protein conjugate of the invention. The neurokine-alpha protein  
 CC conjugate comprises neurokine-alpha protein and chelator, where the  
 CC neurokine-alpha protein (also known as B-lymphocyte stimulator (BLYS),  
 CC TALL-1, THANK and BAPF) is capable of binding neurokine-alpha receptor  
 CC and is selected from full length or mature neurokine-alpha protein. The  
 CC protein conjugate of the invention is useful in a complex with a metal  
 CC ion associated with the chelator which is useful for administering  
 CC radiotherapy to a subject such as human who is in need of radiotherapy,  
 CC which involves administering the complex to the subject, where it is  
 CC administered as an injectable solution, and the subject has a B-cell  
 CC mediated disease. The subject has a condition chosen from non-Hodgkin's  
 CC lymphoma, chronic lymphocytic leukaemia, multiple myeloma, systemic lupus

CC erythematosus, rheumatoid arthritis, multiple sclerosis, Crohn's disease,  
 CC diabetes, Wegener's granulomatosis, myasthenia gravis and asthma,  
 CC preferably non-Hodgkin's lymphoma. The complex is useful for treating  
 CC cancer, which involves administering it to a subject having cancer, where  
 CC a cell of the cancer expresses a neurokine-alpha receptor on its  
 CC surface. The cancer is a B cell cancer, which is chosen from non-  
 CC Hodgkin's lymphoma, multiple myeloma and chronic lymphocytic leukaemia.  
 CC The complex is also useful for treating an autoimmune disease or  
 CC disorder, chosen from systemic lupus erythematosus, rheumatoid arthritis  
 CC and Sjogren's syndrome. The complex may also be used for diagnostic  
 CC imaging. A composition comprising the protein conjugate or the complex is  
 CC useful for killing a cell chosen from a cell bearing a neurokine-alpha  
 CC receptor, and a cell in close proximity to a cell bearing neurokine-  
 CC alpha receptor, which involves contacting the cell with the composition  
 CC to kill the cell. The cell is lymphocyte, B cell or cancerous cell that  
 CC has metastasised into the lymphatic system.

XX SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 8; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 34  
 |||||  
 Db 8 CSQNEYFDSLHACIPQLRCSSTNPPLTCQRYC 41

RESULT 26

ADP56014

ID ADP56014 standard; protein; 184 AA.

XX AC ADP56014;

XX DT 18-NOV-2004 (first entry)

XX DE Human PRO protein sequence SEQ ID NO:1990.

XX KW human; PRO; immune related disease; inflammatory immune response;  
 KW immune response stimulation; anti-allergic; antianemic; antiarthritic;  
 KW antiasthmatic; antidiabetic; antiinflammatory; antiapoptotic;  
 KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;  
 KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;  
 KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;  
 KW virucide; gene therapy.

XX OS Homo sapiens.

XX PN WO2004039956-A2.

XX PD 13-MAY-2004.

XX PF 28-OCT-2003; 2003WO-US034381.

XX PR 29-OCT-2002; 2002US-0422472P.

XX PA (GETH ) GENENTECH INC.

XX PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;

XX PI Wood WI, Wu TD;

XX WPI; 2004-376182/35.

XX DR N-PSDB; ADP56013.

XX CC New PRO polynucleotides and polypeptides, useful in useful in diagnosing  
 CC and treating an immune related disease, e.g. systemic lupus  
 CC erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in  
 CC stimulating an immune response.

XX Claim 1; SEQ ID NO 1990; 3009pp; English.

XX The present invention describes an isolated PRO nucleic acid (1). Also  
 CC described: (1) a vector comprising (1); (2) a host cell comprising the



CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an  
 CC isolated PRO polypeptide; (5) a chimeric molecule comprising the  
 CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an  
 CC antibody which specifically binds to a polypeptide of (4); (7) a  
 CC composition of matter comprising a polypeptide of (4), an agonist or  
 CC antagonist of the polypeptide or an antibody that binds to the  
 CC polypeptide in combination with a carrier; (8) an article of manufacture  
 CC comprising a container, a label on the container and a composition of  
 CC matter of (7); (9) a method of treating an immune related disease in a  
 CC mammal; (10) a method for determining the presence of a PRO polypeptide  
 CC in a sample suspected of having the polypeptide; (11) a method of  
 CC diagnosing an immune related disease or an inflammatory immune response  
 CC in a mammal; (12) a method of identifying a compound that inhibits or  
 CC mimics the activity of or expression of a gene encoding a PRO polypeptide  
 CC ; and (13) a method of stimulating the immune response in a mammal. The  
 CC PRO sequences have anti-allergic, anti-inflammatory, antidiabetic,  
 CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,  
 CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,  
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and  
 CC virucide activities, and can be used in gene therapy. The nucleic acid  
 CC (1) and the encoded polypeptides, compositions, kits and methods are  
 CC useful in diagnosing and treating an immune related disease and in  
 CC stimulating an immune response. The present sequence represents a human  
 CC PRO protein from the present invention.

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 8; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34  
 |||||  
 DB 8 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 41

## RESULT 27

ADW03432  
 ID ADM03432 standard; protein; 184 AA.

AC ADW03432;

DT 24-MAR-2005 (first entry)

XX Human BCMA protein amino acid sequence.

XX B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive;  
 KW non-hodgkin lymphoma; hodgkins disease; cytostatic;  
 KW chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis;  
 KW antiarthritic; antirheumatic; systemic lupus erythematosus;  
 KW wegener granulomatosis; antiallergic; antinflammatory; vasotropic;  
 KW inflammatory bowel disease; gastrointestinal-gen.;  
 KW idiopathic thrombocytopenic purpura; hemostatic; multiple sclerosis;  
 KW asthma; antiasthmatic; psoriasis; antipsoriatic; myasthenia gravis;  
 KW muscular-gen.; neuroprotective; vasculitis; diabetes; antidiabetic;  
 KW glomerulonephritis; nephrotropic; BCMA.

OS Homo sapiens.

XX WO200500351-A2.

PN 06-JAN-2005.

XX 04-JUN-2004; 2004WO-US017693.

XX 05-JUN-2003; 2003US-0476414P.

PR 05-JUN-2003; 2003US-0476481P.

PR 06-JUN-2003; 2003US-0476531P.

XX (GETH ) GENENTECH INC.

XX Chan A, Gong Q, Martin F;

XX WPI; 2005-058069/06.  
 DR N-PSDB; ADW03431.

XX Depleting B cells from a mixed population of cells by contacting the  
 PT cells with a BlyS antagonist and a CD20 binding antibody, useful for  
 PT treating B cell malignancies and autoimmune disorders.

XX Disclosure; Fig 2; 114pp; English.

XX The invention comprises a method of depleting B cells from a mixed  
 CC population of cells, the method involves contacting the mixed population  
 CC of cells with BlyS antagonist (e.g. an immunoadhesin) and a CD20 binding  
 CC antibody (e.g. hu2H7.v16). The method of the invention is useful for  
 CC treating B cell malignancies and autoimmune disorders, such as: non-  
 CC Hodgkin's lymphoma, Hodgkin's disease, follicular center cell lymphomas,  
 CC lymphocytic leukemia, Hairy cell leukemia, rheumatoid arthritis, systemic  
 CC lupus erythematosus, Wegener's disease, inflammatory bowel disease,  
 CC idiopathic thrombocytopenic purpura, multiple sclerosis, asthma,  
 CC psoriasis, IGA nephropathy, myasthenia gravis, vasculitis, diabetes and  
 CC glomerulonephritis. The present amino acid sequence represents a human  
 CC BCMA protein.

XX Sequence 184 AA;

Query Match 100.0%; Score 201; DB 9; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34  
 |||||  
 DB 8 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 41

## RESULT 28

ADZ67760

ID ADZ67760 standard; protein; 184 AA.

XX ADZ67760;

XX 14-JUL-2005 (first entry)

DT Human tumor necrosis factor receptor BCMA.

XX Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;  
 KW cytostatic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 6..45  
 /note= "Cys-rich domain"

XX WO2005037865-A2.

XX 28-APR-2005.

PF 18-OCT-2004; 2004WO-US034375.

XX 16-OCT-2003; 2003US-0511698P.

PR 18-OCT-2004; 2004US-0619552P.

XX (ZYMO ) ZYMOGENETICS INC.

XX Fox BA, Holloway JL, Sheppard PO, Dillon SR;

XX WPI; 2005-315682/32.

XX New tumor necrosis factor receptor (TNFR) polypeptides, useful as  
 PT detecting ligands, and for modulating tumor growth, metastasis and  
 PT immunity, such as separating resting from stimulated immune cells.

XX Disclosure; SEQ ID NO 8; 132pp; English.



XX The invention provides novel tumor necrosis factor receptor ztnfr14  
 CC polynucleotides AD267753 and polypeptides AD267754, expression vectors  
 CC and antibodies. Ztnfr14 polynucleotides are used in claimed methods for  
 CC detecting a genetic abnormality in a patient and for detecting a cancer  
 CC in a patient. Recombinant ztnfr14 polypeptide, optionally conjugated to a  
 CC toxin, is used in a claimed method of killing cancer cells. Ztnfr14  
 CC polypeptides can be used to detect ligands, agonists and antagonists. The  
 CC polypeptides, polynucleotides and antibodies may also be used in methods  
 CC that modulate tumor growth, metastasis, and immunity such as separating  
 CC resting from stimulated immune cells. The present sequence is that of  
 CC human TNFR BCMA. This sequence was compared with that of ztnfr14 in the  
 CC identification of ztnfr14 as a member of the TNFR family.  
 XX  
 SQ Sequence 184 AA;  
 Query Match 100.0%; Score 201; DB 9; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CSQNEVFDLSLLHACIPQCLRCSSNTPLTCQRYC 34  
 Db 8 CSQNEVFDLSLLHACIPQCLRCSSNTPLTCQRYC 41  
 RESULT 29  
 AEA23348  
 ID AEA23348 standard; protein; 184 AA.  
 AC AEA23348;  
 XX  
 DT 11-AUG-2005 (first entry)  
 DE Tumor antigen of hematopoietic origin TAH023.  
 XX  
 KW cytostatic; gene therapy; therapy; cell growth; protein purification;  
 KW DNA purification; hyperproliferation; neoplasm;  
 KW tumor antigen of hematopoietic origin; TAH023.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005049075-A2.  
 XX  
 PD 02-JUN-2005.  
 XX  
 PF 16-NOV-2004; 2004WO-US038262.  
 XX  
 PR 17-NOV-2003; 2003US-0520842P.  
 PR 24-DEC-2003; 2003US-0532426P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Crowley C, Desauvage FJ, Eaton DL, Ebens A, Polson A, Smith V;  
 XX  
 DR WPI; 2005-405198/41.  
 DR N-ESDB; AEA23347.  
 XX  
 PT Inhibiting the growth of a cell that expresses a protein by contacting  
 PT the cell with anti-tumor antigens of hematopoietic origin (TAHO)  
 PT polypeptide, antibody or organic molecule, useful for treating  
 PT hematopoietic and malignant tumors.  
 XX  
 PS Disclosure; SEQ ID NO 46; 367pp; English.  
 XX  
 CC The invention describes a method of inhibiting the growth of a cell that  
 CC expresses a protein comprising contacting the cell with an antibody,  
 CC oligopeptide or organic molecule that binds to the protein, the binding  
 CC of the antibody, oligopeptide or organic molecule to the protein and  
 CC causing an inhibition of growth of the cell. Also described is a method  
 CC for treating or preventing a cell proliferative disorder associated with  
 CC increased expression or activity of a protein having at least 80 % amino  
 CC acid sequence identity to: a polypeptide having any of SEQ ID NO: 2, 8,  
 CC 10, 12, 16, 20, 22, 49 and 51; a polypeptide having the amino acid

CC sequence of (a), lacking its associated signal peptide; an extracellular  
 CC domain of the polypeptide having the amino acid sequence of (a), with or  
 CC without its associated signal peptide; a polypeptide encoded by any of  
 CC SEQ ID NO: 1, 7, 9, 11, 15, 19, 21, 48 and 50; or a polypeptide encoded  
 CC by the full-length coding region of the nucleotide sequence of (d),  
 CC comprising administering to a subject in need of such treatment an  
 CC antagonist of the protein, and effectively treating or preventing the  
 CC cell proliferative disorder. Also disclosed are anti-tumor antigens of  
 CC hematopoietic origin (TAHO) polypeptides, encoding nucleic acids,  
 CC oligopeptides, vectors, host cells and antibodies used in the methods of  
 CC the invention. The methods and compositions of the present invention are  
 CC useful for treating hematopoietic and malignant tumors in mammals. This  
 CC is the amino acid sequence of tumor antigen of hematopoietic origin  
 CC TAH023.  
 XX  
 SQ Sequence 184 AA;

Query Match 100.0%; Score 201; DB 9; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEVFDLSLLHACIPQCLRCSSNTPLTCQRYC 34  
 Db 8 CSQNEVFDLSLLHACIPQCLRCSSNTPLTCQRYC 41

RESULT 30  
 AEC02031  
 ID AEC02031 standard; protein; 184 AA.

AC AEC02031;

DT 20-OCT-2005 (first entry)

DE Amin acid sequence of a BCMA protein.

XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
 KW cytostatic; neoplasm; immunosuppressive; therapeutic; BCMA;  
 KW B-cell maturation antigen.

XX Homo sapiens.

XX WO2005075511-A1.

PD 18-AUG-2005.

PF 04-AUG-2004; 2004WO-US025247.

XX 29-JAN-2004; 2004US-0540271P.

XX (GETH ) GENENTECH INC.

XX Kelley RF, Patel D;

XX WPI; 2005-555932/56.

XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
 PT for treating immune-related disease, cancer or T-cell mediated disease  
 PT such as graft rejection, graft versus host disease (GVHD) and  
 PT inflammation.

PS Disclosure; SEQ ID NO 20; 140pp; English.

XX The specification describes polypeptides that bind APRIL or BAFF. The  
 CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
 CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
 CC polypeptides of the invention are useful for treating immune-related  
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
 CC sclerosis; or T-cell mediated disease such as graft rejection, graft  
 CC versus host disease (GVHD) and inflammation. The present sequence  
 CC represents a BCMA protein.



SQ Sequence 184 AA;  
Query Match 100.0%; Score 201; DB 9; Length 184;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEYFDSLHACIPQCRLCSSTNPPLTCQRYC 34  
|||||  
DB 8 CSQNEYFDSLHACIPQCRLCSSTNPPLTCQRYC 41  
|||||  
RESULT 31  
AAE15488  
ID AAE15488 standard; protein; 283 AA.  
XX  
AC AAE15488;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human BCMA-immunoglobulin Fc region fusion protein.  
XX  
KW Human; transmembrane activator and intracellular CAML interactor; TAC1;  
KW cytosolic; B cell maturation protein; BCMA; tumor necrosis factor; TNF;  
KW lymphoproliferative disorder; tumor; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis; fusion protein.  
XX  
OS Homo sapiens.  
XX  
XX WO200187979-A2.  
PN  
XX 22-NOV-2001.  
XX  
XX 14-MAY-2001; 2001WO-US015567.  
XX  
PR 12-MAY-2000; 2000US-0204039P.  
PR 27-JUN-2000; 2000US-0214591P.  
PR 14-MAY-2001; 2001US-00214591.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Theill LE, Yu G;  
PI  
XX WPI; 2002-066686/09.  
DR  
XX Inhibiting activity of B cell maturation protein and/or transmembrane  
XX activator and intracellular cyclophilin ligand interactor, by  
PT administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX  
PS Disclosure; Fig 10B; 94pp; English.  
XX  
XX The invention relates to a method for inhibiting TAC1 (transmembrane  
CC activator and intracellular CAML interactor) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumor necrosis factor-TNF  
CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence

CC is human BCMA protein-immunoglobulin Fc region fusion protein  
XX  
SQ Sequence 283 AA;  
Query Match 100.0%; Score 201; DB 5; Length 283;  
Best Local Similarity 100.0%; Pred. No. 2.4e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEYFDSLHACIPQCRLCSSTNPPLTCQRYC 34  
|||||  
DB 5 CSQNEYFDSLHACIPQCRLCSSTNPPLTCQRYC 38  
|||||  
RESULT 32  
ABG95060  
ID ABG95060 standard; protein; 288 AA.  
XX  
AC ABG95060;  
XX  
DT 04-DEC-2002 (first entry)  
XX  
DE Human translocation (4; 16)(q26; p13) protein.  
XX  
KW Chromosome aberration; oncogenic fusion protein; cancer;  
KW proliferative disease; cellular protein isoform; heat shock protein 90;  
KW HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;  
KW T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;  
KW acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;  
KW acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;  
KW papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;  
KW rhabdomyosarcoma; synovial sarcoma; viral infection.  
XX  
XX Homo sapiens.  
OS  
XX WO200269900-A2.  
PN  
XX 12-SEP-2002.  
XX  
XX 01-MAR-2002; 2002WO-US006518.  
PF  
XX 01-MAR-2001; 2001US-0272751P.  
PR  
XX (CONF-) CONFORMA THERAPEUTICS CORP.  
PA  
XX Fritz LC, Burrows FJ;  
PI  
XX WPI; 2002-698710/75.  
DR  
XX N-PSDB; ABS73235.  
DR  
XX Treating genetically-defined disease associated with chromosomal  
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative  
PT diseases, involves administering an inhibitor of heat shock protein 90.  
XX  
PS Disclosure; Page 189-190; 389pp; English.  
XX  
XX The invention describes a method of treating genetically-defined disease  
CC associated with chromosomal aberrations yielding oncogenic fusion  
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous  
CC cell population, treating proliferative diseases associated with mutant  
CC protein or cellular protein isoforms (II) dependent on heat shock protein  
CC (HSP)-90, or selectively treating cells expressing (II) involving  
CC administering HSP90-inhibitor. The method is useful for treating  
CC genetically-defined disease with chromosomal aberration yielding  
CC oncogenic fusion protein, treating cancerous cells containing fusion  
CC protein in heterogeneous cell population, treating proliferative disease  
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or  
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.  
CC p53), or selectively treating cells expressing mutant protein or cellular  
CC protein isoform in a patient heterozygous for (II). The method is useful  
CC for treating a disease e.g. haematopoietic disorder such as T or B cell  
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL and CMML,  
CC or a disease characterised by a solid tumour such as papillary thyroid  
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and



CC	synovial sarcoma. The method is also useful for treating viral	CC	and in the treatment of autoimmune disorders, B-cell lymphoproliferative
CC	infections. This represents a protein encoded by the DNA sequence of a	CC	disorders, hypertension and renal disorders. The BAFF-R proteins may also
CC	chromosome aberration	CC	be used in the treatment of immunosuppressive disorders and HIV
XX		CC	infection, and in patients undergoing organ transplantation. The BAFF-R
SQ	Sequence 288 AA;	CC	proteins or BAFF-R specific antibodies may be used for treating,
	Query Match 100.0%; Score 201; DB 5; Length 288;	CC	suppressing or altering an immune response involving a signalling pathway
	Best Local Similarity 100.0%; Pred. No. 2.4e-17; Indels 0; Gaps 0;	CC	between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R
	Matches 34; Conservative 0; Mismatches 0;	CC	inhibits B-cell growth and maturation it is useful for treating diseases
		CC	such as systemic lupus erythematosus, autoimmune haemolytic anaemia,
		CC	Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly
		CC	progressive glomerulonephritis, and lymphomas. Nucleic acids encoding
		CC	human BAFF-R may be used in gene therapy to treat tumours, lymphomas,
		CC	autoimmune disorders and inherited B-cell-associated disorders. The
		CC	present sequence represents the BAFF-R fusion protein BAFF-R-Fc,
		CC	comprising a mouse IgG-kappa signal sequence, residues 1-153 of human
		CC	BAFF-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to
		CC	standardise OS field)
		XX	
		SQ	Sequence 302 AA;
			Query Match 100.0%; Score 201; DB 4; Length 302;
			Best Local Similarity 100.0%; Pred. No. 2.6e-17; Indels 0; Gaps 0;
			Matches 34; Conservative 0; Mismatches 0;
QY	1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34	QY	1 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 34
DB	112 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 145	DB	31 CSQNEYFDSLHACIPQLRCSSNTPLTCQRYC 64
RESULT 33		RESULT 34	
AAB60699		AAE00507	
ID	AAB60699 standard; protein; 302 AA.	ID	AAE00507 standard; protein; 302 AA.
XX		AC	AAE00507;
AC	AAB60699;	XX	11-SEP-2003 (revised)
DT	11-SEP-2003	DT	31-JUL-2001 (first entry)
DT	22-MAY-2001 (first entry)	XX	Human BCMA-Immunoglobulin G Fc region fusion construct.
XX	Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.	XX	Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
XX	Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;	KW	gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease;
KW	immune-related disorder; B-cell growth inhibitor;	KW	carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension;
KW	B-cell maturation inhibitor; immunoglobulin production inhibitor;	KW	systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
KW	autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;	KW	B-cell lympho-proliferative disorder; BCM; immunosuppressive disease;
KW	renal disorder; immunosuppressive disorder; HIV infection;	KW	organ transplantation; HIV; human immunodeficiency virus; TNF; murine;
KW	organ transplantation; antiinflammatory; systemic lupus erythematosus;	KW	tumour necrosis factor; B cell maturation protein; BCMA; fusion protein;
KW	autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;	XX	immunoglobulin G; IgG; Fc region.
KW	B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;	OS	Homo sapiens.
KW	lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.	OS	Mus sp.
XX		OS	Chimeric.
OS	Homo sapiens.	XX	Key Location/Qualifiers
OS	Mus sp.	FT	1..22
OS	Chimeric.	FT	/label= Signal peptide
XX		FT	/note= "Derived from murine Ig kappa sequence"
XX	WO200112812-A2.	FT	23..302
XX	22-FEB-2001.	FT	/label= Mature human BCMA-IgG-Fc fusion protein
XX	16-AUG-2000; 2000WO-US022507.	FT	23..75
XX	17-AUG-1999; 99US-0149378P.	FT	/note= "Derived from human BCMA protein"
PR	11-FEB-2000; 2000US-0181684P.	FT	24..302
PR	18-FEB-2000; 2000US-0183536P.	FT	/label= Cysteine rich domain
XX	(BIOJ ) BIOGEN INC.	FT	/note= "Derived from human BCMA"
PA	(APOT-) APOTEC R & D SA.	FT	76..302
XX		FT	/note= "Derived from human IgG Fc region"
XX	Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;	XX	WO200124811-A1.
PI	Thompson J;	XX	12-APR-2001.
XX	WPI; 2001-202866/20.	XX	05-OCT-2000; 2000WO-US027579.
DR	N-PSDB; AAF59999.		
XX	Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell		
PT	lympho-proliferative disorder by administering BAFF-receptor polypeptide,		
PT	chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.		
XX	Example 4; Fig 2; 59pp; English.		
PS	The invention relates to the use of a BAFF receptor (BAFF-R, also known		
XX	as BCMA) protein, or a BAFF-R fusion protein as an agent for the		
CC	treatment of a variety of immune-related disorders. BAFF-R is a member of		
CC	the TNF (tumour necrosis factor) family, acting as an immunoregulatory		
CC	agent, and also plays a role in the development of hypertension and		
CC	related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-		
CC	specific antibodies can be used for inhibiting B-cell growth, dendritic		
CC	cell-induced B-cell growth and maturation, and immunoglobulin production,		



PR 06-OCT-1999; 99US-0157913P.  
PR 11-FEB-2000; 2000US-0181807P.  
PR 30-JUN-2000; 2000US-0215688P.  
XX  
PA (BIOJ ) BIOGEN INC.  
PA (APOT-) APOTECH R & D SA.  
XX  
XX Schneider P, Thompson J, Cachero T, Ambrose C, Rennert P;  
XX  
XX WPI; 2001-266242/27.  
DR N-PSDB; AAD03847.  
DR  
XX  
XX Treating a mammal for a condition associated with undesired cell  
PT proliferation such as cancer or carcinoma, comprises administering a  
PT composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)  
PT antagonist.  
XX  
XX Example 1; Fig 3B; 85pp; English.  
XX  
XX The invention relates to a method of treating a mammal for a condition  
CC associated with undesired cell proliferation such as cancer or carcinoma.  
CC The method involves administering a composition comprising A  
CC Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell  
CC maturation protein (BCM or BCMA) antagonist that antagonises the  
CC interaction between APRIL and its cognate receptor(s). This method is  
CC useful for treating undesired cell proliferation such as cancer or  
CC carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma,  
CC prostate carcinoma, and other carcinomas whose proliferation is modulated  
CC by APRIL. It is also useful for treating autoimmune diseases (Grave's  
CC disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular  
CC diseases, renal disorders, B-cell lympho-proliferative disorders,  
CC immunosuppressive diseases, organ transplantation, inflammation and human  
CC immunodeficiency virus (HIV), and for treating, suppressing or altering  
CC an immune response involving a signalling pathway between APRIL-R and its  
CC ligand. APRIL-R DNA is also useful in gene therapy. The present sequence  
CC is a fusion construct containing human APRIL-R also referred as BCMA or  
CC BCM protein, FC region of human immunoglobulin G (IgG) and a signal  
CC sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to  
CC standardise OS field)  
XX  
SQ Sequence 302 AA;  
Query Match 100.0%; Score 201; DB 4; Length 302;  
Best Local Similarity 100.0%; Pred. No. 2.6e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEYFDSLHACIFCQLRCSNTPTLTQRYC 34  
|||||  
DB 31 CSQNEYFDSLHACIFCQLRCSNTPTLTQRYC 64  
|||||  
RESULT 35  
ADG43717  
ID ADG43717 standard; protein; 302 AA.  
XX  
XX ADG43717;  
XX  
XX 26-FEB-2004 (first entry)  
XX  
XX Human B-cell maturation antigen-Fc SEQ ID NO:3.  
DE  
DE human; neurodegenerative immunological disorder; demyelination;  
KW Central Nervous System; CNS; inflammation; B-cell maturation antigen;  
KW BCMA; multiple sclerosis; neuroprotective; nontropic; antiinflammatory;  
KW gene therapy; mouse.  
XX  
XX Chimeric.  
OS Homo sapiens.  
OS Mus sp.  
XX  
XX Key Location/Qualifiers  
FH 1..23  
FT /note= "Murine IgGkappa signal sequence"  
FT

FT Region 24..74  
FT /note= "Human BCMA extracellular domain"  
FT 75..302  
FT /note= "Human Ig heavy chain Fc region"  
XX  
XX WO2003072713-A2.  
XX  
XX 04-SEP-2003.  
XX  
XX 21-FEB-2003; 2003WO-US005147.  
XX  
XX 21-FEB-2002; 2002US-0358427P.  
XX (BIOJ ) BIOGEN INC.  
XX Kalled SL, Reid H;  
XX WPI; 2003-721758/68.  
DR N-PSDB; ADG43718.  
XX  
XX Treating a neurodegenerative immunological disorder, e.g. demyelination  
PT or inflammation in a mammal comprises administering a B-cell maturation  
PT antigen (BCMA), an antibody against BCMA or a BCMA ligand.  
XX  
XX Claim 12; Page 70-71; 72pp; English.  
XX  
XX The invention relates to a novel method for treating a neurodegenerative  
CC immunological disorder, demyelination or Central Nervous System (CNS)  
CC inflammation in a mammal. The method comprises administering B-cell  
CC maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand  
CC (the mammal has or is at risk of developing multiple sclerosis). The  
CC method of the invention has neuroprotective, nontropic, and  
CC antiinflammatory activity, and may have a use in gene therapy. The  
CC methods, BCMA, and antibodies are useful for treating a neurodegenerative  
CC immunological disorder such as multiple sclerosis, demyelination or CNS  
CC inflammation. The present sequence is used in the exemplification of the  
XX invention.  
XX  
SQ Sequence 302 AA;  
Query Match 100.0%; Score 201; DB 7; Length 302;  
Best Local Similarity 100.0%; Pred. No. 2.6e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEYFDSLHACIFCQLRCSNTPTLTQRYC 34  
|||||  
DB 31 CSQNEYFDSLHACIFCQLRCSNTPTLTQRYC 64  
|||||  
RESULT 36  
AEC02026  
ID AEC02026 standard; peptide; 34 AA.  
XX  
XX AEC02026;  
XX  
XX 20-OCT-2005 (first entry)  
XX  
XX Formula II derived polypeptide E that binds BAFF.  
DE  
DE APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
XX  
XX Synthetic.  
OS  
XX WO2005075511-A1.  
PN  
XX 18-AUG-2005.  
PD  
XX 04-AUG-2004; 2004WO-US025247.  
PF  
XX 29-JAN-2004; 2004US-0540271P.  
PR  
XX (GETH ) GENENTECH INC.  
PA











PI Kelley RF, Patel D;  
XX WPI; 2005-555932/56.  
XX  
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
XX Claim 13; SEQ ID NO 14; 140pp; English.  
XX  
XX The specification describes polypeptides that bind APRIL or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
CC scleroma; or T-cell mediated disease such as graft rejection, graft  
CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents a polypeptide of the invention, derived from formula II (see  
CC AEC02021), that that bind BAFF.  
XX  
XX Sequence 34 AA;  
SQ

Query Match 95.5%; Score 192; DB 9; Length 34;  
Best Local Similarity 97.1%; Pred. No. 4e-17; 1; Indels 0; Gaps 0;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34  
DB 1 CSQNEAFDSLHACIPQLRCSSNTPPLTCQRYC 34  
RESULT 43  
AEC02033  
ID AEC02033 standard; peptide; 38 AA.  
XX  
XX AEC02033;  
XX  
XX 20-OCT-2005 (first entry)  
XX  
XX Amino acid sequence of an extracellular domain of BCMA.  
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
XX cytostatic; neoplasm; immunosuppressive; therapeutic;  
XX B-cell maturation antigen; BCMA.  
XX  
XX Synthetic.  
XX  
XX WO2005075511-A1.  
XX  
XX 18-AUG-2005.  
XX  
XX 04-AUG-2004; 2004WO-US025247.  
XX  
XX 29-JAN-2004; 2004US-0540271P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Kelley RF, Patel D;  
XX  
XX WPI; 2005-555932/56.  
XX  
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
XX Disclosure; SEQ ID NO 22; 140pp; English.  
XX  
XX The specification describes polypeptides that bind APRIL or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
CC scleroma; or T-cell mediated disease such as graft rejection, graft  
CC versus host disease (GVHD) and inflammation. The present sequence  
CC represents an extracellular domain of BCMA.  
XX  
XX Sequence 38 AA;  
SQ

Query Match 95.5%; Score 192; DB 9; Length 38;  
Best Local Similarity 100.0%; Pred. No. 4.4e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34  
|||||

PI Kelley RF, Patel D;  
XX WPI; 2005-555932/56.  
XX  
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
XX Claim 13; SEQ ID NO 13; 140pp; English.  
XX  
XX The specification describes polypeptides that bind APRIL or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
XX

Query Match 95.5%; Score 192; DB 9; Length 34;  
Best Local Similarity 97.1%; Pred. No. 4e-17; 1; Indels 0; Gaps 0;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 34  
DB 1 CSQNEFDSLHACIPQLRCSSNTPPLTCQRYC 34  
RESULT 42  
AEC02024  
ID AEC02024 standard; peptide; 34 AA.  
XX  
XX AEC02024;  
XX  
XX 20-OCT-2005 (first entry)  
XX  
XX Formula II derived polypeptide C that binds BAFF.  
XX  
XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
XX cytostatic; neoplasm; immunosuppressive; therapeutic.  
XX  
XX Synthetic.  
XX  
XX WO2005075511-A1.  
XX  
XX 18-AUG-2005.  
XX  
XX 04-AUG-2004; 2004WO-US025247.  
XX  
XX 29-JAN-2004; 2004US-0540271P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Kelley RF, Patel D;  
XX  
XX WPI; 2005-555932/56.  
XX  
XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
PT for treating immune-related disease, cancer or T-cell mediated disease  
PT such as graft rejection, graft versus host disease (GVHD) and  
PT inflammation.  
XX  
XX Claim 13; SEQ ID NO 13; 140pp; English.  
XX  
XX The specification describes polypeptides that bind APRIL or BAFF. The  
CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
CC (BCMA). APRIL and BAFF are tumor necrosis family (TNF) members. The  
CC polypeptides of the invention are useful for treating immune-related  
XX







DR WPI; 2005-555932/56.  
 XX New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
 PT for treating immune-related disease, cancer or T-cell mediated disease  
 PT such as graft rejection, graft versus host disease (GVHD) and  
 PT inflammation.  
 XX Claim 13; SEQ ID NO 18; 140pp; English.  
 XX The specification describes polypeptides that bind APRIL or BAFF. The  
 CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
 CC (BCMA). APRIL and BAFF are tumor necrosis factor (TNF) members. The  
 CC polypeptides of the invention are useful for treating immune-related  
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple  
 CC sclerosis; or T-cell mediated disease such as graft rejection, graft  
 CC versus host disease (GVHD) and inflammation. The present sequence  
 CC represents a polypeptide of the invention, derived from formula II (see  
 CC AEC02021), that that bind BAFF.  
 XX Sequence 34 AA;  
 SQ

Query Match 94.0%; Score 189; DB 9; Length 34;  
 Best Local Similarity 94.1%; Pred. No. 9.6e-17;  
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CSQNEVFDLLHACIPCLRCSSNTPPLTCQRYC 34  
 DB 1 CSQNEVFDLLHACIPCLRCSSNTPPLTCQRYC 34  
 RESULT 47  
 AEC02019  
 ID AEC02019 standard; peptide; 34 AA.  
 XX AC AEC02019;  
 XX DT 20-OCT-2005 (first entry)  
 XX DE Formula I derived polypeptide H that binds APRIL.  
 XX APRIL; BAFF; immune disorder; immunomodulator; antiinflammatory; cancer;  
 KW cytostatic; neoplasm; immunosuppressive; therapeutic.  
 KW Synthetic.  
 OS WO2005075511-A1.  
 XX PN 18-AUG-2005.  
 XX PD 04-AUG-2004; 2004WO-US025247.  
 XX PF 29-JAN-2004; 2004US-0540271P.  
 XX PR (GETH ) GENENTECH INC.  
 XX PA Kelley RF, Patel D;  
 XX PI WPI; 2005-555932/56.  
 XX DR New polypeptides that inhibit APRIL and/or BAFF binding to BCMA, useful  
 PT for treating immune-related disease, cancer or T-cell mediated disease  
 PT such as graft rejection, graft versus host disease (GVHD) and  
 PT inflammation.  
 XX Claim 7; SEQ ID NO 8; 140pp; English.  
 XX The specification describes polypeptides that bind APRIL or BAFF. The  
 CC polypeptides inhibit APRIL or BAFF binding to B-cell maturation antigen  
 CC (BCMA). APRIL and BAFF are tumor necrosis factor (TNF) members. The  
 CC polypeptides of the invention are useful for treating immune-related  
 CC diseases, such as rheumatoid arthritis, multiple sclerosis, and systemic  
 CC lupus erythematosus; cancer such as leukemia, lymphoma, or multiple

CC sclerosis; or T-cell mediated disease such as graft rejection, graft  
 CC versus host disease (GVHD) and inflammation. The present sequence  
 CC represents polypeptide of the invention that binds APRIL, derived from  
 CC AEC02012.  
 XX Sequence 34 AA;  
 SQ

Query Match 90.5%; Score 182; DB 9; Length 34;  
 Best Local Similarity 91.2%; Pred. No. 7.5e-16;  
 Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CSQNEVFDLLHACIPCLRCSSNTPPLTCQRYC 34  
 DB 1 CSQNEVFDLLHACIPCLRCSSNTPPLTCQRYC 34  
 RESULT 48  
 AAB60700  
 ID AAB60700 standard; protein; 157 AA.  
 XX AC AAB60700;  
 XX DT 22-MAY-2001 (first entry)  
 XX DE Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.  
 XX KW Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;  
 KW immune-related disorder; B-cell growth inhibitor; BCMA;  
 KW B-cell maturation inhibitor; immunoglobulin production inhibitor;  
 KW autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;  
 KW renal disorder; immunosuppressive disorder; HIV infection;  
 KW organ transplantation; antiinflammatory; systemic lupus erythematosus;  
 KW autoimmune haemolytic anaemia; Grave's disease; multiple myeloma;  
 KW B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;  
 KW lymphoma; Gene therapy; cancer; tumour; plasmid pJST535.  
 XX OS Homo sapiens.  
 XX PN WO200112812-A2.  
 XX PD 22-FEB-2001.  
 XX PF 16-AUG-2000; 2000WO-US022507.  
 XX PR 17-AUG-1999; 99US-0149378P.  
 XX PR 11-FEB-2000; 2000US-018184P.  
 XX PR 18-FEB-2000; 2000US-0183536P.  
 XX PA (BIOJ ) BIOGEN INC.  
 XX PA (APOT-) APOTEC R & D SA.  
 XX PI Mackay F, Browning J, Ambrose C, Tschopp J, Schneider P;  
 XX PI Thompson J;  
 XX DR WPI; 2001-202866/20.  
 XX DR N-PSDB; AAF60000.  
 XX XX Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell  
 PT lympho-proliferative disorder by administering BAFF-receptor polypeptide,  
 PT chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.  
 XX Example 1; Fig 3; 59pp; English.  
 XX The invention relates to the use of a BAFF receptor (BAFF-R, also known  
 CC as BCMA) protein, or a BAFF-R fusion protein as an agent for the  
 CC treatment of a variety of immune-related disorders. BAFF-R is a member of  
 CC the TNF (tumour necrosis factor) family, acting as an immunoregulatory  
 CC agent, and also plays a role in the development of hypertension and  
 CC related disorders. BAFF-R, fusion proteins containing it, and BAFF-R-  
 CC specific antibodies can be used for inhibiting B-cell growth, dendritic  
 CC cell-induced B-cell growth and maturation, and immunoglobulin production,  
 CC and in the treatment of autoimmune disorders, B-cell lymphoproliferative  
 CC disorders, hypertension and renal disorders. The BAFF-R proteins may also



CC be used in the treatment of immunosuppressive disorders and HIV  
 CC infection, and in patients undergoing organ transplantation. The BAPF-R  
 CC proteins or BAPF-R specific antibodies may be used for treating,  
 CC suppressing or altering an immune response involving a signalling pathway  
 CC between BAPF-R and BAPF, thereby inhibiting inflammation. Since BAPF-R  
 CC inhibits B-cell growth and maturation it is useful for treating diseases  
 CC such as systemic lupus erythematosus, autoimmune haemolytic anaemia,  
 CC Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly  
 CC progressive glomerulonephritis, and lymphomas. Nucleic acids encoding  
 CC human BAPF-R may be used in gene therapy to treat tumours, lymphomas,  
 CC autoimmune disorders and inherited B-cell-associated disorders. The  
 CC present sequence represents a human BAPF-R protein sequence as encoded by  
 CC Plasmid pJST535. However, this BAPF-R protein sequence is 27 amino acids  
 CC shorter than that given in AAB60698  
 XX  
 SQ Sequence 157 AA;

Query Match 79.4%; Score 159.5; DB 4; Length 157;  
 Best Local Similarity 90.6%; Pred. No. 2.6e-12;  
 Matches 29; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 3 QNEYFDSLHACIPQQRCSNSTPPLTCQRYC 34  
 DB 7 QNEYFDSLHACIPQQLR---NTPPLTCQRYC 35

RESULT 49  
 ADI53060  
 ID ADI53060 standard; peptide; 26 AA.  
 XX  
 AC ADI53060;  
 XX  
 DT 22-APR-2004 (first entry)  
 DE Human BCMA receptor binding site.  
 XX  
 KW protein co-ordinate data; cytostatic; antiallergic; immunosuppressive;  
 KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;  
 KW antidiabetic; dermatological; antiaesthatic; neurokine-alpha;  
 KW crystallography; cancer; allergic disorder; autoimmune disease;  
 KW rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes;  
 KW systemic lupus erythematosus; asthma; receptor.  
 XX  
 OS Homo sapiens.

XX WO2003050134-A2.  
 XX 19-JUN-2003.  
 XX 07-NOV-2002; 2002WO-US035661.  
 XX 07-NOV-2001; 2001US-0331049P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Li Y, Oren DE, Arnold E, Volevok Y;  
 XX WPI; 2003-532895/50.  
 XX  
 XX New crystalline Neurokine-alpha protein, useful for designing compounds  
 PT that bind, inhibit or mimic a Neurokine-alpha protein or enhance the  
 PT activity of a Neurokine-alpha protein for treating e.g. cancer or  
 PT allergic disorders.  
 XX  
 PS Disclosure; Fig 4; 362pp; English.

XX  
 CC The invention relates to a neurokine-alpha protein in crystalline form.  
 CC The crystalline neurokine-alpha protein is useful for designing  
 CC molecules that have biological activity or compounds that bind, inhibit  
 CC or mimic a neurokine-alpha protein and/or enhance the activity of a  
 CC neurokine-alpha protein. The three-dimensional structure of a neurokine  
 CC -alpha protein is useful in determining the three-dimensional of other  
 CC neurokine-alpha proteins and their homologs. The compounds that mimic,

CC prevent or inhibit the activity of the protein are useful for treating  
 CC cancer, allergic disorders, or autoimmune diseases such as rheumatoid  
 CC arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus  
 CC erythematosus or asthma. This sequence represents the residues in the  
 CC receptor for binding a cytokine ligand.

SQ Sequence 26 AA;

Query Match 75.1%; Score 151; DB 7; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-12;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 EYFDSLHACIPQQRCSNSTPPLTC 30  
 DB 1 EYFDSLHACIPQQRCSNSTPPLTC 26

RESULT 50  
 AAB08844  
 ID AAB08844 standard; peptide; 185 AA.

XX  
 AC AAB08844;  
 XX  
 DT 02-JAN-2001 (first entry)  
 XX

DE Amino acid sequence of murine BCMA polypeptide.

XX BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer;  
 KW anti-cell death gene; apoptosis; viral infection; inflammatory response;  
 KW rheumatoid arthritis; inflammatory bowel disease; septic shock.

XX Mus musculus.

XX  
 FH Key Location/Qualifiers  
 FT Domain 47..72  
 FT /note= "putative transmembrane domain"

XX WO2000050633-A1.

XX 31-AUG-2000.

XX 24-FEB-2000; 2000WO-US004925.

XX 24-FEB-1999; 99US-012148SP.

XX (GEO ) GEN HOSPITAL CORP.

XX Seed B, Ting A;

XX WPI; 2000-558405/51.

XX Identifying a modulator of gene expression for drug designing, by  
 PT contacting a compound library with a cell expressing an anti-cell death  
 PT gene and reporter gene, and determining alteration in reporter gene  
 PT expression.

XX Claim 32; Fig 7B; 53pp; English.

XX The present sequence represents a BCMA (not defined) polypeptide. BCMA is  
 CC a necrosis factor (NF)-kB activator. The method of the invention is used  
 CC to identify compounds which modulate BCMA activity (and thus NF-kB  
 CC activity). The specification describes a method of identifying a  
 CC polypeptide which increases gene expression from a promoter. The method  
 CC involves contacting a library of with a cell which expresses a  
 CC recombinant anti-cell death gene and a reporter gene operably linked to  
 CC the promoter, and then determining whether the expression of the reporter  
 CC gene is altered as a result of contact with library. The method is useful  
 CC for identifying polypeptides which increase or decrease gene expression  
 CC from a promoter. The BCMA polypeptide or nucleic acid are useful for  
 CC preparing a pharmaceutical composition for treating cancer, apoptosis,  
 CC viral infections, inflammatory response, such as rheumatoid arthritis,  
 CC inflammatory bowel disease or septic shock. BCMA is useful for  
 CC identifying compounds that modulate NF-kB expression and thus for drug







CC	with leucocyte infiltration of the skin or organs. The present sequence	
CC	is mouse BCMA protein	
XX		
QQ	Sequence 185 AA;	
	Query Match 67.7%; Score 136; DB 5; Length 185;	
	Best Local Similarity 70.6%; Pred. No. 3e-09;	
	Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;	
QY	1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34	
Db	5 CFHSEYFDSLHACKCHLRCSN--PPATCQPYC 36	
	:	
RESULT 53		
ADZ67762		
ID	ADZ67762 standard; protein; 185 AA.	
XX		
AC	ADZ67762;	
XX		
DT	14-JUL-2005 (first entry)	
DE	Mouse tumor necrosis factor receptor BCMA.	
XX		
KW	Tumor necrosis factor receptor; BCMA; cancer; neoplasm; diagnosis;	
KW	Cytostatic.	
XX		
OS	Mus musculus.	
XX		
PN	WO2005037865-A2.	
XX		
PD	28-APR-2005.	
XX		
PF	18-OCT-2004; 2004WO-US034375.	
XX		
PR	16-OCT-2003; 2003US-0511698P.	
PR	18-OCT-2004; 2004US-0619552P.	
XX		
PA	(ZYMO ) ZYMOGENETICS INC.	
XX		
PI	Fox BA, Holloway JL, Sheppard PO, Dillon SR;	
XX		
DR	WPI; 2005-315682/32.	
XX		
PT	New tumor necrosis factor receptor (TNFR) polypeptides, useful as	
PT	detecting ligands, and for modulating tumor growth, metastasis and	
PT	immunity, such as separating resting from stimulated immune cells.	
XX		
PS	Disclosure; SEQ ID NO 10; 132pp; English.	
XX		
CC	The invention provides novel tumor necrosis factor receptor ztnfr14	
CC	polynucleotides ADZ67753 and polypeptides ADZ67754, expression vectors	
CC	and antibodies. Human ztnfr14 polynucleotides are used in claimed methods	
CC	for detecting a genetic abnormality in a patient and for detecting a	
CC	cancer in a patient. Recombinant ztnfr14 polypeptide, optionally	
CC	conjugated to a toxin, is used in a claimed method of killing cancer	
CC	cells. Ztnfr14 polypeptides can be used to detect ligands, agonists and	
CC	antagonists. The polypeptides, polynucleotides and antibodies may also be	
CC	used in methods that modulate tumor growth, metastasis, and immunity such	
CC	as separating resting from stimulated immune cells. The present sequence	
CC	is that of murine TNFR BCMA. This sequence was compared with that of	
CC	murine ztnfr14 ADZ67756 in the identification of ztnfr14 as a member of	
CC	the TNFR family.	
XX		
QQ	Sequence 185 AA;	
	Query Match 67.7%; Score 136; DB 9; Length 185;	
	Best Local Similarity 70.6%; Pred. No. 3e-09;	
	Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;	
QY	1 CSQNEYFDSLHACIPQLRCSNTPTPLTCQRYC 34	
Db	5 CFHSEYFDSLHACKCHLRCSN--PPATCQPYC 36	
	:	

RESULT 54

AAE15489  
ID AAE15489 standard; protein; 281 AA.

XX AAE15489;

AC AAE15489;

XX 29-AUG-2003 (revised)

DT 12-MAR-2002 (first entry)

XX Mouse BCMA-human immunoglobulin Fc region fusion protein.

DE Mouse BCMA-human immunoglobulin Fc region fusion protein.

XX Human; transmembrane activator and intracellular CAML interactor; TAC1;  
KW Cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
KW rheumatoid arthritis; atherosclerosis; fusion protein; mouse.

XX Homo sapiens.

OS Mus sp.

OS Chimeric.

XX WO200187979-A2.

PN 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

PF 12-MAY-2000; 2000US-0204039P.

PR 27-JUN-2000; 2000US-0214591P.

PR 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

PI WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane

DR activator and intracellular cyclophilin ligand interactor, by  
XX administering a binding partner for APRIL, a tumor necrosis factor family  
PT ligand.  
XX Disclosure; Fig 10B; 94pp; English.

PS The invention relates to a method for inhibiting TAC1 (transmembrane

CC activator and intracellular CAML interactor) and/or B cell maturation  
CC protein (BCMA) activity in a mammal. The method comprises administering a  
CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/  
CC BCMA extracellular consensus sequence, but not the extracellular region  
CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1  
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
CC lymphoproliferative disorders, one or more solid tumours such as lung,  
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1  
CC antagonists are useful for treating inflammation and immune function  
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
CC disease), drug and insect sting allergy, inflammatory bowel disease  
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
CC with leucocyte infiltration of the skin or organs. The present sequence  
CC is mouse BCMA protein-human immunoglobulin Fc region fusion protein.  
CC (updated on 29-AUG-2003 to standardise OS field)

XX Sequence 281 AA;

QQ Query Match 67.7%; Score 136; DB 5; Length 281;



```
Best Local Similarity 70.6%; Pred. No. 4.6e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSNTPTLTQRYC 34
   | : ||||| ||||| ||||| : |||||
Db 5 CFHSEYFDSLHACKPCHLRCN--PPATCQPYC 36

RESULT 55
ID ABJ38417 standard; protein; 42 AA.
XX AC ABJ38417;
XX DT 12-JUN-2003 (first entry)
DE DE TALL-1 related protein SEQ ID No 197.
XX KW TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease;
XX KW systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;
XX KW inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis;
XX KW Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;
XX KW glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
XX KW multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
XX KW gene therapy.
XX OS Homo sapiens.
XX PN WO200292620-A2.
XX PD 21-NOV-2002.
XX PF 13-MAY-2002; 2002WO-US015273.
XX PR 11-MAY-2001; 2001US-0290196P.
XX PA (AMGE-) AMGEN INC.
XX PI Min H, Hsu H;
XX WPI; 2003-156719/15.
XX PT New TALL-1-binding polypeptide, useful for modulating the activity of
PT TALL-1 and in treating, preventing or diagnosing a B-cell-mediated
PT autoimmune diseases, cancers or lymphomas.
XX PS Disclosure; Page 26; 236pp; English.
XX CC The invention relates to a novel TALL-1-binding polypeptide comprising a
XX CC defined sequence in the specification. The composition is useful in
XX CC modulating the activity of TALL-1, and in treating, preventing,
XX CC ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune
XX CC disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or
XX CC lymphoma. The composition may also be used in treating inflammations
XX CC (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease,
XX CC asthma, atherosclerosis, cachexia, cirrhosis, diabetes,
XX CC glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple
XX CC myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis
XX CC and vasculitis. Disorders may be treated with the novel composition using
XX CC gene therapy. This sequence represents a TALL-1 related protein of the
XX CC invention
SQ Sequence 42 AA;
Query Match 61.7%; Score 124; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPQLRRC 21
   | : ||||| ||||| |||||
Db 22 CSQNEYFDSLHACIPQLRC 42

Best Local Similarity 70.6%; Pred. No. 4.6e-09;
Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

RESULT 56
ID AAE15491 standard; protein; 117 AA.
XX AC AAE15491;
XX DT 29-AUG-2003 (revised)
DT 12-MAR-2002 (first entry)
XX DE Human-murine B cell maturation protein (BCMA) consensus sequence.
XX KW Human; transmembrane activator and intracellular CAML interactor; TAC1;
XX KW cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
XX KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
XX KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
XX KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
XX KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
XX KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
XX KW rheumatoid arthritis; atherosclerosis; mouse.
XX OS Homo sapiens.
XX OS Mus sp.
XX OS Chimeric.
XX PN WO200187979-A2.
XX PD 22-NOV-2001.
XX PF 14-MAY-2001; 2001WO-US015567.
XX PR 12-MAY-2000; 2000US-0204039P.
XX PR 27-JUN-2000; 2000US-0214591P.
XX PR 14-MAY-2001; 2001US-00214591.
XX PA (AMGE-) AMGEN INC.
XX PI Theill LE, Yu G;
XX WPI; 2002-066696/09.
XX DR Inhibiting activity of B cell maturation protein and/or transmembrane
XX PT activator and intracellular cyclophilin ligand interactor, by
XX PT administering a binding partner for APRIL, a tumor necrosis factor family
XX PT ligand.
XX PS Disclosure; Fig 11; 94pp; English.
XX CC The invention relates to a method for inhibiting TAC1 (transmembrane
XX CC activator and intracellular CAML interactor) and/or B cell maturation
XX CC protein (BCMA) activity in a mammal. The method comprises administering a
XX CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
XX CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
XX CC BCMA extracellular consensus sequence, but not the extracellular region
XX CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
XX CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
XX CC lymphoproliferative disorders, one or more solid tumours such as lung,
XX CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
XX CC antagonists are useful for treating inflammation and immune function
XX CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
XX CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
XX CC disease), drug and insect sting allergy, inflammatory bowel disease
XX CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
XX CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
XX CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
XX CC with leucocyte infiltration of the skin or organs. The present sequence
XX CC is human-murine B cell maturation protein (BCMA) consensus sequence.
XX CC (Updated on 29-AUG-2003 to standardise OS field)
XX SQ Sequence 117 AA;
Query Match 46.5%; Score 93.5; DB 5; Length 117;
Best Local Similarity 69.7%; Pred. No. 0.0005;
Matches 23; Conservative 1; Mismatches 2; Indels 7; Gaps 4;
```















PT e.g. bacterial infections, allergic asthma, inflammation, allergic  
 PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung  
 PT cancer, or skin cancer.

XX Claim 2; SEQ ID NO 4; 170pp; English.

XX The present invention relates to novel mucin-like proteins (I) and their  
 CC coding sequences. The present sequence is one such human mucin-like  
 CC protein. The mucin-like proteins and coding sequences are useful in the  
 CC therapy or in the prevention of a disease when the increase in the mucin-  
 CC like activity of a polypeptide is needed e.g. bacterial infections,  
 CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced  
 CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial  
 CC wounding, inflammatory bowel disease, Crohn's disease, small  
 CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,  
 CC chronic cholecystitis, or skin cancer.

XX Sequence 2240 AA;

Query Match 34.1%; Score 68.5; DB 8; Length 2240;

Best Local Similarity 45.2%; Pred. No. 15;

Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSNTPLTQ 31

Db 1161 CSQDEYFDHGVCPM-----PPTTPQ 1184

RESULT 64

ADRI8913

ID ADR18913 standard; protein; 2258 AA.

XX AC ADR18913;

XX 04-NOV-2004 (first entry)

XX Human mucin-like protein, SCS0004, variant SEQ ID 3.  
 DE Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;  
 XX Ophthalmological; Auditory; Vulnery; Gastrointestinal; Cytostatic;  
 KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;  
 KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;  
 KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;  
 KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;  
 KW gastric intestinal metaplasia; chronic cholecystitis; skin cancer.

XX Homo sapiens.

XX WO2004069136-A2.

XX 19-AUG-2004.

XX Key Location/Qualifiers

XX Peptide 1..18

XX Protein /label= Signal\_peptide

XX 19..2258

XX /label= Mature\_protein

XX WO2004069136-A2.

XX 19-AUG-2004.

XX 04-FEB-2004; 2004WO-EP050082.

XX 05-FEB-2003; 2003US-0445217P.

XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Bienkowska J, Mcallister G;

XX WPI; 2004-604324/58.

XX New isolated mucin-like polypeptides, useful for diagnosing or treating,  
 PT e.g. bacterial infections, allergic asthma, inflammation, allergic  
 PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung  
 PT cancer, or skin cancer.

PS Claim 2; SEQ ID NO 3; 170pp; English.

XX The present invention relates to novel mucin-like proteins (I) and their  
 CC coding sequences. The present sequence is one such human mucin-like  
 CC protein. The mucin-like proteins and coding sequences are useful in the  
 CC therapy or in the prevention of a disease when the increase in the mucin-  
 CC like activity of a polypeptide is needed e.g. bacterial infections,  
 CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced  
 CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial  
 CC wounding, inflammatory bowel disease, Crohn's disease, small  
 CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,  
 CC chronic cholecystitis, or skin cancer.

XX Sequence 2258 AA;

Query Match 34.1%; Score 68.5; DB 8; Length 2258;

Best Local Similarity 45.2%; Pred. No. 15;

Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSNTPLTQ 31

Db 1179 CSQDEYFDHGVCPM-----PPTTPQ 1202

RESULT 65

ADRI8915

ID ADR18915 standard; protein; 2264 AA.

XX AC ADR18915;

XX 04-NOV-2004 (first entry)

XX His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.  
 DE Antibacterial; Virucide; Antiallergic; Antiasthmatic; Antiinflammatory;  
 XX Ophthalmological; Auditory; Vulnery; Gastrointestinal; Cytostatic;  
 KW Gene Therapy; Mucin-like protein; human; mucin; bacterial infection;  
 KW allergic asthma; inflammation; viral infection; allergic conjunctivitis;  
 KW otitis; tissue injury; epithelial wounding; inflammatory bowel disease;  
 KW Crohn's disease; small adenocarcinoma of the lung; lung cancer;  
 KW gastric intestinal metaplasia; chronic cholecystitis; skin cancer.

XX Homo sapiens.

XX WO2004069136-A2.

XX 19-AUG-2004.

XX 04-FEB-2004; 2004WO-EP050082.

XX 05-FEB-2003; 2003US-0445217P.

XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Bienkowska J, Mcallister G;

XX WPI; 2004-604324/58.

XX New isolated mucin-like polypeptides, useful for diagnosing or treating,  
 PT e.g. bacterial infections, allergic asthma, inflammation, allergic  
 PT conjunctivitis, otitis, inflammatory bowel disease, Crohn's disease, lung  
 PT cancer, or skin cancer.

XX Claim 2; SEQ ID NO 5; 170pp; English.

XX The present invention relates to novel mucin-like proteins (I) and their  
 CC coding sequences. The present sequence is one such human mucin-like  
 CC protein. The mucin-like proteins and coding sequences are useful in the  
 CC therapy or in the prevention of a disease when the increase in the mucin-  
 CC like activity of a polypeptide is needed e.g. bacterial infections,  
 CC allergic asthma, inflammation, respiratory syncytial virus (RSV)-induced  
 CC disease, allergic conjunctivitis, otitis, tissue injury, epithelial  
 CC wounding, inflammatory bowel disease, Crohn's disease, small



CC adenocarcinoma of the lung, lung cancer, gastric intestinal metaplasia,  
 CC chronic cholecystitis, or skin cancer.

SQ Sequence 2264 AA;

Query Match 34.1%; Score 68.5; DB 8; Length 2264;

Best Local Similarity 45.2%; Pred. No. 16;

Matches 14; Conservative 2; Mismatches 8; Indels 7; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSNTPTLTCQ 31

Db 1179 CSQDEYFDHEEGVCVPCM-----PPTTPQ 1202

RESULT 66

ADC71568

ID ADC71568 standard; protein; 1548 AA.

XX AC ADC71568;

DT 18-DEC-2003 (first entry)

DE Mouse subtilisin-like protein convertase 6 (SPC6).

XX neuroleptic; subtilisin-like protein convertase 6 agonist;  
 KW subtilisin-like protein convertase 6 antagonist; transgenic;  
 KW subtilisin-like protein convertase 6; SPC6; schizophrenia.

XX Mus sp.

XX US2003093824-A1.

PN 15-MAY-2003.

PD 25-JUN-2002; 2002US-00180903.

PR 26-JUN-2001; 2001US-0300978P.

PR 24-SEP-2001; 2001US-0324820P.

XX (ALLE/) ALLEN K D.

XX Allen KD;

XX WPI; 2003-777261/73.

DR N-PSDB; ADC71567.

XX New transgenic mouse useful in methods for identifying potential  
 PT therapeutic agents for treating a variety of diseases, including  
 PT schizophrenia, comprises a disruption in a subtilisin-like protein  
 PT convertase 6 (SPC6) gene.

PS Disclosure; SEQ ID NO 2; 34pp; English.

XX The invention describes a transgenic mouse (I) comprising a disruption in  
 CC a subtilisin-like protein convertase (SPC6) gene, where there is no  
 CC native expression of an endogenous SPC6 gene. The therapeutic agent is  
 CC administered by inhalation or insufflation or oral, buccal, parenteral,  
 CC topical, subcutaneous, intraperitoneal, intravenous, intrapleural,  
 CC intraocular, intraarterial, or rectal route. The transgenic mouse and  
 CC associated methods are useful for identifying potential therapeutic  
 CC agents (e.g. SPC6 agonists and antagonists) for treating conditions  
 CC associated with SPC6. The identified agents are potentially useful for  
 CC treating diseases such as schizophrenia. The mouse is useful for  
 CC investigating the biological roles of SPC6. This is the amino acid  
 CC sequence of mouse SPC6.

SQ Sequence 1548 AA;

Query Match 33.6%; Score 67.5; DB 7; Length 1548;

Best Local Similarity 37.8%; Pred. No. 14;

Matches 14; Conservative 4; Mismatches 14; Indels 5; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSNTTP-----LTCOR 32

Db 1152 CAAVEYWDGSHRCQPCCHKKSCRCSPGSDQCYTCPR 1188

RESULT 67

ABB80243

ID ABB80243 standard; protein; 1877 AA.

XX AC ABB80243;

DT 04-DEC-2003 (first entry)

DE Murine subtilase.

XX Subtilase; chromosome 9q21.13; EST; expressed sequence tag; kidney;  
 KW renal cell; head; neck; heart; multiple sclerosis; lesion; cervix;  
 KW pooled germ cell; tumour; uterus; adenocarcinoma; retina II; stomach;  
 KW protein convertase subtilisin; furin-like repeat; Alzheimer's disease;  
 KW Parkinson's disease; pain; colon; pelvic pain; pre-oesophageal dysphagia;  
 KW gastritis; ulcers; urinary incontinence; lupus nephritis;  
 KW renal transplant rejection; myocardial infarction; erectile dysfunction;  
 KW ovary; lung; thyroid; carcinoma; lymphoma; Kaposi's sarcoma;  
 KW congestive heart failure; ischaemia; hypertensive vascular disease.

XX Mus musculus.

XX WO2003060109-A2.

PD 24-JUL-2003.

PF 14-JAN-2003; 2003WO-EP000253.

PR 15-JAN-2002; 2002US-0347876P.

PR 29-JUL-2002; 2002US-0398734P.

XX (FARB ) BAYER AG.

XX Koehler RH;

XX WPI; 2003-608065/57.

XX New subtilase-encoding polynucleotide and its encoded protein, useful for  
 PT identifying modulators of subtilase activity, and in gene therapy for  
 PT treating e.g. Alzheimer's disease, cancers, congestive heart failure or  
 PT ischemia.

PS Disclosure; Page 122-26; 135pp; English.

XX This sequence shows a murine subtilase. The homologous human subtilase  
 CC coding sequence is located on chromosome 9q21.13. Related EST's are  
 CC expressed in kidney (renal cell adenocarcinoma), head and neck tissue,  
 CC heart, multiple sclerosis lesions, cervix, pooled germ cell tumours,  
 CC uterus tumour, adenocarcinoma, retina II and stomach. The subtilisin  
 CC protein is a long membrane bound protein which shows 96% identity to  
 CC human proprotein convertase subtilisin. There are two blocks of 11 furin-  
 CC like repeats in the C-terminal portion of the protein. It has one  
 CC transmembrane domain, also in the C-terminal portion, suggesting that the  
 CC protein is localised on the outside of the membrane. The subtilase  
 CC polynucleotide and polypeptide are useful for identifying test compounds,  
 CC which may act as agonists or antagonists at the receptor site and which  
 CC can be regulated to provide therapeutic effects. Vectors comprising the  
 CC polynucleotide are useful for modulating the activity of subtilase in a  
 CC disease, e.g. a central nervous system disorder, a gastrointestinal  
 CC disorder, cancer, a cardiovascular disorder, a genitourinary disorder, or  
 CC diabetes. In particular, these diseases are Alzheimer's disease,  
 CC Parkinson's disease, pain, colon tumour, pre-oesophageal dysphagia,  
 CC gastritis, ulcers, urinary incontinence, lupus nephritis, renal  
 CC transplant rejection, pelvic pain, erectile dysfunction, ovary tumour,  
 CC lung tumour, thyroid tumour, carcinoma, lymphoma, Kaposi's sarcoma,  
 CC congestive heart failure, myocardial infarction, ischaemia, hypertensive  
 CC vascular diseases, etc. These are also useful for preventing or  
 CC ameliorating the diseases cited above



CC	is human TACI cysteine-rich consensus region	
XX		
QQ	Sequence 33 AA;	
	Query Match 33.1%; Score 66.5; DB 5; Length 33;	
	Best Local Similarity 32.4%; Pred. No. 0.39;	
	Matches 11; Conservative	8; Mismatches 14; Indels 1; Gaps 1;
OY	1 CSQNEYFDSLHACIPQCQLRCSSNTPPLTCQRYC 34	
	:   :   :   :   :   :   :   :   :   :	
DB	1 CPEQYWDPLLTGTCMCKTICNHQS-QRTCAAF 33	
	:   :   :   :   :   :   :   :   :   :	
RESULT 69		
ADA49368		
ID	ADA49368 standard; peptide; 33 AA.	
XX		
AC	ADA49368;	
XX		
DT	20-NOV-2003 (first entry)	
XX		
DE	Human TACII cysteine rich domain.	
XX		
KW	TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory;	
KW	antiarthritic; dermatological; antidiabetic; neuroprotective;	
KW	antihypertensive; antipyrretic; nephrotropic; vasotropic; vaccine;	
KW	autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;	
KW	insulin dependent diabetes mellitus; multiple sclerosis;	
KW	myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;	
KW	autoimmune thrombocytopenic purpura; Goodpasture's syndrome;	
KW	pemphigus vulgaris; acute rheumatic fever;	
KW	post-streptococcal glomerulonephritis; polyarteritis nodosa; TACII; CRD;	
KW	cysteine rich domain.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2003035846-A2.	
XX		
PD	01-MAY-2003.	
XX		
XX	24-OCT-2002; 2002WO-US034376.	
PF		
XX		
PR	24-OCT-2001; 2001US-0345106P.	
PR	14-JAN-2002; 2002US-0348962P.	
PR	07-FEB-2002; 2002US-0354966P.	
PR	13-AUG-2002; 2002US-0403364P.	
XX		
PA	(NAJE-) NAT JEWISH MEDICAL & RES CENT.	
XX		
PI	Zhang G, Shu H, Liu Y, Xu L;	
XX		
XX	WPI; 2003-0403345/38.	
XX		
PT	Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological	
PT	activity in mammal, has a modification in the region connecting beta	
PT	strands D and E that reduces the biological activity of TALL-1	
PT	antagonist.	
PS	Disclosure; Page 617; 618pp; English.	
XX		
CC	The invention relates to a novel TALL-1 antagonist protein, comprising a	
CC	sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID	
CC	NO:2, by at least one modification in the region connecting abgr; strands	
CC	D and E that reduces the biological activity of the TALL- 1 antagonist as	
CC	compared to wild-type TALL-1. A protein of the invention has	
CC	immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,	
CC	dermatological, antidiabetic, neuroprotective, antihypertensive, antipyrretic,	
CC	nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in	
CC	a vaccine. A protein of the invention is useful for inhibiting TALL-1	
CC	biological activity in a mammal. TC is useful for treating autoimmune	
CC	diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin	
CC	dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,	
CC	Grave's disease, autoimmune hemolytic anaemia, autoimmune	



CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,  
 CC acute rheumatic fever, post-streptococcal glomerulonephritis and  
 CC polyarthritis nodosa. The present sequence represents a cysteine rich  
 CC domain (CRD) module of human TAC11.  
 XX  
 SQ Sequence 33 AA;  
 Query Match 33.1%; Score 66.5; DB 6; Length 33;  
 Best Local Similarity 32.4%; Pred. No. 0.39;  
 Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 CSQNEVFDLSLHACIPCOLRCSSNTPLTCQRYC 34  
 Db 1 CPBEQYWDPLLGTCMSCKTICNHQS-QRTCAAF 33  
 RESULT 70  
 AAU10951  
 ID AAU10951 standard; protein; 37 AA.  
 XX  
 AC AAU10951;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human AGP-3 receptor cysteine rich repeat region #1.  
 XX  
 KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;  
 KW dermatological; neuroprotective; nontropic; immunomodulator; metabolic;  
 KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;  
 KW antiparkinsonian; antipsoriasis; vasotropic; antibacterial; asthma;  
 KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;  
 KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;  
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;  
 KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;  
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;  
 KW multiple sclerosis; Parkinson's disease; transgenic animal.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200185782-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 12-FEB-2001; 2001WO-US004568.  
 XX  
 PR 11-FEB-2000; 2000US-0181800P.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Hsu H;  
 XX  
 DR WPI; 2002-049441/06.  
 XX  
 PT Composition, useful for identifying modulator of receptor for treating  
 PT asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor  
 PT ligand family member) receptor and encoding nucleic acids.  
 XX  
 PS Claim 1; Fig 18; 124pp; English.  
 XX  
 CC The invention relates to a composition (I) comprising AGP-3 receptor  
 CC (tumour necrosis factor ligand family member) related protein (II)  
 CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related  
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in  
 CC assays to identify cells and tissues that express AGP-3R or proteins  
 CC related to AGP-3R-related protein and for identifying compounds (agonists  
 CC or antagonists) that interact with AGP-3R proteins. (II) is also useful  
 CC for identifying intracellular proteins that interact with the respective  
 CC cytoplasmic domains by yeast two-hybrid screening processes. (II) is  
 CC involved in B cell growth, survival and activation particularly in lymph  
 CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists  
 CC identified using (II) are used for modulating B cell response and are  
 CC used to treat diseases characterised by inflammatory processes or  
 CC deregulated immune response such as rheumatoid arthritis, graft-versus-

CC host disease, Crohn's disease, lupus, etc. (II) is also useful in the  
 CC production of hybridoma cells which are derived from B cells, which  
 CC involves treating the hybridoma cells with (II). (II) is useful in the  
 CC treatment of inflammatory conditions of joints, e.g., rheumatoid  
 CC arthritis, osteoarthritis, etc. (II), its agonists or antagonists are  
 CC useful for treating acute pancreatitis, amyotrophic lateral sclerosis  
 CC (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia,  
 CC diabetes, fever, glomerulonephritis, inflammatory bowel disease, multiple  
 CC ischaemic injury including cerebral ischaemia, multiple myeloma, multiple  
 CC sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury,  
 CC septic shock, etc. The nucleic acids are also useful for developing the  
 CC transgenic animals expressing (II), which are useful for producing the  
 CC polypeptides and for the study of in vivo biological activity. The  
 CC present sequence represents the amino acid sequence of human AGP-3  
 CC cysteine-rich repeat region #1  
 XX  
 SQ Sequence 37 AA;  
 Query Match 33.1%; Score 66.5; DB 5; Length 37;  
 Best Local Similarity 32.4%; Pred. No. 0.44;  
 Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 CSQNEVFDLSLHACIPCOLRCSSNTPLTCQRYC 34  
 Db 2 CPBEQYWDPLLGTCMSCKTICNHQS-QRTCAAF 34  
 RESULT 71  
 ADZ67772  
 ID ADZ67772 standard; protein; 48 AA.  
 XX  
 AC ADZ67772;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DE Human tumor necrosis factor receptor TAC1 Cys-rich domain.  
 XX  
 KW Tumor necrosis factor receptor; TAC1; cancer; neoplasm; diagnosis;  
 KW cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005037865-A2.  
 XX  
 PD 28-APR-2005.  
 XX  
 PF 18-OCT-2004; 2004WO-US034375.  
 XX  
 PR 16-OCT-2003; 2003US-0511698P.  
 PR 18-OCT-2004; 2004US-0619552P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Fox BA, Holloway JL, Sheppard PO, Dillon SR;  
 XX  
 DR WPI; 2005-315682/32.  
 XX  
 PT New tumor necrosis factor receptor (TNFR) polypeptides, useful as  
 PT detecting ligands, and for modulating tumor growth, metastasis and  
 PT immunity, such as separating resting from stimulated immune cells.  
 XX  
 PS Disclosure; SEQ ID NO 20; 132pp; English.  
 XX  
 CC The invention provides novel tumor necrosis factor receptor (TNFR)  
 CC ztnfr14 polynucleotides ADZ67753 and polypeptides ADZ67754, expression  
 CC vectors and antibodies. Ztnfr14 polynucleotides are used in claimed  
 CC methods for detecting a genetic abnormality in a patient and for  
 CC detecting a cancer in a patient. Recombinant ztnfr14 polypeptide.  
 CC optionally conjugated to a toxin, is used in a claimed method of killing  
 CC cancer cells. Ztnfr14 polypeptides can be used to detect ligands,  
 CC agonists and antagonists. The polypeptides, polynucleotides and  
 CC antibodies may also be used in methods that modulate tumor growth,  
 CC metastasis, and immunity such as separating resting from stimulated















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OM protein - protein search, using sw model

Run on: December 21, 2005, 15:57:04 ; Search time 18.8 Seconds  
(without alignments)  
174.009 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_8\_41  
Perfect score: 201  
Sequence: 1 CSQNEYFDSLLHACIPQLRCSSNTPPLTCQRYC 34

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : PIR 80.\*

1: Pirl.\*

2: Pirl2.\*

3: Pirl3.\*

4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	201	100.0	184	2 S43486	B-cell maturation
2	67.5	33.6	1548	2 S34583	serine proteinase
3	64.5	32.1	5376	2 T42215	zonadhesin - mouse
4	61	30.3	1101	2 T16840	hypothetical prote
5	59	29.4	758	2 T15577	hypothetical prote
6	58	28.9	1299	2 T43251	furin (EC 3.4.21.7
7	57.5	28.6	63	2 S07127	chymotrypsin/elast
8	57.5	28.6	1680	2 A43434	furin (EC 3.4.21.7
9	57	28.4	1717	1 A45558	epidermal growth f
10	56	27.9	2476	2 T34022	zonadhesin - pig
11	55.5	27.6	989	2 T01519	hypothetical prote
12	55	27.4	330	2 T25169	hypothetical prote
13	55	27.4	1513	2 T23681	hypothetical prote
14	54.5	27.1	2155	2 T30197	alpha tectorin - m
15	54	26.9	1980	2 S54307	myosin heavy chain
16	54	26.9	2022	2 A59256	myosin-IXb [simila
17	53.5	26.6	758	2 S46625	finger protein XUL
18	53	26.4	1574	2 T13954	MEGF6 protein - ra
19	53	26.4	2824	2 T22759	hypothetical prote
20	52.5	26.1	118	2 S61051	hypothetical prote
21	52	25.9	255	2 A84544	hypothetical prote
22	52	25.9	294	2 T23682	hypothetical prote
23	52	25.9	547	2 T34318	hypothetical prote
24	52	25.9	1474	2 D88550	protein ZC84.6 [im
25	52	25.9	2844	2 S28291	hypothetical prote
26	51.5	25.6	63	2 S57816	antimicrobial pept
27	51.5	25.6	282	2 I48763	siach-1A protein -
28	51.5	25.6	282	2 S35754	siach-1B protein -
29	51.5	25.6	497	2 T27827	hypothetical prote

hypothetical prote  
hypothetical prote  
hypothetical prote  
alpha tectorin - c  
probable transcrip  
hypothetical prote  
hypothetical prote  
c4b-binding protei  
chymotrypsin/elast  
ubiquitin / riboso  
hypothetical prote  
probable aminotran  
tumor necrosis fac  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable two-compo  
hypothetical prote  
resistance protein  
hypothetical prote  
hypothetical prote  
homeotic protein m  
hypothetical prote  
paired-box-contain  
protein Tf9.18 [i  
tumor necrosis fac  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable vitelloge  
notch-1 protein -  
laminin alpha 5 ch  
hypothetical prote  
serum albumin 1 pr  
serum albumin 2 pr  
hypothetical prote  
seven-pass transme  
trypsin inhibitor  
protein C10G8.4 [i  
tissue factor path  
hypothetical prote  
protein kinase [EC  
protein apx-1 [imp  
CIP synthase (EC 6  
protein C18H9.7 [i  
adenosylhomocyste  
hypothetical prote  
hypothetical prote  
brefeldin A-sensit  
protein MEDEA [imp  
subtilisin-like pr  
subtilisin-like pr  
subtilisin-like pr  
mucin - rat  
gag-Rail-env poly  
Motch B protein -  
laminin beta-2 cha  
hypothetical prote  
gamma-1-microglubu  
probable membrane  
furin (EC 3.4.21.7  
protein F14N23.5 [i  
laminin beta-2 cha  
hypothetical prote  
protein F22A3.8 [i  
hypothetical prote  
laminin alpha chai  
hypothetical 11.7K  
hypothetical prote



103	47	23.4	348	2	T28623	hypothetical prote	176	45	22.4	102	2	S26409	protein 108 precu
104	47	23.4	349	2	D36858	gene G4R protein -	177	45	22.4	104	2	G71202	hypothetical prote
105	47	23.4	350	2	D72175	G2R protein - vari	178	45	22.4	182	2	T28390	ORF MSV229 leucine
106	47	23.4	601	2	C89451	protein T04G9.6 [i	179	45	22.4	187	2	G87521	HNH endonuclease f
107	47	23.4	664	2	AB1136	NADH flavin oxidor	180	45	22.4	320	1	A39479	homeotic protein m
108	47	23.4	664	2	AD1494	NADH flavin oxidor	181	45	22.4	324	2	T24819	hypothetical prote
109	47	23.4	701	2	S62460	hypothetical prote	182	45	22.4	364	2	JC4249	recF protein - Azo
110	47	23.4	877	2	T41794	RNA polymerase LEF	183	45	22.4	370	2	T37282	probable cathepsin
111	47	23.4	932	2	I52527	FACE4A - mouse (fr	184	45	22.4	384	2	S25771	gas1 protein - mou
112	47	23.4	937	2	I53282	gene FACE4 protein	185	45	22.4	396	2	S53325	tissue factor path
113	47	23.4	1650	2	S53457	dominant autoantig	186	45	22.4	420	2	T30507	probable alkaline
114	47	23.4	2616	2	A57096	model protein prec	187	45	22.4	431	2	G75305	hypothetical prote
115	47	23.4	4660	2	T42737	gp330 protein prec	188	45	22.4	450	2	B97297	hydrogenase chain
116	47	23.4	4733	1	A47437	LDL-receptor-relat	189	45	22.4	464	2	T24011	hypothetical prote
117	46.5	23.1	63	1	T1NEB8	proteinase inhibit	190	45	22.4	479	2	AF2146	deoxyribopyrimidin
118	46.5	23.1	135	2	AD2682	transcription regu	191	45	22.4	511	2	JC7682	spermatogenesis as
119	46.5	23.1	135	2	G97469	hypothetical prote	192	45	22.4	557	2	A48434	variant-specific s
120	46.5	23.1	186	2	A45910	ultra-high-sulfur	193	45	22.4	661	2	G97717	hypothetical prote
121	46.5	23.1	202	2	T22327	hypothetical prote	194	45	22.4	672	2	G71719	hypothetical prote
122	46.5	23.1	233	2	T34078	hypothetical prote	195	45	22.4	702	2	T21148	hypothetical prote
123	46.5	23.1	278	2	T05774	hypothetical prote	196	45	22.4	763	2	S51300	probable membrane
124	46.5	23.1	389	2	T29488	hypothetical prote	197	45	22.4	964	2	T30455	hypothetical prote
125	46.5	23.1	413	2	G82422	anaerobic glycerol	198	45	22.4	1397	2	T46354	hypothetical prote
126	46.5	23.1	419	2	S69207	vascular endotheli	199	45	22.4	1839	1	RRWPEM	genome polyprotein
127	46.5	23.1	425	2	T18592	hypothetical prote	200	45	22.4	2548	2	E59435	myosin IXA [import
128	46.5	23.1	461	2	B88953	protein F18B4.8 [i	201	45	22.4	2626	2	T31099	myosin-RhoGAP prot
129	46.5	23.1	461	2	T32863	hypothetical prote	202	45	22.4	4543	1	A53102	alpha-2-macroglobu
130	46.5	23.1	600	2	T18593	hypothetical prote	203	45	22.4	4544	1	S02392	alpha-2-macroglobu
131	46.5	23.1	802	2	T24293	hypothetical prote	204	45	22.4	4545	1	S25111	MHC class II beta
132	46.5	23.1	874	2	JQ0983	genome polyprotein	205	44.5	22.1	142	2	I51063	high-sulfur kerati
133	46.5	23.1	949	2	T24294	hypothetical prote	206	44.5	22.1	175	2	S37649	genome polyprotein
134	46.5	23.1	1124	1	I58388	protein-tyrosine k	207	44.5	22.1	180	2	PC1305	MHC class II beta
135	46.5	23.1	1365	2	S14871	suppressor two of	208	44.5	22.1	217	2	I51062	hypothetical prote
136	46.5	23.1	1597	2	S68420	citron - mouse	209	44.5	22.1	251	2	S23821	hypothetical prote
137	46.5	23.1	1935	2	T39411	RNA helicase - fis	210	44.5	22.1	263	1	ASLJFP	vif protein - feli
138	46.5	23.1	2111	2	T15390	hypothetical prote	211	44.5	22.1	298	2	G69532	conserved hypotet
139	46.5	23.1	3033	1	GNMWJ8	genome polyprotein	212	44.5	22.1	347	2	AC0825	anaerobic sulfate
140	46	22.9	99	2	S60231	gibberellin-regula	213	44.5	22.1	357	2	T21152	hypothetical prote
141	46	22.9	232	2	A40738	hypothetical prote	214	44.5	22.1	368	2	H81059	phosphoserine amin
142	46	22.9	311	2	B64332	hypothetical prote	215	44.5	22.1	396	1	JH0633	cellular tumor ant
143	46	22.9	335	2	T12789	interleukin 12 p40	216	44.5	22.1	400	2	F81432	probable transamin
144	46	22.9	366	2	T15925	hypothetical prote	217	44.5	22.1	481	2	A56429	I-kappa-B-related
145	46	22.9	369	2	S21471	genome polyprotein	218	44.5	22.1	493	2	JC5486	membrane glycoprot
146	46	22.9	404	2	C96549	hypothetical prote	219	44.5	22.1	592	1	A30314	protein kinase C (
147	46	22.9	430	2	AB0811	probable transcrip	220	44.5	22.1	592	1	JC1480	protein kinase C (
148	46	22.9	439	2	T32627	hypothetical prote	221	44.5	22.1	597	1	S53711	C4BP alpha chain p
149	46	22.9	440	2	T41766	ARIF-1 orf20/21 -	222	44.5	22.1	654	2	C96782	unknown protein P2
150	46	22.9	458	2	S61974	SSU1 protein - yea	223	44.5	22.1	949	2	S54020	probable membrane
151	46	22.9	528	2	S14944	regulatory protein	224	44.5	22.1	1115	2	S40241	G protein-coupled
152	46	22.9	593	2	I51213	drebrin - chicken	225	44.5	22.1	1126	2	A49208	transmembrane prot
153	46	22.9	782	2	S18031	genome polyprotein	226	44.5	22.1	1171	2	A42916	metabotropic gluta
154	46	22.9	783	2	A41627	furin (EC 3.4.21.7	227	44.5	22.1	1180	2	JC2132	metabotropic gluta
155	46	22.9	876	2	B72856	late expression fa	228	44.5	22.1	1212	2	JC2131	probable myb-relat
156	46	22.9	1747	2	T43162	vitellogenin - gyp	229	44.5	22.1	1297	2	T52065	head-activator bin
157	46	22.9	1753	2	T00350	hypothetical prote	230	44.5	22.1	1661	2	T31330	hypothetical prote
158	46	22.9	2135	2	T14602	variant-specific s	231	44.5	22.1	1791	2	T02345	hypothetical prote
159	46	22.9	2910	2	T42214	otogelin - mouse	232	44.5	22.1	2150	2	T32497	hypothetical prote
160	46	22.9	3084	1	MMMSA	laminin alpha-1 ch	233	44.5	22.1	2471	2	A49128	cell-fate determin
161	45.5	22.6	131	2	S55380	Norrie disease pro	234	44	21.9	72	2	B27725	small proline-rich
162	45.5	22.6	133	2	A57005	Norrie disease can	235	44	21.9	93	2	JE0159	gibberellin-stimul
163	45.5	22.6	185	2	D82755	conserved hypotet	236	44	21.9	114	2	D75422	hypothetical prote
164	45.5	22.6	201	2	D71190	hypothetical prote	237	44	21.9	118	2	T49515	hypothetical prote
165	45.5	22.6	209	2	A88104	protein W10G11.3 {	238	44	21.9	128	2	T22276	hypothetical prote
166	45.5	22.6	225	2	S57810	hypothetical prote	239	44	21.9	165	2	S74697	hypothetical prote
167	45.5	22.6	318	2	A45522	variant surface gl	240	44	21.9	165	2	AB2113	hypothetical prote
168	45.5	22.6	386	2	A41950	retrovirus-related	241	44	21.9	166	2	H89044	protein B0238.12 {
169	45.5	22.6	392	2	T29519	hypothetical prote	242	44	21.9	167	2	H72579	hypothetical prote
170	45.5	22.6	697	2	E96752	hypothetical prote	243	44	21.9	185	2	A13991	conserved hypotet
171	45.5	22.6	704	2	T50303	hypothetical prote	244	44	21.9	185	2	A95292	hypothetical prote
172	45.5	22.6	749	2	S13518	transposase Tam3 -	245	44	21.9	191	2	B64288	keratin KA5.4 - s
173	45.5	22.6	1077	2	T41146	probable cysteine-	246	44	21.9	199	2	B86288	F9L1.31 protein - s
174	45.5	22.6	1171	2	T13065	PIP82 protein - fr	247	44	21.9	224	2	C81417	probable transcrip
175	45	22.4	99	2	S40012	fill protein - gar	248	44	21.9	242	2	T29699	hypothetical prote



249 44 21.9 304 1 TIHUGK  
 250 44 21.9 319 2 E72852  
 251 44 21.9 334 2 E44221  
 252 44 21.9 338 2 T18715  
 253 44 21.9 340 2 S58770  
 254 44 21.9 361 2 T42992  
 255 44 21.9 405 2 T26678  
 256 44 21.9 405 2 T26678  
 257 44 21.9 418 2 A64508  
 258 44 21.9 441 2 S12707  
 259 44 21.9 455 2 E90316  
 260 44 21.9 469 2 E86421  
 261 44 21.9 502 2 T20130  
 262 44 21.9 548 2 T16642  
 263 44 21.9 601 2 E36346  
 264 44 21.9 659 2 T01520  
 265 44 21.9 661 2 E96596  
 266 44 21.9 667 2 T01999  
 267 44 21.9 669 2 T06702  
 268 44 21.9 683 2 C36346  
 269 44 21.9 685 2 S78040  
 270 44 21.9 705 2 S34968  
 271 44 21.9 761 2 H65083  
 272 44 21.9 776 2 A82787  
 273 44 21.9 780 2 A34102  
 274 44 21.9 780 2 T31548  
 275 44 21.9 782 2 S19876  
 276 44 21.9 838 2 T20125  
 277 44 21.9 862 1 QRM5LD  
 278 44 21.9 879 2 C90879  
 279 44 21.9 879 2 H64888  
 280 44 21.9 879 2 G85739  
 281 44 21.9 915 1 A48225  
 282 44 21.9 1111 2 T26972  
 283 44 21.9 1166 1 S06142  
 284 44 21.9 1221 2 T23472  
 285 44 21.9 1255 1 A24571  
 286 44 21.9 3075 2 S14458  
 287 43.5 21.6 61 2 S57815  
 288 43.5 21.6 155 2 B32669  
 289 43.5 21.6 247 2 I51060  
 290 43.5 21.6 292 2 B42822  
 291 43.5 21.6 312 2 T32379  
 292 43.5 21.6 339 1 KHRTB  
 293 43.5 21.6 347 2 A38453  
 294 43.5 21.6 352 2 S11926  
 295 43.5 21.6 356 2 G88968  
 296 43.5 21.6 481 2 S62427  
 297 43.5 21.6 484 2 JC8020  
 298 43.5 21.6 592 2 JN0877  
 299 43.5 21.6 595 2 T39228  
 300 43.5 21.6 625 2 T37604

ALIGNMENTS

RESULT 1  
 B-cell maturation factor - human  
 N:Alternate names: BCM protein; BCMA protein; BEL protein  
 C:Species: Homo sapiens (man)  
 C>Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text\_change 09-Jul-2004  
 C:Accession: S43486; S31208; S36661  
 R:Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.  
 Nucleic Acids Res. 22, 1147-1154, 1994  
 A:Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidire  
 A:Reference number: S43486; MUID:94218235; PMID:8165126  
 A:Accession: S43486  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-184 <LAA>  
 A:Cross-references: UNIPROT:Q02223; UNIPARC:UPI0000034D1B; EMBL:Z29574; NID:9471244; PID

R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.  
 EMBL J. 11, 3897-3904, 1992  
 A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)  
 A:Reference number: S31208; MUID:93010984; PMID:1396583  
 A:Accession: S31208  
 A:Molecule type: mRNA  
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 C:Genetics:  
 A:Gene: GDB:BCMA  
 A:Cross-references: GDB:135977; OMIM:109545  
 A:Map position: 16p13.1-16p13.1  
 A:Introns: 44/1; 93/1  
 C:Superfamily: human B-cell maturation factor

Query Match 100.0%; Score 201; DB 2; Length 184;  
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 Qy 1 CSQNEYFDSLHACIFCQLRCSNTPLTCQRYC 34  
 Db 8 CSQNEYFDSLHACIFCQLRCSNTPLTCQRYC 41

RESULT 2  
 S34583  
 serine proteinase (EC 3.4.21.-) PC6B - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C:Accession: S34583  
 R:Nakagawa, T.; Murakami, K.; Nakayama, K.  
 FEBS Lett. 327, 165-171, 1993  
 A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a  
 A:Reference number: S34583; MUID:93327934; PMID:8335106  
 A:Accession: S34583  
 A>Status: preliminary  
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 C:Keywords: hydrolase; serine proteinase

Query Match 33.6%; Score 67.5; DB 2; Length 1548;  
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 Qy 1 CSQNEYFDSLHACIFCQLRCSNTTP-----LTCQR 32  
 Db 1152 CAAVEYWDGSHRCQCHKKKRCSPSPDQCYTCPR 1188

RESULT 3  
 T42215  
 zonadhesin - mouse  
 N:Alternate names: sperm-specific membrane protein  
 C:Species: Mus musculus (house mouse)  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C:Accession: T42215  
 R:Gao, Z.; Garbers, D.L.  
 J. Biol. Chem. 273, 3415-3421, 1998  
 A:Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane pro  
 A:Reference number: Z22080; MUID:98123114; PMID:9452463  
 A:Accession: T42215  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
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 A:Cross-references: UNIPROT:O88799; UNIPARC:UPI000002A15E; EMBL:U97068; NID:93327420; PI  
 C:Genetics:  
 A:Gene: Zan







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Qy      1 CSQNEYFDSLHACIP-CO---LRCCSNTPLTTCORYC 34
Db      1851 CSAHSYVTCVPSCLSPQDDPGQCTGAGAPSTCEGC 1898

RESULT 11
T01519
hypothetical protein T10M13.17.1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text:
C:Accession: T01519
R:Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.
Martensen, R.; McCombie, W.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of the Arabidopsis thaliana T
A:Reference number: Z14346
A:Accession: T01519
A:Status: translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-989 <OH>
A:Cross-references: UNIPROT:Q9ZU00; UNIPARC:UPI000000A0E3ED
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4S
A:Introns: 31/3
A>Note: T10M13.17.1

Query Match      27.6%; Score 55.5; DB 2; Lens
Best Local Similarity 41.9%; Pred. No. 45;
Matches 13; Conservative

Qy      1 CSQNEYFDSLHACIPC-----QURCSSNTPP 27
Db      540 CARN-IDDRFLYHCSPCNFTLDRCLVNLNPPP 569

RESULT 12
T25169
hypothetical protein T23F1.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text:
C:Accession: T25169
R:Wilkinson, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19990
A:Accession: T25169
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-330 <WIL>
A:Cross-references: UNIPROT:O18118; UNIPARC:UPI0000006118
A:Experimental source: clone T23F1
C:Genetics:
A:Gene: CESP:T23F1.6
A:Map position: 5
A:Introns: 16/3
C:Superfamily: gliadin

Query Match      27.4%; Score 55; DB 2; Leng
Best Local Similarity 28.6%; Pred. No. 20;
Matches 12; Conservative 7; Mismatches 15; I

Qy      1 CSQNEYFDSLHACIP-----CQLRCSNTPPL---TCORYC
Db      59 CASSQYQLQTSQCMPCQSCSQCCSQSNNTTCQPTCQOSC

RESULT 13
T23681
hypothetical protein M02G9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text:
C:Accession: T23681

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R;Matthews, L.  
submitted to the EMBL Data Library, November 1996

A;Reference number: Z19781

A;Accession: T23681

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1513 <WIL>

A;Cross-references: UNIPROT:O17970; UNIPARC:UPI0000076B6D; EMBL:Z81573; PIDN:CA804625.1;

A;Experimental source: clone M02G9

C;Genetics:

A;Gene: CESP:M02G9.1

A;Map position: 2

A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1

Query Match 27.4%; Score 55; DB 2; Length 1513;

Best Local Similarity 44.8%; Pred. No. 75;

Matches 13; Conservative 3; Mismatches 11; Indels 2; Gaps 2;

QY 8 DSLHAC-IPCQLRC-SSNTPPLTCQRYC 34

Db 141 DSCQNVQVCQACVCSQNSPPAVCQQT 169

RESULT 14

T30197

alpha tectorin - mouse

C;Species: Mus musculus (house mouse)

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T30197

R;Legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.

J. Biol. Chem. 272, 8791-8801, 1997

A;Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to com

A;Reference number: Z20771; MUID:97236843; PMID:9079715

A;Accession: T30197

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-2155 <LEG>

A;Cross-references: UNIPROT:O08523; UNIPARC:UPI000002793C; EMBL:X99805; NID:g1915908; PI

A;Experimental source: strain CDI; whole cochlea

A;Note: non-collagenous protein only expressed in the inner ear, by cells both in and su

Query Match 27.1%; Score 54.5; DB 2; Length 2155;

Best Local Similarity 29.4%; Pred. No. 1.2e+02;

Matches 10; Conservative 6; Mismatches 15; Indels 3; Gaps 1;

QY 1 CSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYC 34

Db 1372 CPNPNHVESCVSQCP---RCAAIRLKSDCNHYC 1402

RESULT 15

S54307

myosin heavy chain - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004

C;Accession: S54307

R;Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M.

EMBO J. 14, 697-704, 1995

A;Title: A novel type of myosin implicated in signalling by rho family GTPases.

A;Reference number: S54307; MUID:95188874; PMID:7882973

A;Accession: S54307

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1980 <REI>

A;Cross-references: UNIPROT:Q63358; UNIPARC:UPI000012PAD6; EMBL:X77609; NID:g639998; PI

C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase C zi

C;Keywords: nucleotide binding; P-loop

F;149-942/Domain: myosin motor domain homology <MMOT>

F;239-246/Region: nucleotide-binding motif A (P-loop)

F;1593-1641/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 26.9%; Score 54; DB 2; Length 1980;

Best Local Similarity 52.9%; Pred. No. 1.2e+02;

Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 16 PCQLRCSSNTPPLTCQR 32

Db 1812 PCLLRCPDNDSDLTSMK 1828

RESULT 16

A52526

myosin-IXb [similarity] - human

C;Species: Homo sapiens (man)

C;Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 31-Dec-2004

C;Accession: A52526; I61700

R;Wirth, J.A.; Jensen, K.A.; Post, P.L.; Bement, W.M.; Mooseker, M.S.

J. Cell Sci. 109, 653-661, 1996

A;Title: Human myosin-IXb, an unconventional myosin with a chimera-like rho/rac GTPase-

A;Reference number: A52526; MUID:97063843; PMID:8907710

A;Accession: A52526

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-2022 <WIR>

A;Cross-references: UNIPROT:Q14788; UNIPARC:UPI0000161189; GB:U42391; NID:g1147782; PIDN:

R;Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.

Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994

A;Title: Identification and overlapping expression of multiple unconventional myosin gene

A;Reference number: A55758; MUID:94294418; PMID:8022818

A;Accession: I61700

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 234-322 <RES>

A;Cross-references: UNIPARC:UPI0000073918; GB:L29149; NID:g457257; PIDN:AAA20912.1; PID:9

C;Genetics:

A;Gene: GDB:WYO9B; OMIM:602129

A;Map position: 19p13.1

C;Superfamily: myosin motor domain homology; protein kinase C zinc-binding repeat homolo

C;Keywords: nucleotide binding; P-loop

F;149-941/Domain: myosin motor domain homology #status atypical <MMO>

F;239-246/Region: nucleotide-binding motif A (P-loop)

Query Match 26.9%; Score 54; DB 2; Length 2022;

Best Local Similarity 52.9%; Pred. No. 1.3e+02;

Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 16 PCQLRCSSNTPPLTCQR 32

Db 1852 PCLLRCPDNDSDLTSMK 1868

RESULT 17

S46625

finger protein YJL206c - yeast (Saccharomyces cerevisiae)

N;Alternate names: probable membrane protein YJL206c; protein J0316

C;Species: Saccharomyces cerevisiae

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Oct-2004

C;Accession: S46625; S56993

R;Purnelle, B.; Coster, F.; Goffeau, A.

Yeast 10, 1235-1249, 1994

A;Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifies

ase gene ACO1 and two homologues to chromosome III genes.

A;Reference number: S46621; MUID:95274326; PMID:7754713

A;Accession: S46625

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-758 <PUR>

A;Cross-references: UNIPROT:P39529; UNIPARC:UPI000013B60A; EMBL:X77688; NID:g1183992; PI

R;Purnelle, B.; Coster, F.; Goffeau, A.

submitted to the Protein Sequence Database, September 1995

A;Reference number: S56977

A;Accession: S56993

A;Molecule type: DNA

A;Residues: 1-758 <PUW>

A;Cross-references: UNIPARC:UPI000013B60A; EMBL:Z49481; NID:g1015584; PIDN:CAA89502.1; PI

C;Genetics:



```
A:Cross-references: SGD:S0003741
A:Map position: 101
C:Keywords: DNA binding; nucleus; transcription regulation; transmembrane protein; zinc
F:42-78/Domain: GAL4 zinc binuclear cluster homology <GAL4>

Query Match      26.6%; Score 53.5; DB 2; Length 758;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 11; Conservative 2; Mismatches 6; Indels 3; Gaps 1;

Qy 13 ACIPC---QLRCSNTPTPLTCQ 31
    ||| | : ||| | ||
Db 46 ACIACRKRKVRCSGNIPRLCQ 67

RESULT 18
Ti3954
MEGF6 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: Ti3954
R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A:Reference number: 214126; MUID:98360089; PMID:9693030
A:Accession: Ti3954
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1574 <NAK>
A:Cross-references: UNIPROT:O88281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:g3449293;
A:Experimental source: strain Sprague-Dawley; brain
C:Genetics:
A:Gene: MEGF6

Query Match      26.4%; Score 53; DB 2; Length 1574;
Best Local Similarity 32.6%; Pred. No. 1.4e+02;
Matches 14; Conservative 6; Mismatches 13; Indels 10; Gaps 3;

Qy 1 CSQNEYFDSLHLHACIPCOL-----RCSNTPTPLT-----CQRYC 34
    ||| | : ||| | ||| | : ||| |
Db 966 CSAGAPCAVGTGSCI-CPAGRWGPRCAQSCPLTFGLNCSQIC 1007

RESULT 19
T22759
hypothetical protein F55H12.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22759
R:Dobson, R.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19610
A:Accession: T22759
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-2824 <WIL>
A:Cross-references: UNIPROT:P90891; UNIPARC:UPI000017BA22; EMBL:Z81091; PIDN:CAB03143.1;
A:Experimental source: clone F55H12
C:Genetics:
A:Gene: CESP:F55H12.3
A:Map position: 1
A:Introns: 87/1; 98/1; 126/2; 201/3; 343/3; 406/1; 576/3; 656/1; 825/3; 869/1; 909/1; 96
7/1; 1755/2; 1800/3; 1850/3; 1896/1; 2003/3; 2035/3; 2082/3; 2119/1; 2144/1; 2200/2; 227
F:243-279/Domain: LDL receptor ligand-binding repeat homology <LDL>

Query Match      26.4%; Score 53; DB 2; Length 2824;
Best Local Similarity 36.1%; Pred. No. 2.2e+02;
Matches 13; Conservative 7; Mismatches 14; Indels 2; Gaps 2;

Qy 1 CSQNEYFD-SLHLHACIPC-QLRCSNTPTPLTCQRYC 34
    ||| | : ||| | ||| | : ||| |
Db 2574 CEQGTQFQVNSDSCIPCSDLSENATSIPTVCQSTC 2609
```

## RESULT 20

S61051

hypothetical protein YDL162c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein D1510

C:Species: Saccharomyces cerevisiae

C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004

C:Accession: S61051; S67714

R:Pohl, T.M.

submitted to the EMBL Data Library, November 1995

A:Reference number: S61010

A:Accession: S61051

A:Molecule type: DNA

A:Residues: 1-118 &lt;POH&gt;

A:Cross-references: UNIPROT:Q12307; UNIPARC:UPI000006A6BC; EMBL:Z67750; NID:g1061256; P11

R:Pohl, T.M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67708

A:Accession: S67714

A:Molecule type: DNA

A:Residues: 1-118 &lt;POW&gt;

A:Cross-references: UNIPARC:UPI000006A6BC; EMBL:Z74210; NID:g1431255; PIDN:CAA98735.1; P

A:Experimental source: strain S288C

C:Genetics:

A:Cross-references: SGD:S0002321

A:Map position: 41

C:Superfamily: Saccharomyces hypothetical protein YDL162c

Query Match 26.1%; Score 52.5; DB 2; Length 118;

Best Local Similarity 34.4%; Pred. No. 17;

Matches 11; Conservative 4; Mismatches 10; Indels 7; Gaps 2;

Qy

1 CSQNEYFDSLHLHACIP-----CQLRCSNTPTPL 28

Db 72 CNRNSYCSRWFCYCLTLSSFCSLRC-----VPPL 100

## RESULT 21

A84544

hypothetical protein At2g16770 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004

C:Accession: A84544

R:Lin, X.; Kaul, S.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84544

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-255 &lt;STO&gt;

A:Cross-references: UNIPROT:Q9SLE1; UNIPARC:UPI00000A1869; GB:AE002093; NID:g4581120; P1

C:Genetics:

A:Gene: At2g16770

A:Map position: 2

Query Match 25.9%; Score 52; DB 2; Length 255;

Best Local Similarity 38.9%; Pred. No. 38;

Matches 14; Conservative 2; Mismatches 14; Indels 6; Gaps 2;

Qy

1 CSQNEYFDSL---HACI---PCQLRCSNTPTPLTC 30

Db 20 CSMDSFDELLRDSHACTHTTCNPPGPENTHTTC 55

## RESULT 22

T23682

hypothetical protein M02G9.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T23682

R:Matthews, L.















C;Species: Ascaris lumbricoidea (common roundworm)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997  
C;Accession: S08572  
R;Babin, D.R.; Peanaaky, R.J.; Goos, S.M.  
Arch. Biochem. Biophys. 232, 143-161, 1984  
A;Title: The isoforms of chymotrypsin/elastase from Ascaris lumbricoidea: the primary structure deduced from complementary DNA sequence  
A;Reference number: S07127; MUID:84255715; PMID:6564898  
A;Accession: S08572  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-63 <BAB>  
A;Cross-references: UNIPARC:UPI0000176391  
C;Superfamily: roundworm trypsin inhibitor

Query Match 24.9%; Score 50; DB 2; Length 63;  
Best Local Similarity 30.8%; Pred. No. 20;  
Matches 12; Conservative 6; Mismatches 9; Indels 12; Gaps 3;

Qy 1 CSQNEYDSSLHACIPCOLRC--SSNTP-----PLTCQ 31  
| | | | : | : | : | : | : | : | : | : | :  
Db 4 CGKNEVWTE----CTGCELKGQDENTPCALMCRRPSPCE 38  
| | | | : | : | : | : | : | : | : | : | :

RESULT 39  
S10332  
ubiquitin / ribosomal protein CEP52 - common tobacco (fragment)  
N;Alternate names: ubiquitin fusion protein  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: S10332  
R;Genschik, P.; Parmentier, Y.; Criqui, M.C.; Fleck, J.  
Nucleic Acids Res. 18, 4007, 1990  
A;Title: Sequence of a ubiquitin carboxyl extension protein of Nicotiana tabacum.  
A;Reference number: S10332; MUID:90326543; PMID:2165257  
A;Accession: S10332  
A;Molecule type: DNA  
A;Residues: 1-74 <GEN>  
C;Cross-references: UNIPROT:P19379; UNIPARC:UPI000017715C; EMBL:X53011  
C;Superfamily: ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52 homology; ubiquitin  
C;Keywords: DNA binding; protein biosynthesis; ribosome; zinc finger  
F;1-2/Product: ubiquitin (fragment) #status predicted <UBI>  
F;3-74/Product: ribosomal protein CEP52 #status predicted <RIB>  
F;3-74/Domain: ribosomal protein CEP52 homology <CPH>  
F;22-61/Region: zinc finger CCCC motif  
F;68-74/Region: nuclear location signal

Query Match 24.9%; Score 50; DB 2; Length 74;  
Best Local Similarity 44.4%; Pred. No. 23;  
Matches 8; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 14 CIPCQLRCSSNTPTPLTCQ 31  
| | | | : | : | : | : | : | : | : | : | :  
Db 22 CRKCVCVRCPRTPTORTCR 39  
| | | | : | : | : | : | : | : | : | : | :

RESULT 40  
T30370  
hypothetical protein ORF23 - Lymantria dispar nuclear polyhedrosis virus  
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV  
C;Date: 29-Oct-1993 #sequence\_revision 29-Oct-1993 #text\_change 09-Jul-2004  
C;Accession: T30370  
R;Kurcio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohrer,  
Virolgy 253, 17-34, 1999  
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d  
A;Reference number: Z20836; MUID:99124785; PMID:9887315  
A;Accession: T30370  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-342 <KUJZ>  
A;Cross-references: UNIPROT:Q9YMW1; UNIPARC:UPI00000F34B2; EMBL:AF081810; PIDN:AAC70208.

Query Match 24.9%; Score 50; DB 2; Length 342;  
Best Local Similarity 50.0%; Pred. No. 85;



Matches 10; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 13 ACIPQQLRCSNTPPTTCQR 32

||||:| | | | |

Db 270 ACIRKSRFPKNNPILYCSR 289

# RESULT 41

C81272 Probable aminotransferase (degt family) Cj1294 [imported] - Campylobacter jejuni (strain

C;Species: Campylobacter jejuni

C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004

C;Accession: C81272

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A;Reference number: A81250; MUID:20150912; PMID:10688204

A;Accession: C81272

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-376 <PAR>

A;Cross-references: UNIPROT:Q9BN05; UNIPARC:UPI000000C1EA5; GB:AL139078; GB:AL111168; NID

A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics:

A;Gene: Cj1294

C;Superfamily: erythromycin resistance protein

Query Match 24.9%; Score 50; DB 2; Length 376;

Best Local Similarity 52.6%; Pred. No. 92;

Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CSQNEYFDSLHACIPCOL 19

| : | | | | | | :

Db 294 CQKEELFESLHAGIGVQV 312

# RESULT 42

GQHU1 tumor necrosis factor receptor 1 precursor [validated] - human

N;Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1

N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A60231; A38

R;Fuchs, P.; Strechl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.

Genomics 13, 219-224, 1992

A;Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to ch

A;Reference number: A38208; MUID:92250049; PMID:131517

A;Accession: A38208

A;Molecule type: DNA

A;Residues: 1-455 <FUC>

A;Cross-references: UNIPROT:P19438; UNIPARC:UPI0000002CE11; GB:M75864; GB:M75865; GB:M758

R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslau

Cell 61, 351-359, 1990

A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep

A;Reference number: A34899; MUID:90235284; PMID:2158862

A;Accession: A34899

A;Molecule type: mRNA

A;Residues: 1-455 <LOE>

A;Cross-references: UNIPARC:UPI0000002CE11; GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36

A;Experimental source: placenta

A;Note: part of this sequence, including the amino end of the mature protein, confirmed

R;Schall, T.J.; Lewis, M.; Kollier, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.

Cell 61, 361-370, 1990

A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.

A;Reference number: A34900; MUID:90235285; PMID:2158863

A;Accession: A34900

A;Molecule type: mRNA

A;Residues: 1-455 <SCH>

A;Cross-references: UNIPARC:UPI0000002CE11; GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:

R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, P.; Lantcz, M.;

, DNA Cell Biol. 9, 705-715, 1990

A;Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor

A;Reference number: A36555; MUID:91090841; PMID:1702293

A;Accession: A36555

A;Molecule type: mRNA

A;Residues: 1-455 <HIM>

A;Cross-references: UNIPARC:UPI0000002CE11; GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:

A;Accession: C36555

A;Molecule type: protein

A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;107-128;162-167,'X',169-20

A;Cross-references: UNIPARC:UPI000002D398; UNIPARC:UPI000002D936; UNIPARC:UPI00001736DE;

A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble

R;Gray, P.W.; Barrett, K.; Chantray, D.; Turner, M.; Feldmann, M.

Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990

A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re

A;Reference number: A38281; MUID:91017509; PMID:2170974

A;Accession: A38281

A;Molecule type: mRNA

A;Residues: 1-455 <GRA>

A;Cross-references: UNIPARC:UPI0000002CE11; GB:M37764

A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372

R;Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann,

EMBO J. 9, 3269-3278, 1990

A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type

1e form of the receptor.

A;Reference number: S12057; MUID:91006021; PMID:1698610

A;Accession: S12057

A;Molecule type: mRNA

A;Residues: 1-455 <NOP>

A;Cross-references: UNIPARC:UPI0000002CE11; EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:

A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, we

R;Kemper, O.; Wallach, D.

Gene 134, 209-216, 1993

A;Title: Cloning and partial characterization of the promoter for the human p55 tumor nec

A;Reference number: JT0758; MUID:94085779; PMID:8262379

A;Accession: JT0758

A;Molecule type: DNA

A;Residues: 1-13 <KEM>

A;Cross-references: UNIPARC:UPI0000155CFB

R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.

Eur. J. Immunol. 20, 1167-1174, 1990

A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence

A;Reference number: A60231; MUID:90292116; PMID:2113477

A;Accession: A60231

A;Molecule type: protein

A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>

A;Cross-references: UNIPARC:UPI0000072FDB

R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Ler

Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990

A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor

tants.

A;Reference number: A38258; MUID:91062364; PMID:2174164

A;Accession: A38258

A;Molecule type: protein

A;Residues: 41-60 <GAT>

A;Cross-references: UNIPARC:UPI00001736E1

A;Experimental source: cancer patient serum

R;Olsson, I.; Lantz, M.; Nilsson, E.; Petre, C.; Thyseil, H.; Grubb, A.; Adolf, G.

Eur. J. Haematol. 42, 270-275, 1989

A;Title: Isolation and characterization of a tumor necrosis factor binding protein from

A;Reference number: A60594; MUID:89171156; PMID:2924890

A;Accession: A60594

A;Molecule type: protein

A;Residues: 41-43,'X',45-53,'V',55-57,'XK',60 <OLS>

A;Cross-references: UNIPARC:UPI00001736E2

A;Experimental source: renal failure patient urine

R;Engelmann, H.; Novick, D.; Wallach, D.

J. Biol. Chem. 265, 1531-1536, 1990

A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence i

A;Reference number: A35010; MUID:90110215; PMID:2153136

A;Accession: A35010

A;Molecule type: protein

A;Residues: 41-45 <ENG>

A;Cross-references: UNIPARC:UPI00001736E3



C;Accession: T27319  
R;McMurray, A.  
submitted to the EMBL Data Library, August 1997  
A;Reference number: Z20343  
A;Accession: T27319  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-626 <WIL>  
A;Cross-references: UNIPROT:O9UT5; UNIPARC:UPI0000164289; EMBL:Z98877; PIDN:CAA54473.1;  
A;Experimental source: clone Y69H2  
C;Genetics:  
A;Gene: CESP:Y69H2.3b  
A;Map position: 5  
A;Introns: 183/1; 247/1; 312/1; 353/1; 383/1; 429/1; 453/2; 522/1; 546/2; 586/3

Query Match 24.9%; Score 50; DB 2; Length 626;  
Best Local Similarity 32.4%; Pred. No. 1.4e+02;  
Matches 12; Conservative 3; Mismatches 12; Indels 10; Gaps 2;

Qy 1 CSQNEYFDSLHACIPCOLRCSS---NTPLTCQRYC 34  
Db 564 CRSNEKFE-----PCKTVCSDTKCNBEPFCFQVC 593

RESULT 45

T23573  
hypothetical protein K10D3.4 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T23573  
R;McMurray, A.  
submitted to the EMBL Data Library, June 1996  
A;Reference number: Z19762  
A;Accession: T23573  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-922 <WIL>  
A;Cross-references: UNIPROT:Q21418; UNIPARC:UPI00000762C2; EMBL:Z75545; PIDN:CAA99886.1;  
A;Experimental source: clone K10D3  
C;Genetics:  
A;Gene: CESP:K10D3.4  
A;Map position: 1  
A;Introns: 60/1; 228/1; 278/1; 355/1; 743/1; 802/1; 885/2

Query Match 24.9%; Score 50; DB 2; Length 922;  
Best Local Similarity 29.3%; Pred. No. 2e+02;  
Matches 12; Conservative 7; Mismatches 14; Indels 8; Gaps 2;

Qy 1 CSQNEYFDSLHAA-CIPQLRCSSNTTP-----LTCQRY 33  
Db 68 CTQNRQCEAVWPFGAYCRSGECRCANNOPPRTRDGLVCLNY 108

RESULT 46

F96596  
hypothetical protein T5A14.15 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: F96596  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
ature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzfall,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: F96596  
A;Status: preliminary  
A;Molecule type: DNA















C;Species: Saccharomyces cerevisiae  
C;Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004  
A;Accession: S30015; #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004  
R;Pascolo, S.; Ghazvini, M.; Boyer, J.; Collea, L.; Thierry, A.; Dujon, B.  
Yeast 8, 987-995, 1992  
A;Title: The sequence of a 9.3 kb segment located on the left arm of the yeast chromosome  
ribosomal protein L10.  
A;Reference number: S30013; MUID:93127732; PMID:1481574  
A;Accession: S30015  
A;Molecule type: DNA  
A;Residues: 1-1483 <PAS>  
A;Cross-references: UNIPROT:P33202; UNIPARC:UPI0000137AD6; GB:SS3418; NID:G263497; PIDN:  
A;Experimental source: strain S288C  
R;Boyer, J.; Pascolo, S.; Richard, G.F.; Ghazvini, M.; Collea, L.; Thierry, A.; Monnier  
submitted to the Protein Sequence Database, March 1994  
A;Reference number: S37813  
A;Accession: S37821  
A;Molecule type: DNA  
A;Residues: 1-1483 <BOY>  
A;Cross-references: UNIPARC:UPI0000137AD6; EMBL:Z28010; NID:G485992; PIDN:CAA81845.1; PI  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: SGD:UFD4  
A;Cross-references: SGD:S0001493; MIPS:YKL010C  
A;Map position: 11L  
Query Match 24.4%; Score 49; DB 2; Length 1483;  
Best Local Similarity 34.4%; Pred. No. 3.9e+02;  
Matches 11; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
QY 2 SQNEYFDSLHACIPCOLRCSSTNPPLTCQRY 33  
DB 499 SNQKFDLSVQCLIPILVEITYTNAADFVRRY 530  
RESULT 61  
T27283  
hypochemical protein Y64G10A.f - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
A;Accession: T27283  
R;Ainscough, R.  
submitted to the EMBL Data Library, September 1999  
A;Reference number: Z20336  
A;Accession: T27283  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1620 <WTL>  
A;Cross-references: UNIPARC:UPI000017BCB4; EMBL:AL110498; NID:el542303; PIDN:CAB54471.1;  
A;Experimental source: clone Y64G10A  
C;Genetics:  
A;Gene: CESP:Y64G10A.f  
A;Introns: 77/1, 116/1, 198/1, 282/1, 365/1, 425/1, 466/1, 548/1, 559/1, 601/1, 625/1, 7  
Query Match 24.4%; Score 49; DB 2; Length 1620;  
Best Local Similarity 23.8%; Pred. No. 4.2e+02;  
Matches 10; Conservative 7; Mismatches 17; Indels 8; Gaps 1;  
QY 1 CSNEYFDSLHACI-----PQLRCSSTNPPLTCQRYC 34  
DB 1409 CENGVCDSSTGSCVCPGVIQTKCEIACQSDRFQPTCEKIC 1450  
RESULT 62  
T13171  
probable vitellogenin receptor - fruit fly (Drosophila melanogaster)  
C;Species: Drosophila melanogaster  
C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004  
A;Accession: T13171  
R;Schonbaum, C.P.; Lee, S.; Mahowald, A.P.  
Proc. Natl. Acad. Sci. U.S.A. 92, 1485-1489, 1995  
A;Title: The Drosophila yolkless gene encodes a vitellogenin receptor belonging to the  
A;Reference number: Z17627; MUID:95183490; PMID:7878005

A;Accession: T13171  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1984 <SCH>  
A;Cross-references: UNIPROT:P98163; UNIPARC:UPI000013B879; EMBL:U13637; NID:G535345; PID  
C;Genetics:  
A;Gene: Y1  
A;Cross-references: FlyBase:FBgn0004649  
A;Map position: 1  
F;90-124/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F;129-166/Domain: LDL receptor ligand-binding repeat homology <LDL8>  
F;184-220/Domain: LDL receptor ligand-binding repeat homology <LDL10>  
F;227-262/Domain: LDL receptor ligand-binding repeat homology <LDL11>  
F;266-304/Domain: LDL receptor ligand-binding repeat homology <LDL12>  
F;1025-1062/Domain: LDL receptor ligand-binding repeat homology <LDL11>  
F;1074-1109/Domain: LDL receptor ligand-binding repeat homology <LDL12>  
F;1118-1152/Domain: LDL receptor ligand-binding repeat homology <LDL3>  
F;1158-1193/Domain: LDL receptor ligand-binding repeat homology <LDL4>  
F;1198-1232/Domain: LDL receptor ligand-binding repeat homology <LDL5>  
F;1243-1279/Domain: LDL receptor ligand-binding repeat homology <LDL6>  
F;1283-1318/Domain: LDL receptor ligand-binding repeat homology <LDL7>  
F;1340-1375/Domain: LDL receptor ligand-binding repeat homology <LDL9>  
Query Match 24.4%; Score 49; DB 2; Length 1984;  
Best Local Similarity 33.3%; Pred. No. 5e+02;  
Matches 11; Conservative 7; Mismatches 11; Indels 4; Gaps 2;  
QY 1 CSQNEY-FDSLHACIPCOLRCSSTNPPLTCOR 32  
DB 1243 CASDQYQCTSNLKIQLFSAVRCNGTT---ECPR 1272  
RESULT 63  
A46019  
notch-1 protein - mouse  
N;Alternate names: notch protein  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Oct-2004  
A;Accession: A46019; S25144; C49175; B46438; A46438; PH1569; S32109  
R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid  
Genomics 15, 259-264, 1993  
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of  
A;Reference number: A46019; MUID:93194170; PMID:8449489  
A;Accession: A46019  
A;Status: not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-2531 <DEL>  
A;Cross-references: UNIPROT:Q01705; UNIPARC:UPI000002922B; GB:Z11886; NID:G28  
A;Note: sequence extracted from NCBI backbone (NCBIP:127318)  
R;Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; i  
submitted to the EMBL Data Library, April 1992  
A;Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggest  
A;Reference number: S25144  
A;Accession: S25144  
A;Molecule type: mRNA  
A;Residues: 1551-2108, 'O', 2110-2114, 'ALP', 2118-2170 <FRA>  
A;Cross-references: UNIPARC:UPI0000177461; EMBL:Z11886  
R;Lardelli, M.; Lendahl, U.  
Exp. Cell Res. 204, 364-372, 1993  
A;Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety o  
A;Reference number: A49175; MUID:93178563; PMID:8440332  
A;Accession: C49175  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1161-1547 <LAR>  
A;Cross-references: UNIPARC:UPI0000177462; EMBL:X68278; NID:G287987; PIDN:CAA48339.1; i  
A;Experimental source: embryo  
A;Note: sequence extracted from NCBI backbone (NCBIP:126159)  
R;Kopan, R.; Weintraub, H.  
J. Cell Biol. 121, 631-641, 1993  
A;Title: Mouse notch: expression in hair follicles correlates with cell fate determinati  
A;Reference number: A46438; MUID:93252998; PMID:8486742  
A;Accession: B46438



A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054  
A:Cross-references: UNIPARC:UPI0000177463  
A:Experimental source: embryo  
A>Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)  
C:Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.  
C:Comment: This protein is one of the neurogenic proteins controlling the decision between  
C:Genetics:  
A:Gene: notch-1  
A:Map position: 2  
A>Note: proximal region of chromosome 2  
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology  
F:106-138/Domain: EGF homology <EGF1>  
F:144-175/Domain: EGF homology <EGF1>  
F:222-254/Domain: EGF homology <EGF1>  
F:261-292/Domain: EGF homology <EGF1>  
F:339-370/Domain: EGF homology <EGF2>  
F:416-449/Domain: EGF homology <EGF3>  
F:456-487/Domain: EGF homology <EGF3>  
F:494-525/Domain: EGF homology <EGF4>  
F:532-563/Domain: EGF homology <EGF4>  
F:607-638/Domain: EGF homology <EGF4>  
F:682-713/Domain: EGF homology <EGF4>  
F:757-788/Domain: EGF homology <EGF4>  
F:795-826/Domain: EGF homology <EGF4>  
F:873-904/Domain: EGF homology <EGF4>  
F:911-942/Domain: EGF homology <EGF4>  
F:949-980/Domain: EGF homology <EGF4>  
F:987-1018/Domain: EGF homology <EGF4>  
F:1025-1056/Domain: EGF homology <EGF4>  
F:1063-1094/Domain: EGF homology <EGF4>  
F:1149-1180/Domain: EGF homology <EGF4>  
F:1187-1218/Domain: EGF homology <EGF4>  
F:1233-1264/Domain: EGF homology <EGF4>  
F:1352-1383/Domain: EGF homology <EGF4>  
F:1391-1425/Domain: EGF homology <EGF4>  
F:1917-1948/Domain: ankyrin repeat homology <AN1>  
F:1949-1981/Domain: ankyrin repeat homology <AN2>  
F:1983-2015/Domain: ankyrin repeat homology <AN3>  
F:2016-2048/Domain: ankyrin repeat homology <AN4>  
F:2049-2081/Domain: ankyrin repeat homology <AN5>  
  
Query Match 24.4%; Score 49; DB 2; Length 2531;  
Best Local Similarity 40.7%; Pred. No. 6.2e+02;  
Matches 11; Conservative 4; Mismatches 10; Indels 2; Gaps 1;  
  
QY 10 LHACI--PCQLRCSSNTPPLTCQRYC 34  
DB 372 LKHACISNFCNCGSNCNDTNPVNGKRIC 398  
  
RESULT 64  
T10053  
laminin alpha 5 chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T10053  
R:Miner, J.H.; Lewis, R.M.; Sanes, J.R.  
Submitted to the EMBL Data Library, November 1997  
A:Reference number: Z16923  
A:Accession: T10053  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-3635 <MIN>  
A:Cross-references: UNIPROT:Q61001; UNIPARC:UPI000004C5E8; EMBL:U37501; NID:g2599231; PIDN:CAAL6417.1  
C:Genetics:  
A:Gene: Lama5  
C:Keywords: Basement membrane; cell binding; extracellular matrix  
F:1888-1939/Domain: laminin-type EGF-like homology <LEG>  
F:1942-1970/Domain: EGF homology <EGF>  
  
Query Match 24.4%; Score 49; DB 2; Length 3635;

Best Local Similarity 26.0%; Pred. No. 8.4e+02;  
Matches 13; Conservative 5; Mismatches 14; Indels 18; Gaps 2;  
  
QY 1 CSONEYFDS---LLHACIPQC-----LRCSNTPPLTCQRC 32  
DB 1763 CAPGYVRDTKGLFLGRCVPCQCHGHSRCLPGSGICVCGQHNTGEGDQCR 1812  
  
RESULT 65  
T27297  
hypothetical protein Y68A4A.5 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T27297  
R:Steward, C.  
Submitted to the EMBL Data Library, January 1998  
A:Reference number: Z20340  
A:Accession: T27297  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-474 <WIL>  
A:Cross-references: UNIPROT:Q9XXQ2; UNIPARC:UPI00000783D7; EMBL:AL021503; PIDN:CAAL6417.1  
A:Experimental source: clone Y68A4A  
C:Genetics:  
A:Gene: CESP:Y68A4A.5  
A:Map position: 5  
A:Introns: 47/2; 80/3; 145/3; 181/2; 196/3; 238/2; 269/2; 306/3; 342/2; 357/3; 418/3  
  
Query Match 24.1%; Score 48.5; DB 2; Length 474;  
Best Local Similarity 42.9%; Pred. No. 1.7e+02;  
Matches 9; Conservative 3; Mismatches 8; Indels 1; Gaps 1;  
  
QY 14 CIPCQLRCSSNTPPLTCQRYC 34  
DB 357 CLPCQ-TCTSFDPMGHASC 376  
  
RESULT 66  
ABON51  
serum albumin 1 precursor - Atlantic salmon  
C:Species: Salmo salar (Atlantic salmon)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: A36238; S13079  
R:Byrnes, L.; Gannon, F.  
DNA Cell Biol. 9, 647-655, 1990  
A:Title: Atlantic salmon (Salmo salar) serum albumin: cDNA sequence, evolution, and tissue  
A:Reference number: A36238; MUID:91083837; PMID:2261082  
A:Accession: A36238  
A:Molecule type: mRNA  
A:Residues: 1-608 <BYR>  
A:Cross-references: UNIPROT:P21848; UNIPARC:UPI00001257B6; GB:X52397; NID:g64375; PIDN:CI  
C:Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds copper, iron  
mones (weak bonds with these hormones promote their transfer across the membranes), thyroxine  
C:Superfamily: serum albumin; serum albumin repeat homology  
C:Keywords: carrier protein; duplication; plasma  
F:1-14/Domain: signal sequence #status predicted <SIG>  
F:15-18/Domain: propeptide #status predicted <PRO>  
F:19-608/Product: serum albumin #status predicted <MAT>  
F:23-196/Domain: serum albumin repeat homology <SA1>  
F:215-390/Domain: serum albumin repeat homology <SA2>  
F:411-591/Domain: serum albumin repeat homology <SA3>  
F:26-72, 71-80, 93-108, 107-118, 142-187, 186-195, 218-264, 263-271, 283-299, 298-309, 336-381, 380-  
  
Query Match 24.1%; Score 48.5; DB 1; Length 608;  
Best Local Similarity 34.4%; Pred. No. 2.1e+02;  
Matches 11; Conservative 5; Mismatches 9; Indels 7; Gaps 1;  
  
QY 8 DSLHACIP-----COLRCSSNTPPLTCQRC 32  
DB 51 DSTLGLDVLPIAEALAMGVKCCSDTPPEDCER 82  
  
RESULT 67



F;15-18/Domain: propeptide #status predicted <PRO>  
F;19-608/Product: serum albumin #status predicted <MAT>  
F;23-196/Domain: serum albumin repeat homology <SA1>  
F;215-390/Domain: serum albumin repeat homology <SA3>  
F;411-591/Domain: serum albumin repeat homology <SA2>  
F;26-72 71-80 93-108 107-118 142-187 186-195 218-264 263-271 283-299 298-309 336-381 380-

A1Status: preliminary  
A1Molecule type: DNA  
A1Residues: 1-98 <STO>







Search completed: December 21, 2005, 16:11:38  
Job time : 22.8 secs

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OM protein - protein search, using sw model

Run on: December 21, 2005, 15:56:49 ; Search time 117.2 Seconds  
(without alignments)  
204.675 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_8\_41  
Perfect score: 201  
Sequence: 1 CSQNEFDLSLHACIPQLRCSSTPTLTCQRYC 34

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201	100.0	184	1 TNR17_HUMAN	Q02223 homo sapien
2	201	100.0	184	2 QPFA6_HUMAN	Q8e45 homo sapien
3	136	67.7	185	1 TNR17_MOUSE	Q8472 mus musculus
4	72.5	36.1	499	2 Q88714_MOUSE	Q88714 mus musculus
5	72.5	36.1	1674	2 Q80218_MOUSE	Q80218 mus musculus
6	72.5	36.1	2850	2 Q80T03_MOUSE	Q80T03 mus musculus
7	71.5	35.6	74	2 Q8U84_MOUSE	Q8u84 mus musculus
8	71.5	35.6	140	2 Q8U83_MOUSE	Q8u83 mus musculus
9	71.5	35.6	249	1 TRL3B_MOUSE	Q9et35 mus musculus
10	71.5	35.6	249	2 Q8U82_MOUSE	Q8u82 mus musculus
11	68.5	34.1	1569	2 Q6W4X9_HUMAN	Q6w4x9 homo sapien
12	67.5	33.6	1877	1 PCSK5_MOUSE	Q04592 mus musculus
13	66.5	33.1	293	1 TRL3B_HUMAN	O14836 homo sapien
14	66.5	33.1	293	2 Q8F3F6_HUMAN	Q8f3f6 homo sapien
15	65.5	32.6	1025	2 Q7R6J7_GIALA	Q7r6j7 giardia lam
16	64.5	32.1	5374	2 Q99ND0_MOUSE	Q99nd0 mus musculus
17	64.5	32.1	5376	1 ZAN_MOUSE	Q88799 mus musculus
18	64	31.8	762	2 Q4I0Y5_GIBZE	Q4i0y5 gibberella
19	63.5	31.6	799	2 Q80L7_ENTHI	Q80l7 entamoeba h
20	63.5	31.6	802	2 Q50Y51_ENTHI	Q50y51 entamoeba h
21	63	31.3	1150	2 Q50PT4_ENTHI	Q50pt4 entamoeba h
22	62.5	31.1	1294	2 Q7QGV0_ANOGA	Q7qgv0 anopheles g
23	61.5	30.6	3005	2 Q6BFG4_PARTA	Q6bf94 paramacium
24	61	30.3	966	2 Q23378_CAENORHABDI	Q23378 caenorhabdi
25	61	30.3	1560	2 Q8U8G7_HUMAN	Q8u8g7 homo sapien
26	60	29.9	830	2 QARTY8_TETNG	Q4ty8 tetraodon n
27	60	29.9	867	1 SSPO_BOVIN	P98167 bos taurus
28	60	29.9	5146	2 Q8SPM4_BOVIN	Q8spm4 bos taurus
29	59.5	29.6	353	2 Q8SZ58_DROSOPHILA	Q8sz58 drosophila
30	59.5	29.6	353	2 Q9VW81_DROME	Q9vw81 drosophila
31	59.5	29.6	484	2 Q5CZ68_HUMAN	Q5cz68 homo sapien

Q8nav8	homo sapien
Q5CZB3	homo sapien
Q55NL5	cryptococcu
Q8nau9	homo sapien
Q81206	homo sapien
Q7zst8	homo sapien
Q86uz9	homo sapien
Q81X30	homo sapien
Q5HYA8	homo sapien
Q84Q3	tetraodon n
Q9GY5	caenorhabdi
Q51ed6	entamoeba h
Q5dd86	schistosoma
Q68f99	mus musculu
Q66PY1	mus musculu
Q8br19	mus musculu
Q9d840	mus musculu
Q8r4x8	mus musculu
Q678B7	lymphocyeta
Q26489	spodoptera
F07851	ascaris suu
O5B110	drosophila
P30432	drosophila
Q51ap4	entamoeba h
Q9mam0	arabidopsia
Q61V24	caenorhabdi
Q7R165	giardia lam
Q26566	schistosoma
Q9WRP4	monosiga br
Q51ef3	entamoeba h
Q60WC9	caenorhabdi
Q8CF47	mus musculu
Q9D351	mus musculu
Q6P233	mus musculu
Q9PVD4	xenopus lae
Q4K1X7	xenopus lae
Q6NUF1	xenopus lae
Q60K18	caenorhabdi
Q28903	sus scrofa
Q9ep28	hepatitis c
Q9e40	drosophila
Q4ifw6	gibberella
Q86Wk8	homo sapien
Q96dn2	homo sapien
Q2u00	arabidopsia
Q61xm7	xenopus lae
Q9v1c6	drosophila
Q8rmb5	vibrio para
O18118	caenorhabdi
Q924K7	meriones un
Q81YJ8	homo sapien
Q6P0M3	homo sapien
Q6bjv7	debaromyce
Q8ult0	homo sapien
O17970	caenorhabdi
Q6q157	rattus norv
Q964D1	entamoeba h
Q50rx4	entamoeba h
Q964d2	entamoeba h
Q51780	entamoeba h
Q50zk2	entamoeba h
Q993K9	callitrichi
Q50rx0	entamoeba h
Q620m9	caenorhabdi
Q50y64	entamoeba h
Q4qcp3	leishmania
Q9ep23	hepatitis c
Q4wc19	aspergillus
Q50m54	entamoeba h
Q9C091	homo sapien
Q51ce3	entamoeba h
O50SS7	entamoeba h
O57484	gallus gall



105	54.5	27.1	2155	1	TECTA_HUMAN	075443	homo sapien	178	52	25.9	72	2	Q28592	SHEEP	Q28592	ovis aries
106	54.5	27.1	2155	1	TECTA_MOUSE	O08523	mus musculus	179	52	25.9	85	1	SPR2D_MOUSE		Q70555	mus musculus
107	54	26.9	98	1	VPI_MESNA	Q8trc7	mesobuthus	180	52	25.9	141	2	Q6WX24_BACCE		Q6WX24	bacllus ce
108	54	26.9	99	2	Q5T871_HUMAN	Q5tr71	homo sapien	181	52	25.9	159	2	Q6BCV4_CABEL		Q6BCV4	caenorhabdi
109	54	26.9	336	2	Q5MAQ8_ENTHI	Q5maq8	dictyosoba h	182	52	25.9	221	2	Q8AXC1_XENLA		Q8AXC1	xenopus lae
110	54	26.9	441	2	Q55DN4_DICDI	C55dn4	dictyosteli	183	52	25.9	249	2	Q8GTS2_ARATH		Q8GTS2	arabidopsis
111	54	26.9	501	2	Q8WVD2_HUMAN	Q8wvd2	homo sapien	184	52	25.9	255	2	Q9SLE1_ARATH		Q9SLE1	arabidopsis
112	54	26.9	695	2	Q93539_CABEL	Q93539	caenorhabdi	185	52	25.9	285	2	Q5U8U7_BACTU		Q5U8U7	baclillus th
113	54	26.9	718	2	Q9BI07_ENTHI	Q9bi07	entamoeba h	186	52	25.9	285	2	Q70E25_BACTU		Q70E25	baclillus th
114	54	26.9	911	2	Q5PQ96_XENLA	Q5pq96	xenopus lae	187	52	25.9	285	2	Q70G28_BACTU		Q70G28	baclillus th
115	54	26.9	1113	2	Q511P5_ENTHI	Q511p5	entamoeba h	188	52	25.9	292	1	KR109_HUMAN		P60411	homo sapien
116	54	26.9	1893	2	Q50PC6_ENTHI	Q50pc6	entamoeba h	189	52	25.9	294	2	Q9XUS0_CABEL		Q9XUS0	caenorhabdi
117	54	26.9	1980	1	MYO9B_RAT	Q63358	rattus norv	190	52	25.9	330	2	Q7ZLX1_DROME		Q7ZLX1	drosohila
118	54	26.9	2010	2	Q4WIH3_RAT	Q4wil3	rattus norv	191	52	25.9	343	2	Q9VMS4_DROME		Q9VMS4	drosohila
119	54	26.9	2015	2	Q4WIH4_RAT	Q4wil4	rattus norv	192	52	25.9	358	2	Q7QEX5_ANOGA		Q7QEX5	anopheles g
120	54	26.9	2028	2	Q4LE74_HUMAN	Q4le74	homo sapien	193	52	25.9	365	2	Q5WML7_XENTR		Q5WML7	xenopus tro
121	54	26.9	2114	1	MYO9B_MOUSE	Q93y06	mus musculus	194	52	25.9	591	2	Q6PC06_BRARE		Q6PC06	brachydanio
122	54	26.9	2158	1	MYO9B_HUMAN	Q13459	homo sapien	195	52	25.9	1452	2	Q4SS61_TETNG		Q4SS61	tetraodon n
123	54	26.9	2447	2	Q9NEF9_DROME	Q9nef9	drosohila	196	52	25.9	1465	2	Q515C0_ENTHI		Q515C0	entamoeba h
124	54	26.9	3215	2	Q8IRV7_DROME	Q8irv7	drosohila	197	52	25.9	1467	2	Q61QNG_CABER		Q61QNG	caenorhabdi
125	54	26.9	4117	2	Q8IRV9_DROME	Q8irv9	drosohila	198	52	25.9	1474	2	Q62504_CABEL		Q62504	caenorhabdi
126	54	26.9	4179	2	Q9W4V4_DROME	Q9w4v4	drosohila	199	52	25.9	1563	1	RIM_CABEL		RIM	echinococcu
127	54	26.9	4223	2	Q8MPN3_DROME	Q8mpn3	drosohila	200	52	25.9	1564	2	Q6MD7_ECHMU		Q6MD7	echinococcu
128	54	26.9	4228	2	Q8IRV8_DROME	Q8irv8	drosohila	201	52	25.9	1582	2	Q61GX5_CABER		Q61GX5	caenorhabdi
129	53.5	26.6	146	2	Q9EP09_9HEPC	Q9ep09	hepatitis c	202	52	25.9	1704	2	Q94446_9DIPY		Q94446	chironomus
130	53.5	26.6	246	2	Q9TUX4_CANFA	Q9tux4	canis famli	203	51.5	25.6	45	2	Q9VM82_DROME		Q9VM82	drosohila
131	53.5	26.6	255	2	Q7Q883_ANOGA	Q7q883	anopheles g	204	51.5	25.6	63	1	AMP2_MIRJA		P25404	mirabilis j
132	53.5	26.6	281	2	Q29475_CANFA	Q29475	canis famli	205	51.5	25.6	77	2	Q16935_ANCCA		Q16935	ancyllostoma
133	53.5	26.6	285	2	Q95326_CANFA	Q95326	canis famli	206	51.5	25.6	91	2	Q16947_ANCCA		Q16947	ancyllostoma
134	53.5	26.6	381	1	P53_CANFA	Q29537	canis famli	207	51.5	25.6	100	2	Q16940_ANCCA		Q16940	ancyllostoma
135	53.5	26.6	396	2	Q5B9F4_EMENI	Q5b9f4	aspergillus	208	51.5	25.6	102	2	Q9DQD5_9VIRU		Q9DQD5	microplitis
136	53.5	26.6	414	2	Q68813_9HEPC	Q68813	hepatitis c	209	51.5	25.6	103	2	Q4ZJY9_9VIRU		Q4ZJY9	microplitis
137	53.5	26.6	464	2	Q511H8_ENTHI	Q511h8	entamoeba h	210	51.5	25.6	104	2	Q5D8U1_SCHJA		Q5D8U1	schistosoma
138	53.5	26.6	601	2	Q4WM60_ASPFU	Q4wm60	aspergillus	211	51.5	25.6	120	2	Q4TDR1_TETNG		Q4TDR1	tetraodon n
139	53.5	26.6	722	2	Q512Z5_MAGGR	Q512z5	magnaporthe	212	51.5	25.6	146	2	Q9ENZ7_9HEPC		Q9ENZ7	hepatitis c
140	53.5	26.6	758	1	YJUE_YEAST	P39529	saccharomyc	213	51.5	25.6	146	2	Q9EP01_9HEPC		Q9EP01	hepatitis c
141	53.5	26.6	1069	2	Q9BFS2_BOMMO	Q9bfs2	bombyx mori	214	51.5	25.6	146	2	Q9EP31_9HEPC		Q9EP31	hepatitis c
142	53.5	26.6	1079	2	Q4SSN7_TETNG	Q4ssn7	tetraodon n	215	51.5	25.6	192	2	Q81383_9HEPC		Q81383	hepatitis c
143	53.5	26.6	1642	2	Q515F7_ENTHI	Q515f7	entamoeba h	216	51.5	25.6	200	2	Q8JHZ7_CHICK		Q8JHZ7	gallus gall
144	53.5	26.6	2843	2	Q9Y6R7_HUMAN	Q9y6r7	homo sapien	217	51.5	25.6	232	2	Q8I7F6_CABEL		Q8I7F6	caenorhabdi
145	53.5	26.6	3084	2	Q7RSJ8_PLAYO	Q7rsj8	plasmodium	218	51.5	25.6	237	2	Q54VG9_DICDI		Q54VG9	dictyosteli
146	53	26.4	131	1	ALK1_MOUSE	P97430	mus musculus	219	51.5	25.6	237	2	Q817F5_CABEL		Q817F5	caenorhabdi
147	53	26.4	131	1	Q548X8_MOUSE	Q548x8	mus musculus	220	51.5	25.6	282	1	SIA1A_MOUSE		P61092	mus musculus
148	53	26.4	271	1	KR105_HUMAN	P60370	homo sapien	221	51.5	25.6	282	1	SIA1B_MOUSE		Q06985	mus musculus
149	53	26.4	303	2	Q4Q6G9_LEIMA	Q4q6g9	leishmania	222	51.5	25.6	282	1	SIAH1_BRARE		Q72V96	brachydanio
150	53	26.4	305	2	Q9F917_9BURK	Q9f917	comamonas s	223	51.5	25.6	282	1	SIAH1_HUMAN		Q81uq4	homo sapien
151	53	26.4	414	2	Q68790_9HEPC	Q68790	hepatitis c	224	51.5	25.6	282	1	SIAH1_RAT		Q920m9	rattus norv
152	53	26.4	415	2	Q68791_9HEPC	Q68791	hepatitis c	225	51.5	25.6	282	2	Q5FVA1_XENTR		Q5fva1	xenopus tro
153	53	26.4	601	2	Q80SU6_MOUSE	Q80su6	mus musculus	226	51.5	25.6	282	2	Q6GQJ5_XENLA		Q6gqj5	xenopus lae
154	53	26.4	721	2	Q6ESH4_ORYSA	Q6esh4	oryza sativ	227	51.5	25.6	352	2	Q5XK19_HUMAN		Q5xk19	homo sapien
155	53	26.4	911	2	Q68KF8_XENLA	Q68kf8	xenopus lae	228	51.5	25.6	365	1	KR106_HUMAN		P60371	homo sapien
156	53	26.4	911	2	Q5EE49_XENLA	Q5ee49	xenopus lae	229	51.5	25.6	407	2	Q8D7Y3_VIRVU		Q8d7y3	vibrio vuln
157	53	26.4	1174	2	Q5EE44_XENLA	Q5ee44	xenopus lae	230	51.5	25.6	410	2	Q7MEZ9_VIRBY		Q7mez9	vibrio vuln
158	53	26.4	1185	2	Q5EE45_XENLA	Q5ee45	xenopus lae	231	51.5	25.6	497	2	Q60VZ2_CABER		Q60vz2	caenorhabdi
159	53	26.4	1321	2	Q4XPC6_PLACH	Q4xpc6	plasmodium	232	51.5	25.6	497	2	Q23460_CABEL		Q23460	caenorhabdi
160	53	26.4	1546	2	Q5EE46_XENLA	Q5ee46	xenopus lae	233	51.5	25.6	596	2	Q4HZ82_GIBZE		Q4hz82	gibberella
161	53	26.4	1574	1	EGFL3_RAT	Q88281	rattus norv	234	51.5	25.6	639	2	Q5B7X4_EMENI		Q5b7x4	aspergillus
162	53	26.4	1632	2	Q5EE47_XENLA	Q5ee47	xenopus lae	235	51.5	25.6	759	2	Q41087_GIBZE		Q41087	gibberella
163	53	26.4	1668	2	Q69ZU6_MOUSE	Q69zu6	mus musculus	236	51.5	25.6	915	2	Q02364_CABEL		Q02364	caenorhabdi
164	53	26.4	1688	2	Q6BFV5_PARTIE	Q6bfv5	paramecium	237	51.5	25.6	926	2	Q61FT7_CABER		Q61ft7	caenorhabdi
165	53	26.4	1849	2	Q5EE48_XENLA	Q5ee48	xenopus lae	238	51.5	25.6	927	2	Q7JXS6_CABEL		Q7jxs6	caenorhabdi
166	53	26.4	2972	2	P90891_CABEL	P90891	caenorhabdi	239	51.5	25.6	979	2	Q9V878_DROME		Q9v878	drosohila
167	52.5	26.1	103	2	Q4ZJZ2_9VIRU	Q4zjz2	microplitis	240	51.5	25.6	999	2	Q17969_CABEL		Q17969	caenorhabdi
168	52.5	26.1	118	2	Q12307_YEAST	Q12307	saccharomyc	241	51.5	25.6	1193	2	Q9Y1X8_9METZ		Q9y1x8	ephydatia f
169	52.5	26.1	142	2	Q50SR1_ENTHI	Q50sr1	entamoeba h	242	51.5	25.6	2120	1	TECTA_CHICK		Q9yxh5	gallus gall
170	52.5	26.1	150	2	Q31475_ONCGO	Q31475	oncorhynch	243	51.5	25.6	2330	1	EGFL4_MOUSE		P60882	mus musculus
171	52.5	26.1	150	2	Q31476_ONCGO	Q31476	oncorhynch	244	51	25.4	138	2	Q5H4V9_XANOR		Q5h4v9	xanthomonas
172	52.5	26.1	741	2	Q4RLP8_TETNG	Q4rlp8	tetraodon n	245	51	25.4	141	2	Q6WX25_BACCE		Q6wx25	bacllus ce
173	52.5	26.1	791	2	Q4I516_GIBZE	Q4i516	gibberella	246	51	25.4	151	2	Q6IK46_DROME		Q6ik46	drosohila
174	52.5	26.1	1018	2	Q5ASW7_EMENI	Q5asw7	aspergillus	247	51	25.4	251	2	Q4YDZ0_PLABE		Q4ydz0	plasmodium
175	52.5	26.1	1562	2	Q4N599_THENI	Q4n599	thellieria p	248	51	25.4	286	2	Q8AXC0_XENLA		Q8axc0	xenopus lae
176	52.5	26.1	1592	1	SORL_CHICK	Q98910	g sortilin-p	249	51	25.4	396	2	Q7T3I6_BRARE		Q7t3i6	brachydanio
177	52	25.9	33	2	Q9UD12_HUMAN	Q9ud12	homo sapien	250	51	25.4	435	2	Q5BH32_EMENI		Q5bh32	aspergillus



251	51	25.4	448	2	O5EP27	CHICK
252	51	25.4	484	2	O7UM25	RHOBA
253	51	25.4	489	2	Q4WLAS	ASPFLU
254	51	25.4	622	2	Q7QWD2	GIADIA
255	51	25.4	641	2	O9FV53	ARATH
256	51	25.4	645	2	O8VY20	ARATH
257	51	25.4	653	2	O9S9J8	ARATH
258	51	25.4	675	2	O94LU3	ORYSA
259	51	25.4	746	2	O9SJ15	ARATH
260	51	25.4	911	2	O68KE9	XENLA
261	51	25.4	911	2	O5G579	XENLA
262	51	25.4	949	2	O4S2B5	TETNG
263	51	25.4	1010	2	O59166	BRARE
264	51	25.4	1010	2	O5G872	BRARE
265	51	25.4	1017	2	O84P66	ORYSA
266	51	25.4	1117	2	O652W3	ORYSA
267	51	25.4	2774	2	O4Z799	PLASMODIUM
268	51	25.4	2980	2	Q8IAK3	PLASMODIUM
269	51	25.4	3087	2	O9WRD2	PLABE
270	51	25.4	3622	2	O6RG85	PARTE
271	51	25.4	4680	2	Q7PV66	ANOGEA
272	51	25.4	37	2	O9SDS1	PHYAM
273	50.5	25.1	102	2	Q6PIK8	HOMO SAPIEN
274	50.5	25.1	146	2	O9EP20	HEPATIC C
275	50.5	25.1	146	2	O9EP32	HEPATIC C
276	50.5	25.1	158	2	O5XQV7	HEPATIC C
277	50.5	25.1	188	2	Q6IM32	CABBR
278	50.5	25.1	263	2	Q9WDU5	9H1V1
279	50.5	25.1	263	2	Q9WDU8	9H1V1
280	50.5	25.1	263	2	Q9WDV0	9H1V1
281	50.5	25.1	263	2	Q9WDV6	9H1V1
282	50.5	25.1	263	2	Q9WDV8	9H1V1
283	50.5	25.1	263	2	Q9WDW7	9H1V1
284	50.5	25.1	263	2	Q9WDW8	9H1V1
285	50.5	25.1	263	2	Q9WDW9	9H1V1
286	50.5	25.1	263	2	Q9WDX0	9H1V1
287	50.5	25.1	263	2	Q9WDX6	9H1V1
288	50.5	25.1	263	2	Q9WE18	9H1V1
289	50.5	25.1	263	2	Q9WE19	9H1V1
290	50.5	25.1	263	2	Q9WEJ0	9H1V1
291	50.5	25.1	263	2	Q9WEJ1	9H1V1
292	50.5	25.1	263	2	Q9WEJ2	9H1V1
293	50.5	25.1	263	2	Q9WEJ4	9H1V1
294	50.5	25.1	263	2	Q9WEJ5	9H1V1
295	50.5	25.1	263	2	Q9WEJ7	9H1V1
296	50.5	25.1	263	2	Q9WEJ9	9H1V1
297	50.5	25.1	263	2	Q9WEJ3	9H1V1
298	50.5	25.1	325	2	O5ZLJ8	CHICK
299	50.5	25.1	599	2	O4TGO4	BRARE
300	50.5	25.1	610	1	C4BP	BOVIN

## ALIGNMENTS

RESULT 1  
 TNR17 HUMAN  
 ID TNR17 HUMAN STANDARD; PRT; 184 AA.  
 AC Q0223;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 13-SEP-2003 (Rel. 48, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).  
 DE Name=TNFRSF17; Synonym=BCM, BCMA;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE, AND CHROMOSOMAL TRANSLOCATION.  
 RC TISSUE=Lymph node, and Peripheral blood leukocyte;

RX MEDLINE=93010984; PubMed=1396583;  
 RA Laabi Y., Gras M.P., Carbonnel P., Brouet J.C., Berger R.,  
 RA Larsen C.-J., Tsapis A.;  
 RT "A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene  
 by a t(4;16)(q26;pl3) translocation in a malignant T cell lymphoma.";  
 RL EMBO J. 11:3897-3904(1992).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=94218235; PubMed=8165126;  
 RA Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;  
 RT "The BCM gene, preferentially expressed during B lymphoid maturation,  
 is bidirectionally transcribed.";  
 RL Nucleic Acids Res. 22:1147-1154(1994).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=99425270; PubMed=10493829; DOI=10.1006/geno.1999.5927;  
 RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,  
 RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,  
 RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,  
 RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;  
 RT "Genome duplications and other features in 12 Mb of DNA sequence from  
 human chromosome 16p and 16q.";  
 RL Genomics 60:295-308(1999).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE, AND VARIANT THR-153.  
 RX MEDLINE=21419161; PubMed=11528522; DOI=10.1038/s1/gene/6363770;  
 RA Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;  
 RT "Presence of four major haplotypes in human BCM gene: lack of  
 association with systemic lupus erythematosus and rheumatoid  
 arthritis.";  
 RL Genes Immun. 2:276-279(2001).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS VAL-54; VAL-65;  
 VAL-75; ASN-81 AND SER-165.  
 RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,  
 RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,  
 RA Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;  
 RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department  
 of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.  
 RX MEDLINE=20363816; PubMed=10903733;  
 RA Hatzoglou A., Rousset J., Bourgeade M.-F., Rogier E., Madry C.,  
 RA Inoue J.-I., Devergne O., Tsapis A.;  
 RT "TNF receptor family member BCMA (B cell maturation) associates with  
 TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and  
 activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-  
 activated protein kinase.";  
 RL J. Immunol. 165:1322-1330(2000).  
 RN [7]  
 RP FUNCTION.  
 RX MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;  
 RA Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,  
 RA Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,  
 RA Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,  
 RA Harrison K., Kindevoel W., Clegg C.H.;  
 RT "TACI and BCMA are receptors for a TNF homologue implicated in B-cell  
 autoimmune disease.";  
 RL Nature 404:995-999(2000).  
 RN [8]  
 RP FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.  
 RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;  
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,  
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,  
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Thell L.E.;  
 RT "APRIL and TRAIL-I and receptors BCMA and TACI: system for regulating  
 humoral immunity.";  
 RL Nat. Immunol. 1:252-256(2000).  
 RN [9]  
 RP INTERACTIONS WITH TRAF5 AND TRAF6.  
 RX MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;  
 RA Shu H.-B., Johnson H.;



RT "B cell maturation protein is a receptor for the tumor necrosis factor  
family member TNF-1.", U.S.A. 97:9156-9161(2000).  
RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).  
CC -1- FUNCTION: Receptor for TNF-1/BLYS/BAFF and TNFSF13/APRIL.  
CC Promotes B-cell survival and plays a role in the regulation of  
CC humoral immunity. Activates NF-kappa-B and JNK.  
CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.  
CC  
CC -1- INTERACTION:  
CC G9Y275:TNFSF13B; NDExp=1; IntAct=EBI-519945, EBI-519169;  
CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane  
CC and perinuclear Golgi-like structures.  
CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-  
CC cells or monocytes.  
CC -1- DISEASE: A chromosomal aberration involving TNFRSF17 is found in a  
CC form of T-cell acute lymphoblastic leukemia (T-ALL). Translocation  
CC t(4;16)(q26;p13) with IL2.  
CC -1- SIMILARITY: Contains 1 TNFR-Cys repeat.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL: Z14954; CAA78679.1; -; mRNA.  
CC EMBL: Z29575; CAA82691.1; -; mRNA.  
CC EMBL: Z29574; CAA82690.1; -; Genomic DNA.  
CC EMBL: U95742; AAB67251.1; -; Genomic DNA.  
CC EMBL: AB052772; BAB360895.1; -; Genomic DNA.  
CC EMBL: AY509112; AAR84240.1; -; Genomic DNA.  
CC PIR: S43486; S43486.  
CC PDB: 1QDQ; X-ray; K/L/M/N/O/P/Q/R=8-46.  
CC PDB: 1XU2; X-ray; R/S/T=5-51.  
CC IntAct: Q02223; -.  
CC HGNC: HGNC:11913; TNFRSF17.  
CC MIM: 109545; -.  
CC GO: 0016021; C: integral to membrane; TAS.  
CC GO: 0005886; C: plasma membrane; TAS.  
CC GO: 0004872; F: receptor activity; TAS.  
CC GO: 0008283; P: cell proliferation; TAS.  
CC GO: 0007275; P: development; TAS.  
CC GO: 0007165; P: signal transduction; TAS.  
CC InterPro: IPR001368; TNFR\_C6.  
CC PROSITE: PS00652; TNFR\_NGFR\_1; FALSE NEG.  
CC PROSITE: PS00650; TNFR\_NGFR\_2; FALSE NEG.  
CC 3D-structure: Chromosomal translocation; Immune response;  
CC Polymorphism: Proto-oncogene; Receptor; Signal-anchor; Transmembrane.  
FT TOPO\_DOM 1 54 Extracellular (Potential).  
FT TRANSMEM 55 77 Signal-anchor for type III membrane  
FT FT TOPO\_DOM 78 184 protein (Potential).  
FT REPEAT 7 41 Cytoplasmic (Potential).  
FT SITE 3 4 Breakpoint for translocation to form  
FT FT DISULFID 8 21 IL2/TNFRSF17 oncogene.  
FT FT DISULFID 24 37 By similarity.  
FT FT DISULFID 28 41 By similarity.  
FT VARIANT 54 54 A -> V.  
FT FT VARIANT 65 65 FTId=VAR\_018755.  
FT FT VARIANT 65 65 I -> V.  
FT FT VARIANT 75 75 FTId=VAR\_018756.  
FT FT VARIANT 81 81 S -> N (in dbSNP:373496).  
FT FT VARIANT 153 153 A -> T.  
FT FT VARIANT 165 165 C -> S.  
FT FT VARIANT 165 165 FTId=VAR\_018759.  
SQ SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;  
Query Match 100.0%; Score 201; DB 1; Length 184;

Best Local Similarity 100.0%; Pred. No. 2.1e-18;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEVFDLSLLHACIPQCLRCSSNTPTLTQRYC 34  
DB 8 CSQNEVFDLSLLHACIPQCLRCSSNTPTLTQRYC 41  
RESULT 2  
Q6PE46 HUMAN  
ID Q6PE46 HUMAN PRELIMINARY; PRT; 184 AA.  
AC Q6PE46;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Tumor necrosis factor receptor superfamily, member 17.  
GN Name=TNFRSF17;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pooled;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pooled;  
RA Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC058291; AAH58291.1; -; mRNA.  
DR GO: GO:0004872; F: receptor activity; IEA.  
KW Receptor.  
SQ SEQUENCE 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;  
Query Match 100.0%; Score 201; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.1e-18;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSQNEVFDLSLLHACIPQCLRCSSNTPTLTQRYC 34  
DB 8 CSQNEVFDLSLLHACIPQCLRCSSNTPTLTQRYC 41  
RESULT 3  
TNFR17\_MOUSE  
ID TNFR17\_MOUSE STANDARD; PRT; 185 AA.  
AC O88472;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 17 (B-cell



DE maturation protein).

GN Name=TNfrsf17; Synonym=Bcm, Bcm;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).

RC STRAIN=BALB/c; TISSUE=Spleen;

RX MEDLINE=99061155; PubMed=9846698; DOI=10.1093/intimm/10.11.1693;

RA Madry C., Laubi Y., Callebaut I., Roussel J., Hatzoglu A.,

RA Le Coniat M., Morion J.P., Berger R., Taapis A.;

RT "The characterization of murine BCMA gene defines it as a new member

RT of the tumor necrosis factor receptor superfamily.";

RL Int. Immunol. 10:1693-1702(1998).

RL [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RC STRAIN=C57BL/6J; TISSUE=Colon;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,

RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltas L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reid J., Ring D.J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RL [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).

RC STRAIN=C57BL/6J; TISSUE=Mammary gland;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywiniski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC CC

CC -!- FUNCTION: Receptor for TNFSF13B/BlyS/BAFF and TNFSF13/APRIL.

CC Promotes B-cell survival and plays a role in the regulation of

CC humoral immunity. Activates NF-kappa-B and JNK (by similarity).

CC -!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (by

CC similarity).

CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=088472-1; Sequence=Displayed;

CC Name=2;

CC IsoId=088472-2; Sequence=VSP\_006507;

CC -!- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and

CC heart, and at lower levels in kidney and lung.

CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC EMBL: AF061505; AAC23799.1; -; mRNA.

CC EMBL: AK020247; BAB32038.1; -; mRNA.

CC EMBL: BC027519; AAH27519.1; -; mRNA.

CC HSSP: Q02223; 1QQD.

CC Ensembl: ENSMUSG0000022496; Mus musculus.

CC MGI: MGI-1343050; Tnfrrsf17.

CC GO: GO:0016021; C:integral to membrane; TAS.

CC InterPro: IPR001368; TNFR\_C6.

CC PROSITE: PS00652; TNFR\_NGFR\_1; FALSE NEG.

CC PROSITE: PS00505; TNFR\_NGFR\_2; FALSE NEG.

CC Alternative splicing; Immune response; Receptor; Signal-anchor;

CC Transmembrane. 1 49 Extracellular (Potential).

CC TOFO\_DOM 50 70 Signal-anchor for type III membrane

CC TRANSMEM 50 70 protein (Potential).

CC FT REPEAT 71. 185 Cytoplasmic (Potential).

CC FT DISULFID 4 36 TNFR-Cys.

CC FT DISULFID 5 18 By similarity.

CC FT DISULFID 21 32 By similarity.

CC FT DISULFID 25 36 By similarity.

CC FT VARSPLIC 87 91 Missing (in isoform 2).

CC FT /FTId=VSP\_006507.

CC SQ SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;

Query Match 67.7%; Score 136; DB 1; Length 185;

Best Local Similarity 70.6%; Pred. No. 7.4e-10;

Matches 24; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

Oy 1 CSONEYFDSLHACIPCOLRCSSNTPLTCORYC 34

Db 5 CFHSEYFDSLHACKPCHLRCSN--PATCQPYC 36

RESULT 4

O88714\_MOUSE PRELIMINARY; PRT; 499 AA.

AC O88714;

DT 01-NOV-1998 (TRENBLrel. 08, Created)

DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Gastric mucin-like protein (Fragment).

GN Name=Muc6; Synonym=gastrectic mucin-like;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Stomach;

RA Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,



RA RIO M.C. ;  
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Stomach;  
RA Tomasetto C.I.;  
RL Submitted (SP-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ010752; CAA09343.1; -; mRNA.

DR HSSP; P56682; ICCV.  
DR Ensembl; ENSMUSG0000048191; Mus musculus.  
DR MGI; MGI:2663233; Muc6.  
DR InterPro; IPRO02919; Prot Inh\_CR\_TIL.  
DR InterPro; IPRO01846; vwp h

```
DR PFAM; PF01826; TIL; 1.  
DR PFAM; PF00094; VWD; 1.  
DR SMART; SM00216; VWD; 1.  
FT NON TER      1      1
```

```

FT  NON_TER  499  499
SQ  SEQUENCE  499  AA;  54190 MW;  04F89EF4F23E61E CRC64;

Query Match  36.1%; Score 72.5; DB 2; Length
              36.2%; 72.5; 45

```

Qy 1 CSQNEYFDSLHLHACIPCOLRCSSNTPPLT 29  
||||| : ||  
Matches 14; Conservative 1; Mismatches 7; Indels  
Best Local Similarity 48.3%; Freq. NO. 0.45;

Db 430 CSQNEYFDHSECTCVP-----APPT 451

RESULT 5

Q80218_MOUSE	
ID	Q80218_MOUSE PRELIMINARY; PRT; 1674 AA.
AC	Q80218;
DT	01-JUN-2003 (TRENBLrel. 24, Created)
DT	01-JUN-2003 (T-EMBLrel. 24, Last sequence update)

01-JUN-2003 (last sequence update)  
 01-MAR-2004 (TREMBLrel. 26, last annotation update)  
 DT Secreted gel-forming mucin (Fragment).  
 DE  
 GN Name=Muc6;  
 OS Mus musculus (Mouse).  
 OS

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

[1]  
KN  
RP  
RC STRAIN=C57BL/6J;  
RX PubMed=14984930; DOI=10.1016/j.bbaexp.2004.01.001;  
PA Escande F., Buistine M. P.;

RT "The mouse secreted gel-forming mucin gene cluster.";  
 RL Biochim. Biophys. Acta 1676:240-250 (2004).  
 DR EMBL; AJ511867; CAD544415.1; -; Genomic DNA.  
 DR EMBL; AJ511868; CAD544415.1; JOINED; Genomic DNA.

DR HSSP; O46162; 1KJ0.  
DR MGI; MGI:2663233; Muc6.  
DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.  
DR InterPro; IPR001846; VWF\_D.  
DR 26.

DK	Pfam; PFU1826; ILL; 2.
DR	Pfam; PF00094; VWD; 3.
DR	SMART; SM00216; VWD; 3.
FT	NON TER 1674 1674
SO	SEQUENCE 1674 AA: 181168 MW: 3BC42CB004476309 CRC64:

Query Match	36.1%	Score	72.5	DB	2	Length
Best Local Similarity	48.3%	Pred. No.	1.6			
Matches	14	Conservative	1	Mismatches	7	Indels

```
Qy      1 CSQNEYFDLLHACIPQICRLCSSNTPPLT 29
         |||||
Db      1181 CSQNEYFDHSEGTCTVPC-----APPTT 1202
           |||||
```

## RESULT 6

ID	Q80T03_MOUSE PRELIMINARY;	PRT; 2850 AA.
AC	Q80T03;	
DT	01-JUN-2003 (TReMBLrel. 24, Created)	
DT	01-JUN-2003 (TReMBLrel. 24, Last sequence update)	

DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	MUC6.
GN	Name=Muc6;
OS	Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OC NCBI\_TaxID=10090;  
PN [1]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=2253400; PubMed=12676567; DOI=10.1016/S0888-7543(03)00036-3;  
RA Desseyn J.-L., Laine A.;

RT "Characterization of mouse muc6 and evidence of conservation of the  
gel-forming mucin gene cluster between human and mouse.";  
RL Genomics 81:433-436(2003).  
DR EMBL: AV184388; AQA47735.1; -; Genomic DNA.  
DR EMBL: AV194385; AQA47735.1; -; Genomic DNA.

DR ENBL; AY184385; AAO47735.1; JOINED; Genomic\_DNA.  
DR ENBL; AY184387; AAO47735.1; JOINED; Genomic\_DNA.  
DR ENBL; AY184386; AAO47735.1; JOINED; Genomic\_DNA.  
DR HSP; O46162; IKJ0.  
DR Ensemble; ENSMUSG00000048191; Mus musculus.

DR MGI; MGI:2663233; Muc6.  
DR InterPro; IPR006207; Cys\_knot\_C.  
DR InterPro; IPR002919; Prot\_Inh\_CR\_Ttl.  
DR InterPro; IPR001846; VWF\_D.

DR PFam; PF01826; TIL; 2.  
DR PFam; PF00094; VWD; 3.  
DR SMART; SM00216; VWD; 3.  
DR PROSITE; PS01225; CTKC 2; 1.  
SC SEQUENCE 2850 AA, 300398 MW, 9C095F08A5C78C9D CPC64.

SEQUENCE	2830 AG,	300396 nm	300396 nm
Query Match		36.1%;	Score 72.5; DB 2; Length 2850;
Best Local Similarity		48.3%;	Pred. No. 2.7;
Matches 14;	Conservative	1;	Mismatches 7; Indels 7; Gaps

```
Qy      1 CSONEYFDSLHACIPCOLRCSSTNPPLT 29  
        ||||| |  
        ||||| :||  
Db     1222 CSONEYFDHSEGTVCPC-----APPTT 1243
```

RESULT 7  
Q5SU84 MOUSE  
ID Q5SU84 MOUSE PRELIMINARY: PRT: 74 AA.

AC	Q5S084		
DT	01-FEB-2005	(TReMBLrel. 29, Created)	
DT	01-FEB-2005	(TReMBLrel. 29, Last sequence update)	
DT	01-FEB-2005	(TReMBLrel. 29, Last annotation update)	

DE Tumor necrosis factor receptor superfamily, member 13b  
DE (Fragment).  
DE  
GN Name=Trnfrsf13b; ORFName=RP23-55I2.2-002;  
OS Mus musculus (Mouse).  
OS

OC Eukaryota; metazoa; Chordata; Mammalia; Eutheria; Sciurognathidae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

RP NUCLEOTIDE SEQUENCE.  
RA Holt K.;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL646093; CAI25894.1; -; Genomic DNA.

DR	GO; GO:0004872; F:receptor activity; IEA.	
KW	Receptor.	
FT	NON_TER	74
SQ	SEQUENCE	74 AA; 8337 MW; DA8A3B06FE191A26 CRC64;

Query Match 35.6%; Score 71.5; DB 2; Length 74;  
Best Local Similarity 35.3%; Pred. No. 0.087;  
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps



Qy 1 CSQNEYEDSLHACIPQLRCSSNTPLTCQRYC 34  
Db 6 CPKQYWDSSRKSCVSCALTCQRS-ORTCTDFC 38

RESULT 8  
Q55U83 MOUSE  
ID Q55U83\_MOUSE PRELIMINARY; PRT; 140 AA.  
AC Q55U83;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Tumor necrosis factor receptor superfamily, member 13b  
DE (Fragment).  
DE Name=TNFRsf13b; ORFNames=RP23-5512.2-003;  
GN Mus musculus (Mouse).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Holt K.;  
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL646033; CA125895.1; -; Genomic DNA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON TER 140 140  
SQ SEQUENCE 140 AA; 15672 MW; 005D8CDF4E8E3D15 CRC64;

Query Match 35.6%; Score 71.5; DB 2; Length 140;  
Best Local Similarity 35.3%; Pred. No. 0.17;  
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy 1 CSQNEYEDSLHACIPQLRCSSNTPLTCQRYC 34  
Db 6 CPKQYWDSSRKSCVSCALTCQRS-ORTCTDFC 38

RESULT 9  
TR13B MOUSE  
ID TR13B\_MOUSE STANDARD; PRT; 249 AA.  
AC Q9ET35; Q9DB23;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane  
DE activator and CAML interactor).  
GN Name=TNFRsf13b; Synonyms=taci;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RX MEDLINE=21177254; PubMed=10881172; DOI=10.1038/76989;  
RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;  
RT "Identification of a receptor for BlyS demonstrates a crucial role in  
RT humoral immunity.";  
RL Nat. Immunol. 1:37-41 (2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC STRAIN=C57BL/6J; TISSUE=lung;  
RX MEDLINE=22354683; PubMed=12466951; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nakaio I., Osato N., Saito R., Suzuki H., Yamanaka I., Miyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gofjoberi T.,  
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayase N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573 (2002).  
RN [3]  
RP FUNCTION.  
RX MEDLINE=20341628; PubMed=10880535; DOI=10.1084/jem.192.1.137;  
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,  
RA Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,  
RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,  
RA Meng S.-Y., Boyle W.J., Hsu H.;  
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis  
RT factor family member involved in B cell regulation.";  
RL J. Exp. Med. 192:137-143 (2000).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=21322748; PubMed=11429548; DOI=10.1038/89782;  
RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,  
RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;  
RT "TACI-ligand interactions are required for T cell activation and  
RT collagen-induced arthritis in mice.";  
RL Nat. Immunol. 2:632-637 (2001).  
CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL/BAPF/BLYS  
CC that binds both ligands with similar high affinity. Mediates  
CC calcineurin-dependent activation of NF-AT, as well as activation  
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-  
CC cell function and the regulation of humoral immunity (By  
CC similarity).  
CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal  
CC domain of CAMLG with its C-terminus (By similarity).  
CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).  
CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC EMBL; AF257673; AAG00081.1; -; mRNA.  
CC EMBL; AK004668; BAB23457.1; -; mRNA.  
CC Ensemble; ENSMUSG0000010142; Mus musculus.  
CC MGI; MGI:1889411; Tnfrsf13b.  
CC GO; GO:0009897; C:external side of plasma membrane; IDA.  
CC GO; GO:0005887; C:integral to plasma membrane; IDA.  
CC GO; GO:0001782; P:B cell homeostasis; IMP.  
CC GO; GO:0030889; P:negative regulation of B cell proliferation; IMP.  
CC InterPro; IPR001368; TNFR\_c6.  
CC PROSITE; PS00652; TNFR\_NGFR\_1; FALSE NEG.  
CC PROSITE; PS00505; TNFR\_NGFR\_2; FALSE NEG.  
KW Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.  
FT TOPO\_DOM 1 128  
FT Signal-anchor for type III membrane  
FT TRANSMEM 129 149  
FT protein (Potential).



FT	TOPO_DOM	150	249	Cytoplasmic (Potential).
FT	REPEAT	5	38	TNFR-Cys 1.
FT	REPEAT	42	76	TNFR-Cys 2.
FT	DISULFID	6	19	By similarity.
FT	DISULFID	22	34	By similarity.
FT	DISULFID	26	38	By similarity.
FT	DISULFID	43	58	By similarity.
FT	DISULFID	61	72	By similarity.
FT	DISULFID	65	76	By similarity.
FT	CONFLICT	137	137	I -> F (in Ref. 2).
SQ	SEQUENCE	249 AA;	26947 MW;	CB2F2D61C2931D81 CRC64;
Query Match 35.6%; Score 71.5; DB 1; Length 249;				
Best Local Similarity 35.3%; Pred. No. 0.3;				
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;				
QY	1	CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC	34	
Db	6	CPKQYWDSSRKSCVSCALTCQRS-QRTCTDFC	38	
RESULT 10				
Q5US82_MOUSE				
ID	Q5US82_MOUSE	PRELIMINARY;	PRT;	249 AA.
AC	Q5US82;			
DT	10-MAY-2005	(T-EMBLrel. 30, Created)		
DT	10-MAY-2005	(T-EMBLrel. 30, Last sequence update)		
DT	10-MAY-2005	(T-EMBLrel. 30, Last annotation update)		
DE	Tumor necrosis factor receptor superfamily, member 13b.			
GN	Name=Tnfrsf13b; ORFNames=RP23-5512.2-001;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Holt K.;			
RL	Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL646093; CAI25896.1; -; Genomic_DNA.			
KW	Receptor.			
SQ	SEQUENCE	249 AA;	26947 MW;	CB2F2D61C2931D81 CRC64;
Query Match 35.6%; Score 71.5; DB 2; Length 249;				
Best Local Similarity 35.3%; Pred. No. 0.3;				
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;				
QY	1	CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC	34	
Db	6	CPKQYWDSSRKSCVSCALTCQRS-QRTCTDFC	38	
RESULT 11				
Q6W4X9_HUMAN				
ID	Q6W4X9_HUMAN	PRELIMINARY;	PRT;	1569 AA.
AC	Q6W4X9;			
DT	05-JUL-2004	(T-EMBLrel. 27, Created)		
DT	05-JUL-2004	(T-EMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(T-EMBLrel. 27, Last annotation update)		
DE	Mucin glycoprotein (Fragment).			
GN	Name=MUC6;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RX	PubMed=15081123; DOI=10.1016/j.ygeno.2003.11.003;			
RA	Rousseau K., Byrne C., Kim J.S., Gum J.R., Swallow D.M.,			
RA	Toribara N.W.;			
RT	"The complete genomic organization of the human MUC6 and MUC2 mucin			
,RT	genes.";			
RL	J. Cell Biol. 135:1261-1275(1996).			
RT	subcellular compartments.";			
RT	"The isoforms of proprotein convertase PC5 are sorted to different			
RA	Bendayan M., Seidah N.G.;			
RA	De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,			
RX	MEDLINE=97103178; PubMed=8947550; DOI=10.1083/jcb.135.5.1261;			
RP	PARTIAL PROTEIN SEQUENCE, AND SUBCELLULAR LOCATION.			
RN	[4]			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).			
RT	nonendocrine cells.";			
RT	candidate proprotein convertase expressed in endocrine and			
RT	"CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a			
RA	Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;			
RX	MEDLINE=93342056; PubMed=8341687;			
RP	NUCLEOTIDE SEQUENCE (ISOFORM PC5A).			
RN	[3]			
RL	J. Biochem. 113:132-135(1993).			
RT	"Identification and functional expression of a new member of the			
RT	mammalian Kex2-like processing endoprotease family: its striking			
RT	structural similarity to PACE4.";			
RL	J. Biochem. 113:132-135(1993).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM PC5A).			
RC	TISSUE=Brain, and Intestine;			
RX	MEDLINE=93224489; PubMed=8468318;			
RA	Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,			
RA	Nakayama K.;			
RT	"Identification and functional expression of a new member of the			
RT	mammalian Kex2-like processing endoprotease family: its striking			
RT	structural similarity to PACE4.";			
RL	FEBS Lett. 327:165-171(1993).			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE OF 330-1877 (ISOFORM PC5B).			
RC	STRAIN=ICR; TISSUE=Intestine;			
RX	MEDLINE=93327934; PubMed=8335106; DOI=10.1016/0014-5793(93)80163-O;			
RA	Nakagawa T., Murakami K., Nakayama K.;			
RT	"Identification of an isoform with an extremely large Cys-rich region			
RT	of PC6, a Kex2-like processing endoprotease.";			
RL	FEBS Lett. 327:165-171(1993).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM PC5A).			
RC	TISSUE=Brain, and Intestine;			
RX	MEDLINE=93224489; PubMed=8468318;			
RA	Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,			
RA	Nakayama K.;			
RT	"Identification and functional expression of a new member of the			
RT	mammalian Kex2-like processing endoprotease family: its striking			
RT	structural similarity to PACE4.";			
RL	J. Biochem. 113:132-135(1993).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM PC5A).			
RC	TISSUE=Adrenal cortex;			
RX	MEDLINE=93342056; PubMed=8341687;			
RA	Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;			
RT	"CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a			
RT	candidate proprotein convertase expressed in endocrine and			
RT	nonendocrine cells.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993).			
RN	[4]			
RP	PARTIAL PROTEIN SEQUENCE, AND SUBCELLULAR LOCATION.			
RX	MEDLINE=97103178; PubMed=8947550; DOI=10.1083/jcb.135.5.1261;			
RA	De Bie I., Marcinkiewicz M., Malide D., Lazure C., Nakayama K.,			
RA	Bendayan M., Seidah N.G.;			
RT	"The isoforms of proprotein convertase PC5 are sorted to different			
RT	subcellular compartments.";			
RL	J. Cell Biol. 135:1261-1275(1996).			
RN	[5]			











ZAN	(Zonadhesin).
GN	Name=Zan.
OS	Mus musculus (Mouse).
EUK	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Mus.
NCBI	TaxID=10090;
[1]	
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=129/Sv;
RX	MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;
RA	Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA	Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA	Miller W., Koop B.F.;
RT	"Comparative analysis of the gene-dense ACHE/TPR2 region on human
RT	chromosome 7q22 with the orthologous region on mouse chromosome 5."
RL	Nucleic Acids Res. 29:1352-1365(2001).
[2]	
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=129/Sv;
RA	Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF312033; AAK28824.1; -; Genomic_DNA.
DR	EMBL; AY046056; AAL04416.1; -; Genomic_DNA.
DR	HSSP; Q90248; 1HX2.
DR	MGI; MGI:106656; Zan.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0007339; P:binding of sperm to zona pellucida; IEA.
DR	GO; GO:0007155; P:cell adhesion; IEA.
DR	InterPro; IPRO00742; EGF 2.
DR	InterPro; IPRO06209; EGF-like.
DR	InterPro; IPRO03645; FcI_N.
DR	InterPro; IPRO06210; IEGF.
DR	InterPro; IPRO00998; MAM.
DR	InterPro; IPRO02919; Prot_Inh_CR_TIL.
DR	InterPro; IPRO03328; TiLa_Cysrich.
DR	InterPro; IPRO01007; VWF_C.
DR	InterPro; IPRO01846; VWF_D.
DR	Pfam; PF00008; EGF_1.
DR	Pfam; PF00629; MAM; 3.
DR	Pfam; PF01826; TIL; 25.
DR	Pfam; PF02345; TIL_assoc; 25.
DR	Pfam; PF00094; VWD; 4.
DR	SMART; SM00181; EGF_2.
DR	SMART; SM00274; FOLN; 20.
DR	SMART; SM00137; MAM; 3.
DR	SMART; SM00214; VWC; 18.
DR	SMART; SM00216; VWD; 4.
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR	PROSITE; PS01186; EGF_2; 18.
DR	PROSITE; PS00026; EGF_3; 1.
DR	PROSITE; PS00740; MAM_1; 1.
DR	PROSITE; PS00060; MAM_2; 3.
SQ	SEQUENCE 5374 AA; 579545 MW; 90D2D8CFE5DE24EB CRC64;
Query Match 32.1%; Score 64.5; DB 2; Length 5374;	
Best Local Similarity 35.1%; Pred.No.58;	
Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps	
Qy	1 CSQNEYDSLHACIP-CQLRCSSNTNP--PLTCQRVC 34
::   ::   ::   ::   ::   ::   ::   ::   :	
Dd	3298 CPTNSQFTCLCPSCVPCSNRCREVTSPVPSSCREGC 3334
RESULT 17	
ZAN_MOUSE	ID_ZAN_MOUSE STANDARD; PRG; 5376 AA.
AD	AC O88799; O08647;
DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)
DT	10-MAY-2005 (Rel. 47, Last annotation update)
DE	Zonadhesin precursor.
GN	Name=Zan;



OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC X OX NCBI\_TaxID=10090;  
RN [1]\_ NUCLEOTIDE SEQUENCE.  
RP TISSUE=Testis;  
RC MEDLINE=98123114; PubMed=9452463; DOI=10.1074/jbc.273.6.3415;  
RX Gao Z., Garbers D.L.;  
RA "Species diversity in the structure of zonadhesin, a sperm-specific  
RT membrane protein containing multiple cell adhesion molecule-like  
RT domains";  
RL J. Biol. Chem. 273:3415-3421(1998).  
RN [2]  
RN NUCLEOTIDE SEQUENCE OF 4864-5376.  
RC TISSUE=Testis;  
RX MEDLINE=97271566; PubMed=9126492; DOI=10.1006/geno.1997.4620;  
RA Gao Z., Harumi T., Garbers D.L.;  
RT "Chromosome localization of the mouse zonadhesin gene and the human  
RT zonadhesin gene (ZAN).";  
RL Genomics 41:119-122(1997).  
CC -|- FUNCTION: Binds in a species-specific manner to the zona pellucida  
CC of the egg. May be involved in gamete recognition and/or  
CC signaling.  
CC -|- SUBUNIT: Probably forms covalent oligomers.  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the  
CC apical region of the sperm head.  
CC -|- TISSUE SPECIFICITY: In testis, primarily in haploid spermatids.  
CC -|- DOMAIN: The MAM domains probably mediates sperm adhesion to the  
CC zona pellucida.  
CC -|- DOMAIN: During sperm migration through the reproductive tracts,  
CC the mucin-like domain might inhibit inappropriate trapping of  
CC spermatozoa or promoting adhesion to the oviductal isthmus.  
CC -|- DOMAIN: The VWFD domain 2 may mediate covalent oligomerization (By  
CC similarity).  
CC -|- SIMILARITY: Contains 1 EGF-like domain.  
CC -|- SIMILARITY: Contains 3 MAM domains.  
CC -|- SIMILARITY: Contains 25 VWFD domains.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC ENBL; U97068; AAC26680.1; -; mRNA.  
DR EMBL; U83190; AAC53125.1; -; mRNA.  
DR PIR; T42215; T42215.  
DR HSSP; Q90248; IHX2.  
DR MGI; MGI:106656; Zan.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR InterPro; IPRO04153; CKXC repeat.  
DR InterPro; IPRO03341; DUF135\_Cys\_rich.  
DR InterPro; IPRO00742; EGF\_2.  
DR InterPro; IPRO06209; EGF\_like.  
DR InterPro; IPRO00998; MAM.  
DR InterPro; IPRO02919; Prot\_Inh CR\_TIL.  
DR InterPro; IPRO03328; TILa\_CysRich.  
DR Pfam; PF02363; C\_tripleX; 18.  
DR Pfam; PF03128; CKXC; 11.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00629; MAM; 3.  
DR Pfam; PF01826; TIL; 25.  
DR Pfam; PF02345; TIL\_assoc; 25.  
DR Pfam; PF00094; WVD; 4.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 18.  
DR PROSITE; PS00026; EGF\_3; 1.  
DR PROSITE; PS00740; MAM\_1; 1.  
DR PROSITE; PS00600; MAM\_2; 3.

KW Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal;  
KW Transmembrane.  
FT SIGNAL 1 17 Potential.  
FT CHAIN 18 5376 Zonadhesin.  
FT TOPO\_DOM 18 5310 Extracellular (Potential).  
FT TRANSMEM 5311 5337 Potential.  
FT TOPO\_DOM 5338 5376 Cytoplasmic (Potential).  
FT DOMAIN 1 210 MAM 1.  
FT DOMAIN 215 374 MAM 2.  
FT DOMAIN 377 542 MAM 3.  
FT DOMAIN 1171 1280 VWFD 1 (partial).  
FT DOMAIN 1281 1669 VWFD 2.  
FT DOMAIN 1670 2056 VWFD 3.  
FT DOMAIN 2057 2459 VWFD 4.  
FT DOMAIN 2460 2579 VWFD 5 (partial).  
FT DOMAIN 2580 2699 VWFD 6 (partial).  
FT DOMAIN 2700 2819 VWFD 7 (partial).  
FT DOMAIN 2820 2939 VWFD 8 (partial).  
FT DOMAIN 2940 3059 VWFD 9 (partial).  
FT DOMAIN 3060 3179 VWFD 10 (partial).  
FT DOMAIN 3180 3299 VWFD 11 (partial).  
FT DOMAIN 3300 3416 VWFD 12 (partial).  
FT DOMAIN 3417 3536 VWFD 13 (partial).  
FT DOMAIN 3537 3656 VWFD 14 (partial).  
FT DOMAIN 3657 3776 VWFD 15 (partial).  
FT DOMAIN 3777 3892 VWFD 16 (partial).  
FT DOMAIN 3893 4028 VWFD 17 (partial).  
FT DOMAIN 4029 4148 VWFD 18 (partial).  
FT DOMAIN 4149 4263 VWFD 19 (partial).  
FT DOMAIN 4264 4283 VWFD 20 (partial).  
FT DOMAIN 4384 4503 VWFD 21 (partial).  
FT DOMAIN 4504 4623 VWFD 22 (partial).  
FT DOMAIN 4624 4743 VWFD 23 (partial).  
FT DOMAIN 4744 4863 VWFD 24 (partial).  
FT DOMAIN 4864 5261 VWFD 25.  
FT DOMAIN 5259 5295 EGF-like.  
FT REGION 547 1170 80 X heptapeptide repeats (approximate)  
(mucin-like domain).  
FT CARBOHYD 339 339 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 499 499 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 1216 1216 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 1239 1239 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 1314 1314 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 1814 1814 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 1908 1908 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 1933 1933 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 2028 2028 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 2111 2111 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 2142 2142 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 2332 2332 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 2533 2533 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 2575 2575 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 2692 2692 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 2812 2812 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 3052 3052 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 3065 3065 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 3144 3144 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 3172 3172 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 3288 3288 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 3292 3292 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 3782 3782 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 4005 4005 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 4136 4136 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 4243 4243 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 4254 4254 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 4335 4335 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 4376 4376 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 4586 4586 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 5136 5136 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 5252 5252 N-linked (GlcNAc... ) (Potential).  
FT DISULFID 5263 5274 By similarity.  
FT DISULFID 5268 5283 By similarity.  
FT DISULFID 5285 5294 By similarity.



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SQ SEQUENCE 5376 AA; 579913 MW; 0E44DB7DF2A2620 CRC64;
Query Match 32.1%; Score 64.5; DB 1; Length 5376;
Best Local Similarity 35.1%; Pred. No. 58;
Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

Qy 1 CSQNEYFDSLHACIP-CQLRCSNTP--PLTCQYC 34
Db 3300 CPTNSQFTDCLPSCVCSNRCVTSFVPSRCGEC 3336

RESULT 18
Q410Y5 GIBZE PRELIMINARY; PRT; 762 AA.
AC Q410Y5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG09123.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Chepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorrts L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Ratta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Snirnov S.,
RA Smith C., Spencer B., Strange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; RACH01000370; EAA78173.1; -; Genomic_DNA.
SQ SEQUENCE 762 AA; 84756 MW; 55B25D037F21A35A CRC64;

Query Match 31.8%; Score 64; DB 2; Length 762;
Best Local Similarity 43.3%; Pred. No. 9.1;
Matches 13; Conservative 3; Mismatches 6; Indels 8; Gaps 2;

Qy 13 ACIPQC---LRCSNTPPLTCQ-----YC 34
Db 17 ACVPCQNSKKRQDSQSPANCRRRDCIPYC 46

RESULT 19
Q50LY7 ENTHI PRELIMINARY; PRT; 799 AA.
AC Q50LY7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

SQ SEQUENCE 5376 AA; 579913 MW; 0E44DB7DF2A2620 CRC64;
Query Match 32.1%; Score 64.5; DB 1; Length 5376;
Best Local Similarity 35.1%; Pred. No. 58;
Matches 13; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

Qy 1 CSQNEYFDSLHACIP-CQLRCSNTP--PLTCQYC 34
Db 3300 CPTNSQFTDCLPSCVCSNRCVTSFVPSRCGEC 3336

RESULT 18
Q410Y5 GIBZE PRELIMINARY; PRT; 762 AA.
AC Q410Y5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG09123.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,
RA Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Chepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorrts L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Ratta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Snirnov S.,
RA Smith C., Spencer B., Strange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; RACH01000370; EAA78173.1; -; Genomic_DNA.
SQ SEQUENCE 762 AA; 84756 MW; 55B25D037F21A35A CRC64;

Query Match 31.8%; Score 64; DB 2; Length 762;
Best Local Similarity 43.3%; Pred. No. 9.1;
Matches 13; Conservative 3; Mismatches 6; Indels 8; Gaps 2;

Qy 13 ACIPQC---LRCSNTPPLTCQ-----YC 34
Db 17 ACVPCQNSKKRQDSQSPANCRRRDCIPYC 46

RESULT 19
Q50LY7 ENTHI PRELIMINARY; PRT; 799 AA.
AC Q50LY7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

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DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Protein kinase, putative (Fragment).
GN ORFNames=650.t00003;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RC PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samueleon J.,
RA Amedeo P., Roncaglia P., Berziman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoef U., Hance Z., Harris B., Harris D.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Omond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sichert-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AAFB01001427; EAL42605.1; -; Genomic_DNA.
GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 4.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding.
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER
SQ SEQUENCE 799 AA; 91662 MW; D8BFE2F2E235989E CRC64;

Query Match 31.6%; Score 63.5; DB 2; Length 799;
Best Local Similarity 35.3%; Pred. No. 11;
Matches 12; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQC---LRCSNTPPLTCQ 31
Db 137 CODNYTYDKELQSCVCSSECLTCSNKDICTCK 170

RESULT 20
Q50Y51 ENTHI PRELIMINARY; PRT; 802 AA.
AC Q50Y51;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE CXXC-rich protein (Fragment).
GN ORFNames=141.t00017;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RC PubMed=15729342; DOI=10.1038/nature03291;

```



```
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFB01000471; EAL46536.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 802 AA; 90126 MW; 1425BF8514DED237 CRC64;

Query Match 31.6%; Score 63.5; DB 2; Length 802;
Best Local Similarity 35.3%; Pred. No. 11;
Matches 12; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

Qy 1 CSONEYFDSLHACIPQC---LRCSNTPPLTCQ 31
Db 654 CQNYYYKELQSCVGCSSCLCTCSNKDICTCK 687

RESULT 21
Q50PT4_ENTHI PRELIMINARY; PRT; 1150 AA.
AC Q50PT4;
DT 13-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DE Receptor protein kinase, putative.
GN ORFNames=359.t00009;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS.
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitsch E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RA "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAFB01000933; EAL43605.1; -; Genomic_DNA.
KW Kinase; Receptor.
SQ SEQUENCE 1150 AA; 128938 MW; 0DBE7051D4B4E286 CRC64;

Query Match 31.3%; Score 63; DB 2; Length 1150;
Best Local Similarity 36.7%; Pred. No. 19;
Matches 11; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

Qy 1 CSONEYFDSLHACIPQLRCSSNTPPLTC 30
Db 138 CGINEYFDVSKNLCLPCKTNCQRCSSAQC 167
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RESULT 22
Q7QGV0_ANOGA PRELIMINARY; PRT; 1294 AA.
AC Q7QGV0;
DT 01-MAR-2004 (TEMBLrel. 26, Created)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE ENSANGP00000012534 (fragment).
GN ORFNames=ENSANGG00000010045;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAB0100823; EAA05574.2; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008565; F:protein transporter activity; IEA.
DR GO; GO:0008886; P:intracellular protein transport; IEA.
DR InterPro; IPR002860; Glyco_Hydro_BNR.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000172; LDL_receptor_A.
DR InterPro; IPR000033; Ldl_receptor_rep.
DR InterPro; IPR006581; VPS10.
DR Pfam; PF02012; BNR; 6.
DR Pfam; PF00057; Ldl_recept_a; 7.
DR Pfam; PF00058; Ldl_recept_b; 4.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00181; EGF; 3.
DR SMART; SM00192; LDLA; 7.
DR SMART; SM00135; LY; 5.
DR SMART; SM00602; VPS10; 1.
DR PROSITE; PS01209; LDLRA_1; 5.
DR PROSITE; PS50068; LDLRA_2; 5.
FT NON TER 1
FT NON TER 1294
SQ SEQUENCE 1294 AA; 146748 MW; 10C251750A3F0586 CRC64;

Query Match 31.1%; Score 62.5; DB 2; Length 1294;
Best Local Similarity 31.7%; Pred. No. 25;
Matches 13; Conservative 8; Mismatches 13; Indels 7; Gaps 1;

Qy 1 CSONEYFDSLHACIPQLRCSS-----NTPPLTCQRYC 34
Db 1131 CRADEPRCNVTNACLPNWRCDTEKDCPDGTPPPRRKDRTC 1171

RESULT 23
Q6BFG4_PARTE PRELIMINARY; PRT; 3005 AA.
AC Q6BFG4;
DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Putative surface protein with EGF domains and furin-like repeats.
GN ORFNames=PFMB.409;
OS Paramaecium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Paramaecium.
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OX NCBI\_TaxID=5888;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Stock d4-2;  
RA PubMed=15296759; DOI=10.1016/j.j.cub.2004.07.029;  
RX Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,  
RA Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Kellier A.M.,  
RA Cohen J., Meyer E., Sperling L.,  
RT "High Coding Density on the Largest Paramecium tetraurelia Somatic Chromosome."  
RL Curr. Biol. 14:1397-1404(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Stock d4-2;  
RA Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;  
RT "Paramecium megabase sequencing project."  
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR548612; CAHQ3606.1; -; Genomic\_DNA.  
DR InterPro; IPR006058; 2Fe2S fd BS.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR006212; Furin\_repeat.  
DR InterPro; IPR006210; IEGF.  
DR SMART; SM00181; EGF; 22.  
DR SMART; SM00261; FU; 29.  
DR PROSITE; PS00197; 2FE2S FERREDOXIN; UNKNOWN\_1.  
DR PROSITE; PS01186; EGF\_2; 12.  
SQ SEQUENCE 3005 AA; 343821 MW; D8CG6A247876A5AS CRC64;  
Query Match 30.6%; Score 61.5; DB 2; Length 3005;  
Best Local Similarity 40.6%; Pred. No. 80;  
Matches 13; Conservative 3; Mismatches 7; Indels 9; Gaps 2;  
QY 6 YFDSLHACIPQLRCSNTPLPFCQ----RYC 34  
DB 1190 YFESSNQICQDLSC-----FTCGSSKYC 1215  
RESULT 24  
Q22378 CAEEL  
ID Q22378 CAEEL PRELIMINARY; PRT; 966 AA.  
AC Q22378;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Hypothetical protein T10E10.4;  
GN ORFNames=T10E10.4;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG WormBase; WBGene00020421; T10E10.4.  
RT The C. elegans sequencing consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology."  
RL Science 282:2012-2018(1998).  
DR EMBL; U39644; AAA80360.2; -; Genomic\_DNA.  
DR PIR; T16840; T16840.  
DR HSP; P10969; 1WGT.  
DR IntAct; Q22378; -.  
DR Ensembl; T10E10.4; Caenorhabditis elegans.  
DR WormBase; WBGene00020421; T10E10.4.  
DR WormPep; T10E10.4; CE25989.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008066; F:chitin binding; IEA.  
DR GO; GO:0006030; P:chitin metabolism; IEA.  
DR InterPro; IPR002557; Chitin bind\_perA.  
DR InterPro; IPR006149; EB region.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR000794; Ketoacyl\_synth.  
DR InterPro; IPR003571; Snake\_toxin.

DR InterPro; IPR006150; Worm\_repeat\_1.  
DR Pfam; PF01607; CBM\_14; 2.  
DR Pfam; PF01683; EB; 1.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00289; WRI; 12.  
DR PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; UNKNOWN\_1.  
DR PROSITE; PS00272; SNAKE\_TOXIN; UNKNOWN\_1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 966 AA; 102461 MW; B565A3CDD25216D9 CRC64;  
Query Match 30.3%; Score 61; DB 2; Length 966;  
Best Local Similarity 37.5%; Pred. No. 29;  
Matches 12; Conservative 7; Mismatches 11; Indels 2; Gaps 1;  
QY 1 CSQNEVFDSLHACIPQLR--CSSNTPPLTC 30  
DB 216 CSQSTFVNSDLNVCVPLAQNCSSTQQPVC 247  
RESULT 25  
Q5JSG7 HUMAN  
ID Q5JSG7 HUMAN PRELIMINARY; PRT; 1560 AA.  
AC Q5JSG7;  
DT 10-MAY-2005 (TRENBLrel. 30, Created)  
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)  
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
DE Protease convertase subtilisin/kexin type 5 (Fragment).  
GN Name=PCSK5; ORFNames=RP11-422N19.4-002;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Mashreghi-Mohammadi M.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Pelan S.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Peck A.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL391868; CAI40675.1; -; Genomic\_DNA.  
DR EMBL; AL589653; CAI40809.1; -; Genomic\_DNA.  
DR EMBL; AL353607; CAI41234.1; -; Genomic\_DNA.  
DR EMBL; AL353607; CAI40675.1; JOINED; Genomic\_DNA.  
DR EMBL; AL353607; CAI40809.1; JOINED; Genomic\_DNA.  
DR EMBL; AL589653; CAI40675.1; JOINED; Genomic\_DNA.  
DR EMBL; AL391868; CAI40809.1; JOINED; Genomic\_DNA.  
DR EMBL; AL391868; CAI41234.1; JOINED; Genomic\_DNA.  
DR EMBL; AL589653; CAI41234.1; JOINED; Genomic\_DNA.  
DR GO; GO:0004289; F:subtilase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR003460; APP.  
DR InterPro; IPR005560; DUF326.  
DR InterPro; IPR006212; Furin\_repeat.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR000209; Pept\_S8\_S53.  
DR InterPro; IPR002884; PrprotnconvertP.  
DR Pfam; PF02420; AFP; 1.  
DR Pfam; PF03860; DUF326; 2.  
DR Pfam; PF01483; P\_protein; 1.  
DR ProDom; PD000717; PrprotnconvertP; 1.  
DR SMART; SM00181; EGF; 16.  
DR SMART; SM00261; FU; 22.  
DR PROSITE; PS00138; SUBTILASE\_SER; 1.  
FT NON\_TER 1  
SQ SEQUENCE 1560 AA; 173890 MW; 7211FBC127A8A08C CRC64;  
Query Match 30.3%; Score 61; DB 2; Length 1560;



Best Local Similarity 28.0%; Pred. No. 47;  
Matches 14: Conservative 6; Mismatches 14: Indels 16; Gaps 2;

**Qy** 1 CSQNEYFDSLHACIPQLRC-----SSTPPL-----TCQRYC 34  
||:||: |||::| |::| |:  
**Db** 1155 CSPSEYDWDAPGCKPHVCFHCWGPAEDOCOTCPMNSLLNTTVCWKC 1204

**RESULT 26**

Q4RT8\_TETNG  
ID Q4RT8\_TETNG PRELIMINARY; PRT; 830 AA.  
AC Q4RT8;  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE Chromosome 12 SCAF14996, whole genome shotgun sequence.  
DE (Fragment).  
DN OPFNames=GSTENG00029038001;  
GN Tetraodon nigroviridis (Green puffer).  
OS Tetraodon nigroviridis  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Tetraodon.  
ON NCBI\_TaxID=99883;  
RX [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Dasilva S., Jaffe D., Fisher S., Lutfalla G., Bessat C., Segurens B.,  
RA Nascica C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Catellio L., Katina M., Vacherie B.,  
RA Blemont C., Skalli Z., Catellio L., Poulain J., De Bernardis V.,  
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gousy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schacherer V., Quetier F., Saurin W., Scarpelli C.,  
RA Winkler P., Lander E.S., Weissbach J., Roest Croillius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RL the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).

## [2]

RP	NUCLEOTIDE SEQUENCE.	
RG	Genoscope; Whitehead Institute Centre for Genome Research;	
RL	Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.	
CC	-! CAUTION: The sequence shown here is derived from an	
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is	
CC	preliminary data.	
DR	EMBL; CAAE01014996; CAG08144.1; -; Genomic_DNA.	
DR	InterPro; IPR000742; EGF_2.	
DR	InterPro; IPR006209; EGF_like.	
DR	InterPro; IPR006210; IEGF.	
DR	InterPro; IPR002049; Laminin EGF.	
DR	Pfam; PF00053; Laminin EGF; I.	
DR	PRINTS; PR00011; EGFLAMININ.	
DR	SMART; SM00181; EGF; 7.	
DR	SMART; SM00180; EGF Lam; 6.	
DR	PROSITE; PS00022; EGF 1; 7.	
DR	PROSITE; PS01186; EGF 2; 4.	
DR	PROSITE; PS50026; EGF_3; 4.	
KW	Laminin EGF-like domain.	
FT	NON_TER 1	
FT	NON_TER 830	
FT	SEQUENCE 830 AA; 91073 MW; 94415DC15C27B26A CRC64;	

### Query Match

Best Local Similarity 24.1%; Pred. No. 34; Matches 14; Conservative 6; Mismatches 14; Indels 24; Gaps 2;

**Qy** 1 CSQNEYFDLSLLHACI-----PQLRCSSTNPPL-----TCORYC 34  
||| ||:: | :||| | :|||  
**Db** 144 C\$VNSICDAMTGRCLSPGWGTNRNGCIQC\$NNSPCDOFTGRCOCERLWGPCCRYC 201  
||||| ::| :||| | :|||

RESULT 27	SSPO_BOVIN	STANDARD;	PRT;	867 AA.
AC	P98167;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	SCO-spondin (Fragment).			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;			
OC	Pecora; Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RP	[1]			
RN	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Endomycyte;			
RX	MEDLINE=96338614; PubMed=8743952;			
RA	Gabron S., Monnerie H., Meiniel R., Creveaux I., Lehmann W.,			
RA	Lamalle D., Dastugue B., Meiniel A.;			
RT	"SCO-spondin: a new member of the thrombospondin family secreted by			
RT	the subcutaneous organ is a candidate in the modulation of neuronal			
RT	aggregation.";			
RL	J. Cell Sci. 109:1053-1061(1996).			
CC	-1- FUNCTION: Involved in the modulation of neuronal aggregation.			
CC	-1- SUBCELLULAR LOCATION: Extracellular.			
CC	-1- TISSUE SPECIFICITY: Subcutaneous organ.			
CC	-1- DEVELOPMENTAL STAGE: Embryo.			
CC	-1- SIMILARITY: Belongs to the thrombospondin family.			
CC	-1- SIMILARITY: Contains at least 2 EGF-like domains.			
CC	-1- SIMILARITY: Contains at least 1 F5/8 type C domain.			
CC	-1- SIMILARITY: Contains at least 3 LDL-receptor Class A domains.			
CC	-1- SIMILARITY: Contains at least 4 TSP type-1 domains.			
CC	-1- SIMILARITY: Contains 1 VWFC domain.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collabora-			
CC	tion between the Swiss Institute of Bioinformatics and the EMBL outstation			
CC	at the European Bioinformatics Institute. There are no restrictions on			
CC	use as long as its content is in no way modified and this statement is			
CC	removed.			
CC	-----			
DR	EMBL; X93922; CAA63815.1; -; mRNA.			
DR	HSP; P01130; 1AJJ.			
DR	InterPro; IPR000742; EGF_2.			
DR	InterPro; IPR006209; EGF_like.			
DR	InterPro; IPR000421; FAS8_C.			
DR	InterPro; IPR002172; LDL_receptor_A.			
DR	InterPro; IPR002919; Prot_Inh_CR_TIL.			
DR	InterPro; IPR000884; TSP1.			
DR	InterPro; IPR008085; TSP_1.			
DR	InterPro; IPR01007; VWFC_C.			
DR	Pfam; PF00754; F5_F8_type_C; 1.			
DR	Pfam; PF00057; Ldl_recept_a; 3.			
DR	Pfam; PF01826; TIL; 1.			
DR	Pfam; PF00090; TSP_1; 4.			
DR	Pfam; PF00093; VWFC_1.			
DR	PRINTS; PR00261; LDLRECEPTOR.			
DR	PRINTS; PR01705; TSP1REPEAT.			
DR	PROSITE; PS00022; EGF_1; FALSE NEG.			
DR	PROSITE; PS01186; EGF_2; FALSE NEG.			
DR	PROSITE; PS50026; EGF_3; FALSE NEG.			
DR	PROSITE; PS01285; FAS8C_1; 1.			
DR	PROSITE; PS01286; FAS8C_2; 1.			
DR	PROSITE; PS50022; FAS8C_3; 1.			
DR	PROSITE; PS01209; LDLRA_1; 3.			
DR	PROSITE; PS50068; LDLRA_2; 3.			
DR	PROSITE; PS50092; TSP1_4.			
DR	PROSITE; PS50184; VWFC_2; 1.			
KW	Calcium; Cell adhesion; EGF-like domain; Glycoprotein; Repeat.			
FT	DOMAIN 29 87			
FT	DOMAIN 103 142			
FT	DOMAIN 143 180			
FT	DOMAIN 188 244			
FT	TSP type-1 1.			
FT	EGF-like 1.			
FT	EGF-like 2.			
FT	TSP type-1 2.			



FT	DOMAIN	245	304		WFPC.
FT	DOMAIN	344	502		F5/8 type C.
FT	DOMAIN	506	544		LDL-receptor class A 1.
FT	DOMAIN	663	701		LDL-receptor class A 2.
FT	DOMAIN	723	761		LDL-receptor class A 3.
FT	DOMAIN	761	814		TSP type-1 3.
FT	DOMAIN	816	866		TSP type-1 4.
FT	CARBOHYD	88	88		N-linked (GLCNAC. .) (Potential).
FT	CARBOHYD	309	309		N-linked (GLCNAC. .) (Potential).
FT	CARBOHYD	409	409		N-linked (GLCNAC. .) (Potential).
FT	DISULFID	107	122		By similarity.
FT	DISULFID	116	127		By similarity.
FT	DISULFID	129	141		By similarity.
FT	DISULFID	147	166		By similarity.
FT	DISULFID	149	169		By similarity.
FT	DISULFID	171	179		By similarity.
FT	DISULFID	344	502		By similarity.
FT	DISULFID	508	520		By similarity.
FT	DISULFID	515	533		By similarity.
FT	DISULFID	527	542		By similarity.
FT	DISULFID	665	677		By similarity.
FT	DISULFID	672	690		By similarity.
FT	DISULFID	684	699		By similarity.
FT	DISULFID	725	737		By similarity.
FT	DISULFID	732	750		By similarity.
FT	DISULFID	744	759		By similarity.
FT	NON_TER	1	1		
FT	NON_TER	867	867		
SQ	SEQUENCE	867 AA;	91817 MW;	9538F2108E787B49 CRC64;	
Query Match 29.9%; Score 60; DB 1; Length 867;					
Best Local Similarity 42.9%; Pred.No. 35;					
Matches 9; Conservative 3; Mismatches 9; Indels 0; Gaps 0;					
Qy	10 LLHACIPCOLRCSSTNPPLTC 30 :          :				
Db	96 VFHACVCPCLTCDISQATC 116 :          :				
RESULT 28					
ID	Q8SPM4_BOVIN				
ID	Q8SPM4_BOVIN PRELIMINARY;	PRT;	5146 AA.		
AC	Q8SPM4;				
DT	01-JUN-2002 (TrEMBLrel. 21, Created)				
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)				
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				
DE	SCO-spondin.				
GN	Name=sco-spondin;				
OS	Bos taurus (Bovine);				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;				
OC	Pecora; Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Subcommissural organ;				
EX	MEDLINE=20465125; PubMed=11008217;				
DX	DOI=10.1002/1098-1136(200011)32:2<177::AID-GLIA70>3.0.CO;2-V;				
RA	Gobron S.;				
RT	"Subcommissural organ/Reissner's fiber complex: characterization of				
RT	sco-spondin, a glycoprotein with potent activity on neurite				
RT	outgrowth.";				
RL	Glia 32:177-191(2000).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Subcommissural organ;				
RA	Meinl A.;				
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL; AJ416457; CAC94914.1; -; mRNA.				
DR	HSP; F98162; 1K7B.				
DR	GO; GO:0005576; C:extracellular region; IEA.				
DR	GO; GO:0005179; F:hormone activity; IEA.				
DR	GO; GO:0030414; F:protease inhibitor activity; IEA.				



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RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY071103; AAU48725.1; -; mRNA.
DR Ensembl; CG7348; Drosophila melanogaster.
DR FlyBase; FBgn0036940; CG7348.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR Pfam; PF01607; CBM 14; 4.
DR SMART; SM00494; ChEBD2; 3.
DR PROSITE; PS0940; CHIT BIND II; 4.
SQ SEQUENCE 353 AA; 39712 MW; F5AB27B9A6FF9921 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 353;
Best Local Similarity 31.8%; Pred. No. 16;
Matches 14; Conservative 4; Mismatches 15; Indels 11; Gaps 2;

Qy 1 CSQNEVFDLSLLHACIPCOL-----RCSNTP-----PLTCQRY 33
Db 119 CSVGNFDPARRACLPVAISAAHQSCVLPDNATLANPDSOCETY 162

RESULT 30
Q9VW81 DROME
ID Q9VW81 DROME PRELIMINARY; PRT; 353 AA.
AC Q9VW81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG7348-PA.
GN Name=CG7348; ORFNames=CG7348;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mankov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Stadling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,

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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003514; AAF49068.1; -; Genomic DNA.
DR Ensembl; CG7348; Drosophila melanogaster.
DR FlyBase; FBgn0036940; CG7348.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_Pera.
DR Pfam; PF01607; CBM 14; 4.
DR SMART; SM00494; ChEBD2; 3.
DR PROSITE; PS0940; CHIT BIND II; 4.
SQ SEQUENCE 353 AA; 39713 MW; 1C66916504FD130B CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 353;
Best Local Similarity 31.8%; Pred. No. 16;
Matches 14; Conservative 4; Mismatches 15; Indels 11; Gaps 2;

Qy 1 CSQNEVFDLSLLHACIPCOL-----RCSNTP-----PLTCQRY 33
Db 119 CSVGNFDPARRACLPVAISAAHQSCVLPDNATLANPDSOCETY 162

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RESULT 31
Q5CZ68 HUMAN PRELIMINARY; PRT; 484 AA.
AC Q5CZ68;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein DKFZp686D20108 (Fragment).
GN Name=DKFZp686D20108;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The German cDNA Consortium;
RG Tissue=Fetal kidney;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
OS Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR936873; CAI59785.1; -.
DR InterPro; IPR000859; CUB.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 484 AA; 53895 MW; 8895A663B9DB369C CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 484;
Best Local Similarity 28.9%; Pred. No. 22;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOL-----RCSNT 25
|||:::|:::|:::|:::|:::|
Db 241 CSPGHYNTSIHRCAMGYSQDPFRNFCRCPCGNT 278

RESULT 32
Q8NAV8 HUMAN PRELIMINARY; PRT; 581 AA.
AC Q8NAV8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ34691.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura N., Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

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RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohnori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isigai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45 (2004).
DR EMBL; AK092010; BAC03789.1; -. mRNA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR011641; GCC2_GCC3.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00042; CUB; 1.
DR PROSITE; PS01180; CUB; 1.
SQ SEQUENCE 581 AA; 64343 MW; D17BC28CDA1E4EE1 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 581;
Best Local Similarity 28.9%; Pred. No. 27;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

Qy 1 CSQNEYFDSLHACIPCOL-----RCSNT 25
|||:::|:::|:::|:::|:::|
Db 337 CSPGHYNTSIHRCAMGYSQDPFRNFCRCPCGNT 374

RESULT 33
Q5CZB3 HUMAN PRELIMINARY; PRT; 852 AA.
AC Q5CZB3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein DKFZp686B1223 (Fragment).
GN Name=DKFZp686B1223;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The German cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR936607; CAI56752.1; -. mRNA.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004988; P:transmembrane receptor activity; IEA.
DR GO; GO:0007536; P:blood coagulation; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011641; GCC2_GCC3.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001491; Thrombomodulin.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF07645; EGF_CA; 1.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR PRINTS; PR00907; THROMBOMODULN.
DR SMART; SM00042; CUB; 1.

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DR SMART; SM00181; EGF; 7.
DR SMART; SM00179; EGF CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01187; EGF CA; 3.
KW EGF-like domain, Hypothetical protein.
FT NON_TER
SQ SEQUENCE 852 AA; 93812 MW; 514918CDD126C7B2 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 852;
Best Local Similarity 28.9%; Pred. No. 40;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEYFDSLHACIPQL-----RCSNNT 25
|||:::|||||
Db 608 CSPGHYNTSIHRCIRCAMGSYQDPFRQNFCSCRCPGNT 645

RESULT 34
Q55NL5 CRYNE PRELIMINARY; PRT; 861 AA.
AC Q55NL5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNAMES=CNBH0730;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiellia.
OX NCBI_TaxID=283643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary.
DR EMBL; AA00100041; EAL19380.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 861 AA; 93346 MW; 8745729FBD869366 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 861;
Best Local Similarity 37.1%; Pred. No. 40;
Matches 13; Conservative 4; Mismatches 13; Indels 5; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSNTPP-----LTC 30
|||:::|||||
Db 321 CSSGLYDSTSCSCSPACSTCTGPTGTSCLSC 355

RESULT 35
Q8NAU9 HUMAN PRELIMINARY; PRT; 880 AA.
AC Q8NAU9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ34743.
GN Name=SCUBE3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14702039; DOI=10.1038/ng1285;
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RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakanatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahori K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togai S., Komai F., Hara R., Takeuchi K., Arica M.,
RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Negase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Iwogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK092062; BAC03798.1; -; mRNA.
DR HSSP; P35555; ILMJ.
DR Ensembl; ENSG00000146197; Homo sapiens.
DR HGNC; HGNC:13655; SCUBE3.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011641; GCC2_GCC3.
DR InterPro; IPR001491; Thrbomodulin.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF07645; EGF CA; 2.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR PRINTS; PR00907; THRBOMODULN.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF CA; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01187; EGF CA; 3.
SQ SEQUENCE 880 AA; 97239 MW; F0BDE6E85266FD60 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 880;
Best Local Similarity 28.9%; Pred. No. 41;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

QY 1 CSQNEYFDSLHACIPQL-----RCSNNT 25
|||:::|||||
Db 636 CSPGHYNTSIHRCIRCAMGSYQDPFRQNFCSCRCPGNT 673

RESULT 36
Q8IZ06 HUMAN PRELIMINARY; PRT; 985 AA.
ID Q8IZ06_HUMAN
AC Q8IZ06;
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DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC26979 protein.
GN Name=MGC26979;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC032835; AAH32835.1; -; mRNA.
DR InterPro; ENSG00000164953; Homo sapiens.
DR ProSITE; PS01228; COF 1; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 985 AA; 110872 MW; 571B5626C726B384 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 985;
Best Local Similarity 21.6%; Pred. No. 46;
Matches 11; Conservative 9; Mismatches 12; Indels 19; Gaps 1;

Qy 1 CSQNEYFDSLHACIPC-----QLRCSNTPPLTCOR 32
Db 39 CDNNQYFDISALSCVPCGANQRDARGTSCVCLPGFQMISNNGGPAIICKK 89

RESULT 37
Q725T8 HUMAN
ID Q725T8 HUMAN PRELIMINARY; PRT; 985 AA.
AC Q725T8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MGC26979.
GN Name=MGC26979;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC054338; AAH54338.1; -; mRNA.
DR InterPro; IPR000150; Hypothet cof.
DR ProSITE; PS01228; COF 1; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 985 AA; 110858 MW; 711109F095C12E89 CRC64;

Query Match 29.6%; Score 59.5; DB 2; Length 985;
Best Local Similarity 21.6%; Pred. No. 46;
Matches 11; Conservative 9; Mismatches 12; Indels 19; Gaps 1;

Qy 1 CSQNEYFDSLHACIPC-----QLRCSNTPPLTCOR 32
Db 39 CDNNQYFDISALSCVPCGANQRDARGTSCVCLPGFQMISNNGGPAIICKK 89

RESULT 38
Q86U29 HUMAN
ID Q86U29 HUMAN PRELIMINARY; PRT; 992 AA.
AC Q86U29;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Signal peptide, CUB domain, EGF-like 3.
GN Name=SCUBE3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,

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RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.",  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Pancreas;  
RA Strauberg R.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC052263; AAHS2263.2; -, mRNA.  
DR HSSP; P35555; IEMN.  
DR GO; GO:0005509; F:Calcium ion binding; IEA.  
DR InterPro; IPR000152; Aex\_hydroxyl\_S.  
DR InterPro; IPR000859; CUB\_2.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR011641; GCC2\_GCC3.  
DR InterPro; IPR006210; IBGF.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 5.  
DR Pfam; PF07645; EGF\_CA; 4.  
DR Pfam; PF07699; GCC2\_GCC3; 3.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 10.  
DR SMART; SM00179; EGF\_CA; 7.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 6.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS01186; EGF\_2; 7.  
DR PROSITE; PS50026; EGF\_3; 6.  
DR PROSITE; PS01187; EGF\_CA; 6.  
SQ SEQUENCE 992 AA; 109165 MW; 24093050738932E1 CRC64;  
  
Query Match 29.6%; Score 59.5; DB 2; Length 992;  
Best Local Similarity 28.9%; Pred. No. 47;  
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;  
  
QY 1 CSQNEYFDSLHACIPCOL-----RCSNT 25  
DB 748 CSFGHYNTSIHRCIRCMGSGYQDFRQNFCSRCPGNT 785  
  
RESULT 39  
Q8IX30\_HUMAN PRELIMINARY; PRT; 993 AA.  
AC Q8IX30;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE CUB and EGF containing protein (Signal peptide, CUB and EGF-like  
DE domain containing protein 3 precursor) (ORFTHUMP00000016250).  
GN Name=SCUBE3; Synonyms=CEGF3; ORFNames=RP3-329A5.4-001;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Pfarr N., Bahr A., Cichutek A., Loebbert R., Zabel B.U., Schmidt E.R.,  
RA Hankeln T., Winterpacht A.;  
RT "Novel human gene family (CEGF) encoding mosaic proteins with EGF-  
RT like, SVT2R and a CUB module: cloning and expression analysis.";  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
[2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15234972; DOI=10.1074/jbc.M405912200;  
RA Wu B.T., Su Y.H., Tsai M.T., Wasserman S.M., Topper J.N., Yang R.B.;  
RT "A novel secreted, cell-surface glycoprotein containing multiple  
RT epidermal growth factor-like repeats and one CUB domain is highly  
RT expressed in primary osteoblasts and bones.";  
RL J. Biol. Chem. 279:37485-37490(2004).  
[3]

RP NUCLEOTIDE SEQUENCE.  
RA Williams S.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF452494; AAN76808.1; -, mRNA.  
DR EMBL; AY639608; AAU08347.1; -, mRNA.  
DR EMBL; Z97832; CAI20187.1; -, Genomic\_DNA.  
DR HSSP; P35555; IEMN.  
DR Ensembl; ENSG00000146197; Homo sapiens.  
DR HGNC; HGNC:13655; SCUBE3.  
DR GO; GO:0005509; F:Calcium ion binding; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000859; CUB\_2.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR011641; GCC2\_GCC3.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 6.  
DR Pfam; PF07645; EGF\_CA; 3.  
DR Pfam; PF07699; GCC2\_GCC3; 3.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00179; EGF\_CA; 6.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 6.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS01186; EGF\_2; 7.  
DR PROSITE; PS50026; EGF\_3; 6.  
DR PROSITE; PS01187; EGF\_CA; 6.  
KW Signal.  
FT SIGNAL  
SQ SEQUENCE 993 AA; 109282 MW; 19BBE0E5627EEAF4 CRC64;  
  
Query Match 29.6%; Score 59.5; DB 2; Length 993;  
Best Local Similarity 28.9%; Pred. No. 47;  
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;  
  
QY 1 CSQNEYFDSLHACIPCOL-----RCSNT 25  
DB 749 CSFGHYNTSIHRCIRCMGSGYQDFRQNFCSRCPGNT 786  
  
RESULT 40  
QSHYA8\_HUMAN PRELIMINARY; PRT; 995 AA.  
AC QSHYA8;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Hypothetical protein DKFZp686F1937.  
GN Name=DKFZp686F1937;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RG The German cDNA Consortium;  
RA Bahr A., Lauber J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,  
RA Han M., Wiemann S.;  
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX648768; CAI45999.1; -, mRNA.  
DR InterPro; IPR000150; Hypothet\_cof.  
DR PROSITE; PS01228; COF\_1; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 995 AA; 111730 MW; AEBD4A6B84F759A8 CRC64;  
  
Query Match 29.6%; Score 59.5; DB 2; Length 995;  
Best Local Similarity 21.6%; Pred. No. 47;  
Matches 11; Conservative 9; Mismatches 12; Indels 19; Gaps 1;  
  
QY 1 CSQNEYFDSLHACIPC-----QLRCSNTPTLTCOR 32



Db 49 CDNNQYFDISALSCVPCGANQRDAGTSCVCLPGFMISNNGPALICK 99

RESULT 41  
Q4SAQ3\_TETNG PRELIMINARY; PRT; 184 AA.

ID Q4SAQ3\_TETNG PRELIMINARY; PRT; 184 AA.  
AC Q4SAQ3;  
DT 13-SEP-2005 (TEMBLrel. 31, Created)  
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)  
DE Chromosome 2 SCFA174738, whole genome shotgun sequence.  
ORFNames=GSTENG0024082001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontoidea; Tetraodontidae; Tetraodon.  
OX NCBI\_TaxID=99883;  
RN [1]  
NP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.-M., Brunet F., Petit J.L., Stange-Thomann M.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Cottier L., Poullain J., De Bernardis V.,  
RA Cruaud C., Duprat S., Bottier P., Coutanceau J.P., Gousy J.,  
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RP [2]  
NP NUCLEOTIDE SEQUENCE.  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAAB01014738; CAG04379.1; -- Genomic DNA.  
SQ SEQUENCE 184 AA; 1913 MW; 3B2167E5E4FB1BB7 CRC64;

Query Match 29.4%; Score 59; DB 2; Length 184;  
Best Local Similarity 27.3%; Pred. No. 9.7;  
Matches 9; Conservative 10; Mismatches 4; Indels 10; Gaps 1;  
  
Oy 1 CSONEYFDSLHACTPQLCRSSNTPLPTCORY 33  
|||:::|::|::|:  
Db 94 CSSSEFFNSDDVCVPCE-----SCKKY 116  
  
RESULT 42  
Q9GYR5\_CAEEL PRELIMINARY; PRT; 937 AA.  
ID Q9GYR5\_CAEEL PRELIMINARY; PRT; 937 AA.  
AC Q9GYR5;  
DT 01-MAR-2001 (TEMBLrel. 16, Created)  
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TEMBLrel. 26, Last annotation update)  
DE Hypothetical protein C23G10.8.  
GN ORFNames=C23G10.8;  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabdittida; Rhabditoidea;  
OC Rhabdittidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
NP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=Bristol N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RG The C. elegans sequencing consortium;  
RT "Genome sequence of the nematode C. elegans: a platform for



Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalao D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smillius D.E., Schnerch A., Schein J.Z., Jones S.J.M., Maier M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Director MGC Project;  
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC079849; AAH79849.1; -; mRNA.  
MGI; MGI:3045253; Scube3.  
GO; GO:0005509; Fcalcium ion binding; IEA.  
DR InterPro; IPR000152; Asx\_hydroxyl\_S.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR011641; GCC2\_GCC3.  
DR InterPro; IPR006210; IEGF.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 5.  
DR Pfam; PF07645; EGF\_CA; 3.  
DR Pfam; PF07699; GCC2\_GCC3; 2.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 9.  
DR SMART; SM00179; EGF\_CA; 7.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 5.  
DR PROSITE; PS01180; CUB\_1.  
DR PROSITE; PS01186; EGF\_2; 6.  
DR PROSITE; PS00026; EGF\_3; 4.  
DR PROSITE; PS01187; EGF\_CA; 4.  
KW EGF-like domain.  
FT NON TER 1 1  
SQ SEQUENCE 827 AA; 90870 MW; DF6BB3337B4CE91D CRC64;

Query Match 29.1%; Score 58.5; DB 2; Length 827;  
Best Local Similarity 28.9%; Pred. No. 53;  
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;  
  
QY 1 CSQNEYFDLSLLHACIPCQL-----RCSNNT 25  
Db 611 CSPGHYYNTSIHRCAVGSYPDFRQNFRCTRCPGNT 648  
|:::|||||:  
|||

RESULT 46  
Q66PY1\_MOUSE PRELIMINARY; PRT; 993 AA.  
AC Q66PY1;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Signal peptide, CUB and EGF-like domain containing protein 3 precursor.  
DE Name=Scube3; Synonyms=SCUBE3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
RN PRELIMINARY NUCLEOTIDE SEQUENCE.



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RC STRAIN=C57BL/6;
RX PubMed=15234972; DOI=10.1074/jbc.M405912200; Topper J.N., Yang R.B.;
RA Wu B.F., Su Y.H., Tsai M.T., Wasserman S.M.;
RT "A novel secreted, cell-surface glycoprotein containing multiple
RT epidermal growth factor-like repeats and one CUB domain is highly
RT expressed in primary osteoblasts and bones.";
RL J. Biol. Chem. 279.37485-37490(2004).
DR EMBL; AY39609; AAU08348.1; -; mRNA.
DR MGI; MGI:3045253; Scubes.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR00152; ASx hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR011641; GCC2_GCC3.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF07645; EGF_CA; 4.
DR Pfam; PF07699; GCC2_GCC3; 3.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 10.
DR SMART; SM00179; EGF_CA; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 6.
KW Signal.
FT SIGNAL
FT SIGNAL
SQ SEQUENCE 993 AA; 108983 MW; E43989ACACCC345F CRC64;

Query Match 29.1%; Score 58.5; DB 2; Length 993;
Best Local Similarity 28.9%; Pred. No. 63;
Matches 11; Conservative 5; Mismatches 9; Indels 13; Gaps 1;

Qy 1 CSQNEYFDLLHACIPCOL-----RCSSNT 25
Db 749 CSPGHYNTSIHRCIRCAVGSQPDFRQNFCTRCPGNT 786

RESULT 47
ID QBRI19_MOUSE PRELIMINARY; PRT; 101 AA.
AC QBRI19;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
DE enriched library, clone:B230316E19 product:hypothetical protein, full
DE insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa K., Hara A., Fukuishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Batsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita P., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohleuli S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagasaki S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Tota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
KW Hypothetical protein.
SQ SEQUENCE 101 AA; 11571 MW; E899420B6F215D23 CRC64;

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Query Match 28.9%; Score 58; DB 2; Length 101;
Best Local Similarity 31.9%; Pred. No. 7.1;
Matches 15; Conservative 5; Mismatches 9; Indels 18; Gaps 2;

Qy 6 YFDSLLHACIPPC-----QRCSSNTTP-----ITCQRYC 34
Db 4 YFNSLLFLSLFCFKRLTLRLCTSHPPPPPPPPPPSHSLACGYC 50

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RESULT 51
Q26489_SPOFR Q26489_SPOFR PRELIMINARY; PRT; 1299 AA.
ID ID
AC Q26489;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Endoprotease FURIN.
GN Name=FURIN;
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Amphipyridinae; Spodoptera.
NCBI_TaxID=7108;
[1]
RN NUCLEOTIDE SEQUENCE.
RP RCP TISSUE=sf9;
RA Cieplik M., Klenk H.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; Z68886; CAA93116.1; -; mRNA.
DR PIR; T43251; T43251.
DR HSSP; P23188; 1P8J.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . ; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR002029; Pept S8 S53.
DR InterPro; IPR002884; PrprotcnconvertSP.
DR Pfam; PF01483; P_proprotein; 1.
DR Pfam; PF00082; Peptidase S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR SMART; SMO0261; FU; 10.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN_1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
SQ SEQUENCE. 1299 AA; 142020 MW; 4C3799C7BBC572AB CRC64;

Query Match 28.9%; Score 58; DB 2; Length 1299;
Best Local Similarity 37.1%; Pred. No. 97;
Matches 13; Conservative 5; Mismatches 9; Indels 8; Gaps

Oy 1 CSONEVFDSLHACIFCQLRCS-----SNTPLTC 30
||| ||| ||| ||| ||| ||| |||
Db 1150 CSRPLRIDRLNNQCVC---CSERGVTNSTPTDTC 1181

RESULT 52
ICEI_ASCSU ICEI_ASCSU STANDARD; PRT; 63 AA.
ID ID
AC P07851; O77419;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Chymotrypsin/elastase isoform inhibitor 1 (C/E-1 inhibitor) (ASC/B-1).
OS Ascaris suum (pig roundworm) (Ascaris lumbricoidea).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
OC Ascaridae; Ascaris.
NCBI_TaxID=6253;
[1]
RN NUCLEOTIDE SEQUENCE.
RP RCP PROTEIN SEQUENCE.
RA MEDLINE=84255715; PubMed=6564898;
RX Babin D.R., Peanasky R.J., Goos S.M.;
RT "The isoforms of chymotrypsin/elastase from Ascaris lumbricoidea:
the primary structure.";
RL Arch. Biochem. Biophys. 232:143-161 (1984).
[2]
RN NUCLEOTIDE SEQUENCE.

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RX MEDLINE=98297373; PubMed=9635450; DOI=10.1006/expr.1998.4284;
RA Lu C.C., Nguyen T., Morris S., Hill D., Sakanari J.A.;
RT "Anisakis simplex: mutational bursts in the reactive site centers of
RL serine protease inhibitors from an ascarid nematode.";
RN Exp. Parasitol. 89:257-261(1998).
RP [3]
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.
RA MEDLINE=95006335; PubMed=7922044;
RA Huang K., Strynadka N.C., Bernard V.D., Penaskey R.J., James M.N.;
RT "The molecular structure of the complex of Ascaris
RL chymotrypsin/elastase inhibitor with porcine elastase.";
RN Structure 2:679-689(1994).
CC -|- FUNCTION: Defends the organism against the host's proteinases.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Contains 1 TIL (trypsin inhibitory-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U94499; AAC61300.1; -; mRNA.
CC PDB; 1EAI; X-ray; C/D=1-61.
CC InterPro; IPR002919; Prot_Inh_CR_TIL.
CC Pfam; PF01826; TIL; 1.
KW 3D-structure; direct protein sequencing; Protease inhibitor;
KW Serine protease inhibitor.
FT DOMAIN 5 60 TIL.
FT SITE 31 32 Reactive bond.
FT DISULFID 5 38
FT DISULFID 14 33
FT DISULFID 17 29
FT DISULFID 21 60
FT DISULFID 40 54
FT CONFLICT 4 4
FT CONFLICT 23 24
FT TURN 3 4
FT TURN 7 8
FT STRAND 10 12
FT STRAND 15 15
FT STRAND 20 20
FT TURN 25 26
FT STRAND 28 30
FT STRAND 34 34
FT STRAND 37 39
FT HELIX 42 44
FT TURN 45 45
FT STRAND 46 48
FT TURN 50 51
FT STRAND 54 56
FT HELIX 57 59
SQ SEQUENCE 63 AA; 6862 MW; 5DC10DE75B375F16 CRC64;

Query Match 28.6%; Score 57.5; DB 1; Length 63;
Best Local Similarity 37.1%; Pred. No. 5.1;
Matches 13; Conservative 5; Mismatches 10; Indels 7; Gaps 3;

QY 1 CSQNEYFDSLHACIPQLRC--SSNTP-PLTCOR 32
Db | | | | | | | | | | | | | | | | |
5 CGNEVWTE---CTGCMKGGPDENTPCPLMCR 35

RESULT 53
Q5BI10 DROME PRELIMINARY; PRT; 1061 AA.
AC Q5BI10;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE LD05524p.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
```

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OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT021414; AAX33562.1; -; mRNA.
DR InterPro; IPR010980; Cyt_c_b562.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR012286; FCC3 N cyt.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR011025; GproteinA_insert.
DR InterPro; IPR012287; Homeodomain-rel.
DR InterPro; IPR006210; IEGP.
DR InterPro; IPR010503; LT-11B.
DR InterPro; IPR002186; NCS-type chromop.
DR InterPro; IPR000070; Pectinesterase.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR004094; Prot_inh_antistn.
DR InterPro; IPR002884; Ppilotnconvertsp.
DR InterPro; IPR008919; Retrov_capsid_N.
DR Pfam; PF01483; P_protein; 1.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
DR SEQUENCE 1061 AA; 115699 MW; 4E71FC5388FF229 CRC64;

Query Match 28.6%; Score 57.5; DB 2; Length 1061;
Best Local Similarity 34.3%; Pred. No. 92;
Matches 12; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

QY 1 CSQNEYFDSLHACIPQLRCSS-NTPPLTCORYC 34
Db | | | | | | | | | | | | | | | | |
580 CSESEFYSQVQCRPCPCGSCGNGPDTCTSC 614

RESULT 54
FUR2 DROME
ID FUR2 DROME STANDARD; PRT; 1679 AA.
AC P30432; Q24301; Q8SZS2;
DT 01-APR-1993 (Rel. 25, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Furin-like protease 2 precursor (EC 3.4.21.75) (Furin-2).
GN Names=Fur2; ORFNames=CG18734;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM D).
RC STRAIN=iso-1; Oregon-R, and Tuebingen;
RX MEDLINE=92381036; PubMed=1512259;
RA Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dunke U.,
RA Roebroek M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.M.;
RT "Cloning and functional expression of Dfurin2, a subtilisin-like
RT proprotein processing enzyme of Drosophila melanogaster with multiple
RT repeats of a cysteine motif.";
RL J. Biol. Chem. 267:17208-17215(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM D).
RC STRAIN=iso-1;
RX MEDLINE=95186060; PubMed=7880443;
RA Roebroek A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L.,
RA van de Ven W.J.M.;
RT "The Dfur2 gene of Drosophila melanogaster: genetic organization,
RT expression during embryogenesis, and pro-protein processing activity
RT of its translational product Dfurin2.";
RL DNA Cell Biol. 14:223-234(1995).
```



[3] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
STRAIN=Berkeley; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celnikner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin N.L., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.J., Pacle J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:2185-2195 (2000).  
[4] GENOME REANNOTATION, AND ALTERNATIVE SPLICING.  
RX MEDLINE=22426069; PubMed=12537572;  
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
RA Hradecky P., Huang Y., Kinkler J.S., Millburn G.H., Prochkin S.E.,  
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
RA Bettencourt B.R., Celnikner S.E., de Grey A.D.N.J., Drysdale R.A.,  
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.;  
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
systematic review."  
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).  
[5] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 305-1679 (ISOFORM A).  
RX MEDLINE=22426066; PubMed=12537569;  
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,  
RA George R.A., Guarin H., Krommiller B., Pacle J.M., Park S., Wan K.H.,  
RA Rubin G.M., Celnikner S.E.;  
RT "A *Drosophila* full-length cDNA resource."  
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).  
CC -!- FUNCTION: Furin is likely to represent the ubiquitous endoprotease  
activity within constitutive secretory pathways and capable of  
cleavage at the RX(K/R)R consensus motif (By similarity).  
CC -!- CATALYTIC ACTIVITY: Release of mature proteins from their  
precursors by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa  
can be any amino acid and Yaa is Arg or Lys. Releases albumin,  
complement component C3 and von Willebrand factor from their  
respective precursors.  
CC -!- INTERACTION:







```
DR GO; GO:0008061; F:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin_bind_PeA.
DR InterPro; IPR006149; EB_region.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR003571; Snake_toxin.
DR InterPro; IPR006150; Worm_repeat_1.
DR Pfam; PF01607; CBM_14; 2.
DR Pfam; PF01683; EB; 1.14.
DR SMART; SMO0289; WRI; 14.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
DR PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
DR KW Hypothetical protein.
DR SEQUENCE 919 AA; 96816 MW; B3EFC096CE53DFD CRC64;

Query Match 28.4%; Score 57; DB 2; Length 919;
Best Local Similarity 34.4%; Pred. No. 92;
Matches 11; Conservative 7; Mismatches 12; Indels 2; Gaps 1;

Qy 1 CSQNEYFDSLHACIPQLR--CSNTPTPLTC 30
Db 164 CSQSTVFNAELSCVPLAIONSCDSSTQQPVC 195

RESULT 58
Q7R165 GIALA
ID Q7R165 GIALA PRELIMINARY; PRT; 1210 AA.
AC Q7R165;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE GLP_447_61408.57776.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OC NCBI_TaxID=184922;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G.; McArthur A.G.; Adam R.D.; Alley S.B.; Gillin F.D.;
RA Olsen G.J.; Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000029; EAA41074.1; -; Genomic_DNA.
DR HSSP; P25963; 1IKN.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; Ank; 20.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 2.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR ANK repeat; Repeat.
SQ SEQUENCE 1210 AA; 132501 MW; 0AC83EEA78A5D726 CRC64;

Query Match 28.4%; Score 57; DB 2; Length 1210;
Best Local Similarity 35.7%; Pred. No. 1.2e+02;
Matches 15; Conservative 4; Mismatches 9; Indels 14; Gaps 2;

Qy 1 CSQNEYFDSLH-----ACIPC-----QLRCSSNTPTPL 28
Db 549 CIRNNGYDTHALHIAVASKSFACIPCLAAVEAIRDSHNRNAL 590

RESULT 59
Q26566 SCHMA
ID Q26566 SCHMA PRELIMINARY; PRT; 1717 AA.
AC Q26566;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Epidermal growth factor receptor precursor.
GN Name=SER;

OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Puerto Rican;
RC MEDLINE=92365727; PubMed=1501637; DOI=10.1016/0166-6851(92)90003-3;
RA Shoemaker C.B.; Ramachandran H.; Landa A.; dos Reis M.G.; Stein L.;
RT "Alternative splicing of the Schistosoma mansoni gene encoding a
RT homologue of epidermal growth factor receptor.";
RL Mol. Biochem. Parasitol. 53:17-32(1992).
DR EMBL; M86396; AAA29866.1; -; mRNA.
DR PIR; A45558; A45558.
DR HSP; P11362; IFGK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005824; P:ATP binding; IEA.
DR GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA.
DR InterPro; IPR000494; EGFR_L.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008265; Tyr_kinase_AS.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00757; Furin-like; 2.
DR Pfam; PF01030; Recep_L domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SMO0261; FU; 6.
DR SMART; SMO0219; TyKc; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
DR Receptor; Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 1717 epidermal growth factor receptor.
SQ SEQUENCE 1717 AA; 192303 MW; 1101A338C1653D8C CRC64;

Query Match 28.4%; Score 57; DB 2; Length 1717;
Best Local Similarity 40.9%; Pred. No. 1.8e+02;
Matches 9; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CSQNEYFDSLHACIPQLRCS 22
Db 646 CPRNTYIDPQTRHCLPCNCS 667

RESULT 60
Q8WRF4 MONBE
ID Q8WRF4 MONBE PRELIMINARY; PRT; 1476 AA.
AC Q8WRF4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Receptor tyrosine kinase.
GN Name=MBRTK1;
OS Monosiga brevicollis.
OC Eukaryota; Choanoflagellida; Codonosigidae; Monosiga.
OX NCBI_TaxID=81824;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ATCC 50154;
RC MEDLINE=21625102; PubMed=11752452; DOI=10.1073/pnas.261477698;
RA King N.; Carroll S.B.;
RT "A receptor tyrosine kinase from choanoflagellates: molecular insights
RT into early animal evolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:15032-15037(2001).
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ATCC 50154;
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SQ SEQUENCE 341 AA; 38046 MW; 62BB8F5059125A2B CRC64;

Query Match 27.9%; Score 56; DB 2; Length 341;
Best Local Similarity 29.4%; Pred.No.45;
Matches 10; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 CSQNEYFDLSLLHACIPQLCRCSSTNTPLTQCQYC 34
   ::::|::|::|::|::|::|::|::|::|::|::|
Db 60 CNEREWESQLIRSLPEHGVRCPSQLAPIPFQNYC 93

RESULT 66
Q9PVD4_XENLA PRELIMINARY; PRT; 387 AA.
ID Q9PVD4_XENLA PRELIMINARY; PRT; 387 AA.
AC Q9PVD4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE p75-like transmembrane protein fullback (Neurotrophin receptor-related
DE protein la).
DE Name=NRHla;
GN Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_TaxID=8355;
[1]
RN NCLEOTIDE SEQUENCE.
RP Hick E., Sun B.I., Collins-Racie L., Lavallie E., Sive H.L.;
RA Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
RL [2]
RN NCLEOTIDE SEQUENCE.
RX PubMed=15258592; DOI=10.1038/ncbl1158;
RA Sasai N., Nakazawa Y., Haraguchi T., Sasai Y.;
RT "The neurotrophin-receptor-related protein NRH1 is essential for
RT convergent extension movements.";
RT Nat. Cell Biol. 6:741-748(2004).
DR EMBL; AF131890; AAD54072.1; -; mRNA.
DR EMBL; AB162703; BAD36761.1; -; mRNA.
DR HSSP; P07174; INGR.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
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DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
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QY 32 RYC 34
Db 162 TEC 164

RESULT 67
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FT DISULFID 2392 2401 By similarity.  
FT CONFLICT 823 823 C -> V (in Ref. 1; AA sequence).  
FT CONFLICT 923 923 S -> Y (in Ref. 1; AA sequence).  
FT CONFLICT 965 965 W -> Y (in Ref. 1; AA sequence).  
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DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Polyprotein (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN NUCLEOTIDE SEQUENCE.  
RA Shinzawa H., Shao L., Jiang Q., Togashi H., Zhang X., Ishibashi M.,  
RA Watanabe H., Saio T., Takahashi T., Ohba K., Mizokami M.,  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB030968; BAB11770.1; -; Genomic RNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR CO; GO:0019031; C:viral envelope; IEA.  
DR InterPro; IPR002519; HCVenv.  
DR Pfam; PF01539; HCV\_env; I.  
KW Envelope protein; Polyprotein; Transmembrane.  
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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
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GN ORFNames=CG7114;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
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RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
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RN NUCLEOTIDE SEQUENCE.  
RP MEDLINE=22426065; PubMed=12537568;  
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RP MEDLINE=22426069; PubMed=12537572;  
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RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
RA Lewis S.E.,  
RT "Annotation of the Drosophila melanogaster euchromatic genome: a







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OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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RT "Complete sequencing and characterization of 21,243 full-length human  
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RL Nat. Genet. 36:40-45(2004).  
DR EMBL; AK056571; BAB71219.1; -; mRNA.  
DR HSSP; P00743; 1CCP.  
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117	44	15.5	1255	7	US-11-113-202-10	Sequence 10, Appl	190	41	14.5	769	7	US-11-107-028-5	Sequence 5, Appl1
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143	43	15.2	1368	6	US-10-995-561-539	Sequence 539, App	216	40	14.1	47	7	US-11-000-463-408	Sequence 408, App
144	43	15.2	2725	7	US-11-113-424-52	Sequence 52, Appl	217	40	14.1	161	7	US-11-113-424-38	Sequence 38, Appl
145	42.5	15.0	160	6	US-10-846-172A-10	Sequence 10, Appl	218	40	14.1	196	6	US-10-995-561-579	Sequence 579, App
146	42.5	15.0	338	6	US-10-632-150-12	Sequence 12, Appl	219	40	14.1	219	6	US-10-995-561-580	Sequence 580, App
147	42.5	15.0	338	7	US-11-073-457-12	Sequence 12, Appl	220	40	14.1	250	6	US-10-131-826A-320	Sequence 320, App
148	42.5	15.0	338	7	US-11-073-460-12	Sequence 12, Appl	221	40	14.1	297	6	US-10-467-657-8438	Sequence 8438, Ap
149	42.5	15.0	526	6	US-10-606-302-5	Sequence 5, Appl1	222	40	14.1	334	6	US-10-995-561-822	Sequence 822, App
150	42.5	15.0	526	6	US-10-606-302-7	Sequence 7, Appl1	223	40	14.1	379	6	US-10-763-712A-40	Sequence 40, Appl
151	42.5	15.0	755	7	US-11-067-121-6	Sequence 6, Appl1	224	40	14.1	397	6	US-10-878-556A-165	Sequence 165, App
152	42.5	15.0	886	6	US-10-821-234-1390	Sequence 1390, Ap	225	40	14.1	414	6	US-10-131-826A-418	Sequence 418, App
153	42.5	15.0	1121	7	US-11-113-751-24	Sequence 24, Appl	226	40	14.1	418	6	US-10-312-954-4	Sequence 4, Appl1
154	42.5	15.0	1159	7	US-11-113-751-27	Sequence 27, Appl	227	40	14.1	421	6	US-10-763-712A-13	Sequence 13, Appl
155	42	14.8	26	6	US-10-967-527A-6	Sequence 6, Appl1	228	40	14.1	421	6	US-10-763-712A-41	Sequence 41, Appl
156	42	14.8	148	6	US-10-467-657-5478	Sequence 5478, Ap	229	40	14.1	447	6	US-10-632-150-10	Sequence 10, Appl
157	42	14.8	184	6	US-10-742-634-5	Sequence 5, Appl1	230	40	14.1	447	7	US-11-073-457-10	Sequence 10, Appl
158	42	14.8	184	6	US-10-967-527A-5	Sequence 5, Appl1	231	40	14.1	447	7	US-11-073-460-10	Sequence 10, Appl
159	42	14.8	211	6	US-10-980-388-97	Sequence 97, Appl	232	40	14.1	488	6	US-10-995-561-860	Sequence 860, App
160	42	14.8	235	7	US-11-126-126-16	Sequence 16, Appl	233	40	14.1	727	6	US-10-995-561-864	Sequence 864, App
161	42	14.8	333	6	US-10-980-388-119	Sequence 119, App	234	40	14.1	782	6	US-10-995-561-861	Sequence 861, App
162	42	14.8	379	6	US-10-131-826A-308	Sequence 308, App	235	40	14.1	847	6	US-10-995-561-863	Sequence 863, App
163	42	14.8	444	7	US-11-029-003-16	Sequence 16, Appl	236	40	14.1	847	6	US-10-995-561-865	Sequence 865, App
164	42	14.8	461	7	US-11-132-285-6	Sequence 6, Appl1	237	39.5	14.0	72	6	US-10-467-657-4880	Sequence 4880, Ap
165	42	14.8	461	7	US-11-182-946-4	Sequence 4, Appl1	238	39.5	14.0	95	6	US-10-131-826A-62	Sequence 62, Appl
166	42	14.8	631	6	US-10-995-561-546	Sequence 546, App	239	39.5	14.0	118	7	US-11-116-144-158	Sequence 158, App
167	42	14.8	820	7	US-11-147-047-31	Sequence 31, Appl	240	39.5	14.0	143	6	US-10-821-234-1216	Sequence 1216, Ap
168	42	14.8	2644	6	US-10-770-726-45	Sequence 45, Appl	241	39.5	14.0	255	6	US-10-793-626-1304	Sequence 1304, Ap
169	41.5	14.7	395	7	US-11-075-185-13	Sequence 13, Appl	242	39.5	14.0	348	6	US-10-793-626-1702	Sequence 1702, Ap
170	41.5	14.7	830	6	US-10-995-561-899	Sequence 899, App	243	39.5	14.0	351	6	US-10-793-626-338	Sequence 338, App
171	41.5	14.7	842	6	US-10-645-441-2	Sequence 2, Appl1	244	39.5	14.0	386	6	US-10-131-826A-340	Sequence 340, App







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; LENGTH: 40
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(40)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-9

Query Match      81.3%; Score 230; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 9.4e-23;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASV 45
DB      1 GQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASV 40

RESULT 4
US-10-967-527A-10
; Sequence 10, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 185
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-10

Query Match      64.0%; Score 181; DB 6; Length 185;
Best Local Similarity 70.8%; Pred. No. 4.7e-16;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

QY      4 MAQCQSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 51
DB      1 MAQCQCFHSEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTNSVKG 46

RESULT 5
US-10-967-527A-21
; Sequence 21, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 249
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-21

Query Match      25.3%; Score 71.5; DB 6; Length 249;
Best Local Similarity 35.3%; Pred. No. 0.025;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYC 41
DB      6 CPKQDYWDSSRRKSCVSCALTCQRS-QRTCTDFC 38

RESULT 6
US-10-967-527A-20
; Sequence 20, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 48
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(48)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-20

Query Match      23.9%; Score 67.5; DB 6; Length 48;
Best Local Similarity 30.6%; Pred. No. 0.018;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNA 43
DB      13 CPEQYWDPLLGTCTCMCKTICNHQS-QRTCAAFCS 47

RESULT 7
US-10-967-527A-19
; Sequence 19, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 292
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-19

Query Match      23.9%; Score 67.5; DB 6; Length 292;
Best Local Similarity 30.6%; Pred. No. 0.092;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNA 43
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Query Match          22.3%; Score 63; DB 6; Length 175;
Best Local Similarity 50.0%; Pred. No. 0.21;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 QCSQNEYFDLSLHACIPCOL 26
Db 21 QCNQTECFDPLVRNCVSCEL 40

RESULT 12
US-11-110-082-30
; Sequence 30, Application US/111110082
; Publication No. US200502366558A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Hall, Claire
; APPLICANT: Norriss, Michael Geoffrey
; APPLICANT: Saulebury, Keith Martin
; TITLE OF INVENTION: Compositions Isolated from Forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.1074UC1
; CURRENT APPLICATION NUMBER: US/11/110,082
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/563,723
; PRIOR FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: 10/655,799
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: 60/408,782
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1149
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-11-110-082-30

Query Match          19.6%; Score 55.5; DB 7; Length 1149;
Best Local Similarity 29.7%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 14 FDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVK 50
Db 632 FDSYVLAAV-CALSCELQFLPILCKNVTKSNIKDSIK 667

RESULT 13
US-10-995-561-1016
; Sequence 1016, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1016
; LENGTH: 3690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1016

Query Match          19.6%; Score 55.5; DB 6; Length 3690;
Best Local Similarity 26.7%; Pred. No. 29;
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 7 QCSQNEYFD---SLHACIPCO-----LRCSNTPPLTCQRYCNASVTNS 48
Db 1844 ECAPGFYRDVKGLFLGRVCPCQCHGHSRCLPLSGVGVCDQHNTGHAHCE-CQAGFVSS 1902

Query Match          22.3%; Score 63; DB 6; Length 175;
Best Local Similarity 50.0%; Pred. No. 0.21;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 QCSQNEYFDLSLHACIPCOL 26
Db 21 QCNQTECFDPLVRNCVSCEL 40

RESULT 12
US-11-110-082-30
; Sequence 30, Application US/111110082
; Publication No. US200502366558A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Hall, Claire
; APPLICANT: Norriss, Michael Geoffrey
; APPLICANT: Saulebury, Keith Martin
; TITLE OF INVENTION: Compositions Isolated from Forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.1074UC1
; CURRENT APPLICATION NUMBER: US/11/110,082
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/563,723
; PRIOR FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: 10/655,799
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: 60/408,782
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 1149
; TYPE: PRT
; ORGANISM: Festuca arundinacea
US-11-110-082-30

Query Match          19.6%; Score 55.5; DB 7; Length 1149;
Best Local Similarity 29.7%; Pred. No. 10;
Matches 11; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 14 FDSLHACIPCOLRCSNTPPLTCQRYCNASVTNSVK 50
Db 632 FDSYVLAAV-CALSCELQFLPILCKNVTKSNIKDSIK 667

RESULT 13
US-10-995-561-1016
; Sequence 1016, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1016
; LENGTH: 3690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1016

Query Match          19.6%; Score 55.5; DB 6; Length 3690;
Best Local Similarity 26.7%; Pred. No. 29;
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 7 QCSQNEYFD---SLHACIPCO-----LRCSNTPPLTCQRYCNASVTNS 48
Db 1844 ECAPGFYRDVKGLFLGRVCPCQCHGHSRCLPLSGVGVCDQHNTGHAHCE-CQAGFVSS 1902

Query Match          19.6%; Score 55.5; DB 6; Length 3714;
Best Local Similarity 26.7%; Pred. No. 29;
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 7 QCSQNEYFD---SLHACIPCO-----LRCSNTPPLTCQRYCNASVTNS 48
Db 1845 ECAPGFYRDVKGLFLGRVCPCQCHGHSRCLPLSGVGVCDQHNTGHAHCE-CQAGFVSS 1903

RESULT 15
US-10-821-234-1076
; Sequence 1076, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1076
; LENGTH: 3717
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1076

Query Match          19.6%; Score 55.5; DB 6; Length 3717;
Best Local Similarity 26.7%; Pred. No. 29;
Matches 16; Conservative 6; Mismatches 19; Indels 19; Gaps 3;

QY 7 QCSQNEYFD---SLHACIPCO-----LRCSNTPPLTCQRYCNASVTNS 48
Db 1866 ECAPGFYRDVKGLFLGRVCPCQCHGHSRCLPLSGVGVCDQHNTGHAHCE-CQAGFVSS 1924

RESULT 16
US-11-108-172-1116
; Sequence 1116, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
```



APPLICANT: Stolk, John A.  
APPLICANT: Wang, Tongtong  
APPLICANT: Jiang, Yugu  
APPLICANT: Smith, Carole L.  
APPLICANT: King, Gordon E.  
APPLICANT: Wang, Aijun  
APPLICANT: Clapper, Jonathan D.  
APPLICANT: Skeiky, Yasir A. W.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Vedvick Thomas S.  
APPLICANT: Carter, Darrick  
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE  
FILE REFERENCE: 210121.471C15  
CURRENT APPLICATION NUMBER: US/11/108,172  
CURRENT FILING DATE: 2005-04-15  
PRIOR APPLICATION NUMBER: US 10/025,380  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: US 09/922,217  
PRIOR FILING DATE: 2001-08-03  
PRIOR APPLICATION NUMBER: US 09/833,263  
PRIOR FILING DATE: 2001-04-10  
PRIOR APPLICATION NUMBER: US 09/649,811  
PRIOR FILING DATE: 2000-08-28  
PRIOR APPLICATION NUMBER: US 09/609,448  
PRIOR FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: US 09/575,251  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: US 09/519,444  
PRIOR FILING DATE: 2000-03-06  
PRIOR APPLICATION NUMBER: US 09/504,629  
PRIOR FILING DATE: 2000-02-15  
PRIOR APPLICATION NUMBER: US 09/480,321  
PRIOR FILING DATE: 2000-01-10  
PRIOR APPLICATION NUMBER: US 09/476,296  
PRIOR FILING DATE: 1999-12-30  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 1130  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1116  
LENGTH: 5405  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-108-172-1116  
Query Match 19.6%; Score 55.5; DB 7; Length 5405;  
Best Local Similarity 33.3%; Pred. No. 41;  
Matches 12; Conservative 6; Mismatches 13; Indels 5; Gaps 2;  
Qy 7 QCSQNEYFDSLHACI-PCOLRCSSNTPPLTCQRYC 41  
Db 2732 ECPQNSHYE----LCADTCSLGCALSAPLQCPDGC 2763  
RESULT 17  
US-11-153-880-4  
Sequence 4, Application US/11153880  
Publication No. US20050256050A1  
GENERAL INFORMATION:  
APPLICANT: HU, JING-SHAN  
APPLICANT: ROSEN, CRAIG A.  
APPLICANT: CAO, LIANG  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 NEW YORK AVENUE  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM: Floppy disk  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/153,880  
FILING DATE: 16-Jun-2005  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/219,442  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/999,811  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MARKOWICZ, KAREN R.  
REGISTRATION NUMBER: 36,351  
REFERENCE/DOCKET NUMBER: 1488.1000004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-11-153-880-4  
Query Match 19.3%; Score 54.5; DB 7; Length 350;  
Best Local Similarity 35.0%; Pred. No. 4.5;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;  
Qy 7 QCSQNEYFDSLHACI-PCOLRCSSNTP--PLTCQRYCNAS 44  
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296  
RESULT 18  
US-11-064-769-2  
Sequence 2, Application US/11064769  
Publication No. US20050256075A1  
GENERAL INFORMATION:  
APPLICANT: Alitalo, Kari  
APPLICANT: Yl-Herttuala, Seppo  
APPLICANT: Hiltunen, Mikko O  
APPLICANT: Jeltsch, Markku M  
APPLICANT: Acher, Marc G  
TITLE OF INVENTION: Use of VEGF-C or VEGF-D Gene or Protein to Prevent Restenosis  
FILE REFERENCE: 28967/35601A  
CURRENT APPLICATION NUMBER: US/11/064,769  
CURRENT FILING DATE: 2005-02-24  
PRIOR APPLICATION NUMBER: US/09/427,657  
PRIOR FILING DATE: 1999-10-26  
PRIOR APPLICATION NUMBER: US 60/105,587  
PRIOR FILING DATE: 1998-10-26  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-064-769-2  
Query Match 19.3%; Score 54.5; DB 7; Length 419;  
Best Local Similarity 35.0%; Pred. No. 5.3;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;  
Qy 7 QCSQNEYFDSLHACI-PCOLRCSSNTP--PLTCQRYCNAS 44



Db 327 QCGANREFDNTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 19

US-11-153-880-2

; Sequence 2, Application US/11153880

; Publication No. US20050256050A1

; GENERAL INFORMATION:

; APPLICANT: HU, JING-SHAN

; APPLICANT: ROSEN, CRAIG A.

; APPLICANT: CAO, LIANG

; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2

; NUMBER OF SEQUENCES: 15

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX

; STREET: 1100 NEW YORK AVENUE

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.10

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/11/153,880

; FILING DATE: 16-Jun-2005

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/219,442

; FILING DATE: 23-DEC-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/999,811

; FILING DATE:

; APPLICATION DATA: US 08/465,968

; FILING DATE: 08-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: MARKOWICZ, KAREN R.

; REGISTRATION NUMBER: 36,351

; REFERENCE/DOCKET NUMBER: 1488.1000004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)371-2600

; TELEFAX: (202)371-2540

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 419 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-11-153-880-2

Query Match 19.3%; Score 54.5; DB 7; Length 419;

Best Local Similarity 35.0%; Pred. No. 5.3;

Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLRCSSNTP--PLTCORYCNAS 44

Db 327 QCGANREFDNTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 20

US-11-064-774A-22

; Sequence 22, Application US/11064774A

; Publication No. US20050267024A1

; GENERAL INFORMATION:

; APPLICANT: Alitalo et al.

; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWTH FACTOR 2

; FILE REFERENCE: 28967/35977B2

; CURRENT APPLICATION NUMBER: US/11/064,774A

; CURRENT FILING DATE: 2005-02-24

; PRIOR APPLICATION NUMBER: 09/795,006

; PRIOR FILING DATE: 2001-02-26

; PRIOR APPLICATION NUMBER: US 60/205,331

; PRIOR FILING DATE: 2000-05-18

; PRIOR APPLICATION NUMBER: US 60/185,205

; PRIOR FILING DATE: 2000-02-25

; NUMBER OF SEQ ID NOS: 1212

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 22

; LENGTH: 419

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-064-774A-22

Query Match 19.3%; Score 54.5; DB 7; Length 419;

Best Local Similarity 35.0%; Pred. No. 5.3;

Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLRCSSNTP--PLTCORYCNAS 44

Db 327 QCGANREFDNTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 21

US-11-113-424-37

; Sequence 37, Application US/11113424

; Publication No. US20050260713A1

; GENERAL INFORMATION:

; APPLICANT: Gangolli et al.

; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-225

; CURRENT APPLICATION NUMBER: US/11/113,424

; CURRENT FILING DATE: 2005-04-21

; PRIOR APPLICATION NUMBER: 60/256,704

; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: 60/311,590

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/257,314

; PRIOR FILING DATE: 2000-12-20

; PRIOR APPLICATION NUMBER: 60/311,613

; PRIOR FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: 60/315,617

; PRIOR FILING DATE: 2001-08-29

; PRIOR APPLICATION NUMBER: 60/307,506

; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: 60/322,358

; PRIOR FILING DATE: 2001-09-14

; PRIOR APPLICATION NUMBER: 60/294,075

; PRIOR FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: 60/288,153

; PRIOR FILING DATE: 2001-05-02

; NUMBER OF SEQ ID NOS: 190

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 37

; LENGTH: 997

; TYPE: PRT

; ORGANISM: Mus musculus

US-11-113-424-37

Query Match 19.3%; Score 54.5; DB 7; Length 997;

Best Local Similarity 28.2%; Pred. No. 12;

Matches 11; Conservative 4; Mismatches 11; Indels 13; Gaps 1;

QY 7 QCSQNEYFDSLHACIPQL-----RCSNNT 32

Db 751 QCSPGHFYNTTTHRCIRCPCTGYQPEFGKNNVCVSCPGNT 789

RESULT 22

US-11-110-082-29

; Sequence 29, Application US/11110082

; Publication No. US20050266558A1



```

; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Hall, Claire
; APPLICANT: Norries, Michael Geoffrey
; APPLICANT: Saulsbury, Keith Martin
; TITLE OF INVENTION: Compositions Isolated from Forage
; TITLE OF INVENTION: Grasses and methods for their use.
; FILE REFERENCE: 11000.1074Uc1
; CURRENT APPLICATION NUMBER: US/11/110,082
; CURRENT FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/563,723
; PRIOR FILING DATE: 2004-04-20
; PRIOR APPLICATION NUMBER: 10/655,799
; PRIOR FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: 60/408,782
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Lolium perenne
; US-11-110-082-29

Query Match      19.3%; Score 54.5; DB 7; Length 1148;
Best Local Similarity 29.7%; Pred. No. 13;
Matches 11; Conservative 8; Mismatches 17; Indels 1; Gaps 1;

QY      14  FDSLHACIPQCLRCSSNTPLTCQRYCNASVTSVK 50
Db      631  FDSVLAHV-CALSCQLPFLCKNVTNKTNIKDSIK 666

RESULT 23
US-11-126-126-2
; Sequence 2, Application US/11126126
; Publication No. US20050250696A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
; TITLE OF INVENTION: Type-II Receptors
; FILE REFERENCE: 02-006-A
; CURRENT APPLICATION NUMBER: US/11/126,126
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: 09/882,735
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/214,613
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: PCT/US97/12244
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: 60/039,792
; PRIOR FILING DATE: 1997-03-04
; PRIOR APPLICATION NUMBER: 60/039,314
; PRIOR FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: 60/037,737
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 60/032,534
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: 60/021,443
; PRIOR FILING DATE: 1996-07-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-126-126-2

Query Match      18.7%; Score 53; DB 7; Length 161;
Best Local Similarity 33.3%; Pred. No. 3.4;
Matches 14; Conservative 5; Mismatches 19; Indels 4; Gaps 2;

QY      3  QVAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNAS 44
Db      295  QFCGCLRNRYGVEVDALDPNWHC-----PP--CRGICNCS 330

RESULT 25
US-11-186-284-14
; Sequence 14, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-11-186-284-16

Query Match      18.7%; Score 53; DB 7; Length 371;
Best Local Similarity 31.0%; Pred. No. 7.3;
Matches 13; Conservative 5; Mismatches 18; Indels 6; Gaps 2;

QY      3  QVAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNAS 44
Db      295  QFCGCLRNRYGVEVDALDPNWHC-----PP--CRGICNCS 330

RESULT 25
US-11-186-284-14
; Sequence 14, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
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; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-14

Query Match      18.7%; Score 53; DB 7; Length 450;
Best Local Similarity 31.0%; Pred. No. 8.7;
Matches 13; Conservative 5; Mismatches 18; Indels 6; Gaps 2;

Qy      3 QMACCCSQNEYFDSLHACIPCOLRCSSNTPLTTCQRYCNAS 44
Db      374 QFCGCLRNRYGEEVRDALLDPNWHC-----PP--CRGICNCS 409

RESULT 26
US-11-182-946-3
; Sequence 3, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-3

Query Match      18.7%; Score 53; DB 7; Length 455;
Best Local Similarity 33.3%; Pred. No. 8.8;
Matches 14; Conservative 5; Mismatches 19; Indels 4; Gaps 2;

Qy      8 CSONE---YFDSLHACIPCOLRCSSNTPLTTCQRYCNASVT 46
Db      127 CRKNQYRWSENUFQCFNCSL-CLNGTVHLSCQEKQNTVCT 167

RESULT 27
US-11-076-187-4
; Sequence 4, Application US/11076187
; Publication No. US20050244857A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Pan, James G
; APPLICANT: Gentz, Reiner L
; APPLICANT: Dixit, Vishva M
; TITLE OF INVENTION: Death Domain Containing Receptor-4
; FILE REFERENCE: PF355P3
; CURRENT APPLICATION NUMBER: US/11/076,187
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 60/035,722
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 60/037,829
; PRIOR FILING DATE: 1997-02-05

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QY	7	QCSQNEFYDLSLLHACIPQC-----LRCSSNT	32
Db	753	QCSPGHFYNTTTHRCIRCPVGTQYQPEFGKNCVSCPNT	791
RESULT 29			
US-11-080-991-50			
; Sequence 50, Application US/11080991			
; Publication No. US20050266437A1			
; GENERAL INFORMATION:			
; APPLICANT: Veiby, Petter Ole			
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR			
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST			
; TITLE OF INVENTION: AND OVARIAN CANCER			
; FILE REFERENCE: MRI-039			
; CURRENT APPLICATION NUMBER: US/11/080,991			
; CURRENT FILING DATE: 2005-03-11			
; PRIOR APPLICATION NUMBER: US/10/176,847			
; PRIOR FILING DATE: 2002-06-21			
; NUMBER OF SEQ ID NOS: 112			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 50			
; LENGTH: 997			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-11-080-991-50			
Query Match 18.2%; Score 51.5; DB 7; Length 997;			
Best Local Similarity 25.6%; Pred. No. 28;			
Matches 10; Conservative 5; Mismatches 11; Indels 13; Gaps 1;			
QY	7	QCSQNEFYDLSLLHACIPQC-----LRCSSNT	32
Db	751	QCSPGHFYNTTTHRCIRCPVGTQYQPEFGKNCVSCPNT	789
RESULT 30			
US-11-113-424-36			
; Sequence 36, Application US/11113424			
; Publication No. US20050260713A1			
; GENERAL INFORMATION:			
; APPLICANT: Gangolli et al.			
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same			
; FILE REFERENCE: 21402-225			
; CURRENT APPLICATION NUMBER: US/11/113,424			
; CURRENT FILING DATE: 2005-04-21			
; PRIOR APPLICATION NUMBER: 60/256,704			
; PRIOR FILING DATE: 2000-12-19			
; PRIOR APPLICATION NUMBER: 60/311,590			
; PRIOR FILING DATE: 2001-08-10			
; PRIOR APPLICATION NUMBER: 60/257,314			
; PRIOR FILING DATE: 2000-12-20			
; PRIOR APPLICATION NUMBER: 60/311,613			
; PRIOR FILING DATE: 2001-08-10			
; PRIOR APPLICATION NUMBER: 60/315,617			
; PRIOR FILING DATE: 2001-08-29			
; PRIOR APPLICATION NUMBER: 60/307,506			
; PRIOR FILING DATE: 2001-07-24			
; PRIOR APPLICATION NUMBER: 60/322,358			
; PRIOR FILING DATE: 2001-09-14			
; PRIOR APPLICATION NUMBER: 60/294,075			
; PRIOR FILING DATE: 2001-05-29			
; PRIOR APPLICATION NUMBER: 60/288,153			
; PRIOR FILING DATE: 2001-05-02			
; NUMBER OF SEQ ID NOS: 190			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 36			
; LENGTH: 999			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-11-113-424-36			
Query Match 18.2%; Score 51.5; DB 7; Length 999;			
Best Local Similarity 25.6%; Pred. No. 28;			
Matches 10; Conservative 5; Mismatches 11; Indels 13; Gaps 1;			
QY	9	SQNEFYDLSLLHACIPQCQLRCSNSTPPLTCQRYCNAS	44
Db	75	SRNH-----LPACLSNGRCNSQVE---TRSCNTT	103
RESULT 31			
US-11-182-946-13			
; Sequence 13, Application US/11182946			
; Publication No. US20050255100A1			
; GENERAL INFORMATION:			
; APPLICANT: Wei, Ying-Fei			
; APPLICANT: Ni, Jian			
; APPLICANT: Gentz, Reiner			
; APPLICANT: Ruben, Steven			
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5			
; FILE REFERENCE: 1488.1280004			
; CURRENT APPLICATION NUMBER: US/11/182,946			
; CURRENT FILING DATE: 2005-07-18			
; PRIOR APPLICATION NUMBER: US/10/186,643			
; PRIOR FILING DATE: 2002-07-02			
; PRIOR APPLICATION NUMBER: US/09/573,986			
; PRIOR FILING DATE: 2000-05-18			
; NUMBER OF SEQ ID NOS: 27			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 13			
; LENGTH: 349			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-11-182-946-13			
Query Match 17.5%; Score 49.5; DB 7; Length 349;			
Best Local Similarity 36.1%; Pred. No. 19;			
Matches 13; Conservative 5; Mismatches 11; Indels 7; Gaps 2;			
QY	9	SQNEFYDLSLLHACIPQCQLRCSNSTPPLTCQRYCNAS	44
Db	75	SRNH-----LPACLSNGRCNSQVE---TRSCNTT	103
RESULT 32			
US-10-131-826A-82			
; Sequence 82, Application US/10131826A			
; Publication No. US20050245730A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Beresini, Maureen			
; APPLICANT: DeForge, Laura			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Sherwood, Steven			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stewart, Timothy A.			
; APPLICANT: Tumas, Daniel			
; APPLICANT: Watanabe, Colin K			
; APPLICANT: Wood, William			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME			
; FILE REFERENCE: P3330R1C128			
; CURRENT APPLICATION NUMBER: US/10/131,826A			
; CURRENT FILING DATE: 2002-04-24			
; PRIOR APPLICATION NUMBER: 60/049911			
; PRIOR FILING DATE: 1997-06-18			
; PRIOR APPLICATION NUMBER: 60/056974			
; PRIOR FILING DATE: 1997-08-26			
; PRIOR APPLICATION NUMBER: 60/059113			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/059115			



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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 82
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-82

Query Match      17.5%; Score 49.5; DB 6; Length 406;
Best Local Similarity 34.3%; Pred. No. 22;
Matches 12; Conservative 5; Mismatches 15; Indels 3; Gaps 2;

QY      6 GGCQNEFYDLSLLHACIPQLRCSNTPTLTQRY 40
DB      83 GGCIPEDY-DVCAEA--PCEQQCTDNFGRVLCTCY 114

RESULT 33
US-10-995-561-1033
; Sequence 1033, Application US/10995561
; Publication No. US2005072054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1033
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1033

Query Match      17.5%; Score 49.5; DB 6; Length 1798;
Best Local Similarity 26.8%; Pred. No. 84;
Matches 15; Conservative 4; Mismatches 12; Indels 25; Gaps 3;

QY      5 AGCQSQNEFYDLSLL-----HACIP-----COL-RCSNTPTPL 35
DB      940 ATSCHQDEYSQQIVCHRCAGYTGRLCEACAPGHGDPSPRGRCQLCECSGNIDPM 995

RESULT 34
US-10-995-561-1034
; Sequence 1034, Application US/10995561
; Publication No. US2005072054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 1034
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1034

Query Match      17.5%; Score 49.5; DB 6; Length 1798;
Best Local Similarity 26.8%; Pred. No. 84;
Matches 15; Conservative 4; Mismatches 12; Indels 25; Gaps 3;

QY      5 AGCQSQNEFYDLSLL-----HACIP-----COL-RCSNTPTPL 35
DB      940 ATSCHQDEYSQQIVCHRCAGYTGRLCEACAPGHGDPSPRGRCQLCECSGNIDPM 995

RESULT 35
US-10-967-527A-18
; Sequence 18, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Znf14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 42
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-967-527A-18

Query Match      17.3%; Score 49; DB 6; Length 42;
Best Local Similarity 47.6%; Pred. No. 3.1;
Matches 10; Conservative 3; Mismatches 6; Indels 2; Gaps 2;

QY      8 CSQNEFYDLSLLHACIPCOLRC 28
DB      2 CQENEYWDQ-WGRCVTCQ-RC 20

RESULT 36
US-11-132-285-61
; Sequence 61, Application US/11132285
; Publication No. US20050244876A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
; FILE REFERENCE: PFS11P1
; CURRENT APPLICATION NUMBER: US/11/132,285
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/10/046,433
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
```







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; FILE REFERENCE: PF511P1
; CURRENT APPLICATION NUMBER: US/11/132,285
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/10/046,433
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-285-41

Query Match      17.1%; Score 48.5; DB 7; Length 350;
Best Local Similarity 22.8%; Pred. No. 25;
Matches 18; Conservative 3; Mismatches 15; Indels 43; Gaps 3;

QY      6 GQCSONEY-----FDSL-----LHACIPCO 25
DB      30 GKCKDNEYRHHLCCLSCPPGTYASRLCDSKNTNTQCTPCGSDTFTSRNNHLPACLSCN 89

QY      26 LRCSSTNTPLTCQRYCNAS 44
DB      90 GRCDNSQVE---TRSCNTT 105

RESULT 44
US-11-182-946-14
; Sequence 14, Application US/11/182,946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-14

Query Match      17.1%; Score 48.5; DB 7; Length 355;
Best Local Similarity 22.8%; Pred. No. 25;
Matches 18; Conservative 3; Mismatches 15; Indels 43; Gaps 3;

QY      6 GQCSONEY-----FDSL-----LHACIPCO 25
DB      28 GKCKDNEYRHHLCCLSCPPGTYASRLCDSKNTNTQCTPCASDTFTSRNNHLPACLSCN 87

QY      26 LRCSSTNTPLTCQRYCNAS 44
DB      90 GRCDNSQVE---TRSCNTT 105
```

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; FILE REFERENCE: PF511P1
; CURRENT APPLICATION NUMBER: US/11/132,285
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/10/046,433
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-285-41

Query Match      17.1%; Score 48.5; DB 7; Length 350;
Best Local Similarity 22.8%; Pred. No. 25;
Matches 18; Conservative 3; Mismatches 15; Indels 43; Gaps 3;

QY      6 GQCSONEY-----FDSL-----LHACIPCO 25
DB      30 GKCKDNEYRHHLCCLSCPPGTYASRLCDSKNTNTQCTPCGSDTFTSRNNHLPACLSCN 89

QY      26 LRCSSTNTPLTCQRYCNAS 44
DB      90 GRCDNSQVE---TRSCNTT 105

RESULT 44
US-11-182-946-14
; Sequence 14, Application US/11/182,946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-14

Query Match      17.1%; Score 48.5; DB 7; Length 355;
Best Local Similarity 22.8%; Pred. No. 25;
Matches 18; Conservative 3; Mismatches 15; Indels 43; Gaps 3;

QY      6 GQCSONEY-----FDSL-----LHACIPCO 25
DB      28 GKCKDNEYRHHLCCLSCPPGTYASRLCDSKNTNTQCTPCASDTFTSRNNHLPACLSCN 87

QY      26 LRCSSTNTPLTCQRYCNAS 44
DB      90 GRCDNSQVE---TRSCNTT 105
```

```
; FILE REFERENCE: PF511P1
; CURRENT APPLICATION NUMBER: US/11/132,285
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/10/046,433
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-285-41

Query Match      17.1%; Score 48.5; DB 7; Length 350;
Best Local Similarity 22.8%; Pred. No. 25;
Matches 18; Conservative 3; Mismatches 15; Indels 43; Gaps 3;

QY      6 GQCSONEY-----FDSL-----LHACIPCO 25
DB      30 GKCKDNEYRHHLCCLSCPPGTYASRLCDSKNTNTQCTPCGSDTFTSRNNHLPACLSCN 89

QY      26 LRCSSTNTPLTCQRYCNAS 44
DB      90 GRCDNSQVE---TRSCNTT 105

RESULT 44
US-11-182-946-14
; Sequence 14, Application US/11/182,946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-14

Query Match      17.1%; Score 48.5; DB 7; Length 355;
Best Local Similarity 22.8%; Pred. No. 25;
Matches 18; Conservative 3; Mismatches 15; Indels 43; Gaps 3;

QY      6 GQCSONEY-----FDSL-----LHACIPCO 25
DB      28 GKCKDNEYRHHLCCLSCPPGTYASRLCDSKNTNTQCTPCASDTFTSRNNHLPACLSCN 87

QY      26 LRCSSTNTPLTCQRYCNAS 44
DB      90 GRCDNSQVE---TRSCNTT 105
```

```
; FILE REFERENCE: PF511P1
; CURRENT APPLICATION NUMBER: US/11/132,285
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/10/046,433
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-285-41

Query Match      17.1%; Score 48.5; DB 7; Length 350;
Best Local Similarity 22.8%; Pred. No. 25;
Matches 18; Conservative 3; Mismatches 15; Indels 43; Gaps 3;

QY      6 GQCSONEY-----FDSL-----LHACIPCO 25
DB      30 GKCKDNEYRHHLCCLSCPPGTYASRLCDSKNTNTQCTPCGSDTFTSRNNHLPACLSCN 89

QY      26 LRCSSTNTPLTCQRYCNAS 44
DB      90 GRCDNSQVE---TRSCNTT 105

RESULT 44
US-11-182-946-14
; Sequence 14, Application US/11/182,946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-14

Query Match      17.1%; Score 48.5; DB 7; Length 355;
Best Local Similarity 22.8%; Pred. No. 25;
Matches 18; Conservative 3; Mismatches 15; Indels 43; Gaps 3;

QY      6 GQCSONEY-----FDSL-----LHACIPCO 25
DB      28 GKCKDNEYRHHLCCLSCPPGTYASRLCDSKNTNTQCTPCASDTFTSRNNHLPACLSCN 87

QY      26 LRCSSTNTPLTCQRYCNAS 44
DB      90 GRCDNSQVE---TRSCNTT 105
```







```

; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 556
; LENGTH: 4655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-556

Query Match      17.0%; Score 48; DB 6; Length 4655;
Best Local Similarity 25.9%; Pred. No. 3.1e+02;
Matches 14; Conservative 8; Mismatches 18; Indels 14; Gaps 2;

QY 2 LQAG-----QCSQNEFYDSLHACIPCLRC-----SSNTPPLTCQRYC 41
DB 3500 LQLSGSTYCMPCSSQFLCANNEKCIPIWKCQKDCGSDGDELALCPORFC 3553

RESULT 50
US-10-821-234-1504
; Sequence 1504, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preseclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1504
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1504

Query Match      16.8%; Score 47.5; DB 6; Length 419;
Best Local Similarity 37.0%; Pred. No. 39;
Matches 17; Conservative 3; Mismatches 17; Indels 9; Gaps 3;

QY 2 LQAGQCSQNEFYDSLHHA-----CIPCLR--CSSNTPPLTCQRY 40
DB 181 LHMparVvANSgFDVLCHALESYTTLPHYLRSPCPSN--PITRPAY 224

RESULT 51
US-10-821-234-1412
; Sequence 1412, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preseclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1412
; LENGTH: 703
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1412

```

```

Query Match      16.8%; Score 47.5; DB 6; Length 703;
Best Local Similarity 21.4%; Pred. No. 63;
Matches 12; Conservative 6; Mismatches 25; Indels 13; Gaps 2;

QY 7 QCSQNEFYDSLHACIP-----CQLRCSSNTPPLTCQRYCNASVTNSVKG 51
DB 383 ECKGTGYFDGISRMCVDVNEQRYPGRLCGHKCENTLGSYLCS--CSVGPRLSVDG 436

RESULT 52
US-11-182-946-5
; Sequence 5, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-5

Query Match      16.6%; Score 47; DB 7; Length 427;
Best Local Similarity 30.0%; Pred. No. 46;
Matches 12; Conservative 5; Mismatches 19; Indels 4; Gaps 3;

QY 7 QCSQNEFYDSLHHA--CIPCLRCSNTPPL--TCQRYCNA 43
DB 148 ECPDGTYSDEANHVDPCLCTV--CEDTERQLRECTRWADA 186

RESULT 53
US-11-182-946-9
; Sequence 9, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-9

Query Match      16.6%; Score 47; DB 7; Length 595;
Best Local Similarity 29.1%; Pred. No. 62;
Matches 16; Conservative 6; Mismatches 19; Indels 14; Gaps 4;

QY 7 QCSQNEFYDSL--LHACIPC-----CQLRCSSNTPPLTCQ----RYCNASVTNS 48

```



```

DB      243  QCPEPDYLDAGRGACTACVSCSDDLVEKTPCAWNS-SRTCECRPGMICATSATNS 296
      || : | | | || : | : | : | : || : | | |
RESULT 54
US-10-131-826A-60
; Sequence 60, Application US/10131826A
; Publication NO. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131.826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 60
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-60
Query Match 16.6%; Score 47; DB 6; Length 724;
Best Local Similarity 28.6%; Pred. No. 75;
Matches 22; Conservative 4; Mismatches 15; Indels 36; Gaps 6;
QY      6  GCQSQN-----EYFDSLH-AC-----IPCQLRCS-----SNTTP- 33
      || : | : | || || || || || || || || || || || || || || || ||
DB      68  GCCDQHKKDRRIAARYWDIMEYFDLKRHELCDGYIKDILCQ-ECSPYAAHLYDAENTQPL 126
      || : | : | || || || || || || || || || || || || || || || ||
QY      34  ---PLTCQRYCNASVTN 47
      || : | : | || || || || || || || || || || || || || || || ||
DB      127  RNLPLCLSDYCSAFHSN 143
      || : | : | || || || || || || || || || || || || || || || ||
RESULT 55

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; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 670
; LENGTH: 4347
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-670
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Query Match      16.6%; Score 47; DB 6; Length 4347;
Best Local Similarity 36.4%; Pred. No. 3.9e+02;
Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
```

```
OY 3 QMAGCQSQNEYFDSLHACIPC 24
    |||||::|||
Db 456 ORAGPCPDGHFYLEHSAACLPC 477
```

## RESULT 58

```
US-10-821-234-1155
; Sequence 1155, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Suean
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1155
; LENGTH: 4419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1155
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```
Query Match      16.6%; Score 47; DB 6; Length 4419;
Best Local Similarity 36.4%; Pred. No. 3.9e+02;
Matches 8; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
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```
OY 3 QMAGCQSQNEYFDSLHACIPC 24
    |||||::|||
Db 528 ORAGPCPDGHFYLEHSAACLPC 549
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## RESULT 59

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US-11-147-047-50
; Sequence 50, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoqing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPS0016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
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; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-50
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Query Match      16.4%; Score 46.5; DB 7; Length 487;
Best Local Similarity 23.7%; Pred. No. 60;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;
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```
OY 8 CSQNEYFDSLHACIPCO-----LRCSSNT 32
    |||||::|||
Db 242 CSPGHYNTTTHRCIRCPVGTYPQPEFGNHCIICPGNT 279
```

## RESULT 60

```
US-10-770-726-66
; Sequence 66, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-66
```

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Query Match      16.4%; Score 46.5; DB 6; Length 712;
Best Local Similarity 28.6%; Pred. No. 85;
Matches 12; Conservative 11; Mismatches 12; Indels 7; Gaps 3;
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```
OY 1 MLQAGCQSQNEYFDSLHACIP-----CQLRCSNT-PPLT 36
    ::|||::|||::|||::|||
Db 271 IVDFAGYCAQNGFY-CLVYGFLPNGSLDLRLHCQTQACPPLS 311
```

## RESULT 61

```
US-10-770-726-57
; Sequence 57, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 883
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-57

Query Match      16.4%; Score 46.5; DB 6; Length 883;
Best Local Similarity 30.3%; Pred. No. 1e+02;
```



```

; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-58

Query Match      16.4%; Score 46.5; DB 7; Length 964;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

QY      8 CSONEYFDSLHACIPQ-----LRCSNNT 32
      ||:::|||||:||
Db      743 CSPGHYNTTTHRCIRCPVGTYPQEFQGNHCITCPGNT 780

RESULT 64
US-11-113-424-2
; Sequence 2, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-2

Query Match      16.4%; Score 46.5; DB 7; Length 965;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

QY      8 CSONEYFDSLHACIPQ-----LRCSNNT 32
      ||:::|||||:||
Db      744 CSPGHYNTTTHRCIRCPVGTYPQEFQGNHCITCPGNT 781

RESULT 65
US-11-147-047-51
; Sequence 51, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.

```



```
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoqing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 965
; TYPE: PRT
; ORGANISM: Homo sapiens
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
US-11-147-047-51

Query Match      16.4%; Score 46.5; DB 7; Length 965;
Best Local Similarity 23.7%; Pred. No. 1.1e-02;
Matches 9; Conservative 5; Mismatches 11; Indels 13; Gaps 1;

QY      8 CSONEYFDSLHACIPQC-----LRCSNT 32
DB      743 CSPGHYNTTTRCIRCPVGTQYQPFQGNHCITCPGNT 780

RESULT 66
US-11-055-822-100
; Sequence 100, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158

; SEQ ID NO 100
; LENGTH: 1045
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-100

Query Match      16.4%; Score 46.5; DB 7; Length 1045;
Best Local Similarity 30.4%; Pred. No. 1.2e+02;
Matches 14; Conservative 9; Mismatches 22; Indels 1; Gaps 1;

QY      1 MLOWAGOC-SONEYFDSLHACIPQCQLRCSNTPLTTCQRYCNASV 45
DB      711 MLTVQEVCSLSLVWDVAIDALDAEIRAALNDPKDQPLANISV 756

RESULT 67
US-11-078-735-12
; Sequence 12, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-078-735-12

Query Match      16.3%; Score 46; DB 7; Length 63;
Best Local Similarity 30.4%; Pred. No. 11;
Matches 7; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY      19 HACIPQCQLRCSNTPLTTCQRYC 41
DB      12 HLELQIRVRCDENYYSATCNKFC 34

RESULT 68
US-11-078-735-13
; Sequence 13, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
```



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; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-078,735-13

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Query Match	16.3%	Score 46;	DB 7;	Length 63;
Best Local Similarity	30.4%;	Pred. NO. 11;		
Matches 7; Conservative	5;	Mismatches 11;	Indels 0;	Gaps 0;

QY 19 HACIPQLRCSSNTPTLCQRYC 41  
| : : : | : : :  
Db 12 HLEQLRVRCDENYYSATCNKEC 34

RESULT 69  
US-11-078-735-14  
; Sequence 14, Application US/11078735  
; Publication No. US20050261477A1  
; GENERAL INFORMATION:  
; APPLICANT: CHAMPION, BRIAN ROBERT  
; APPLICANT: LENNARD, ANDREW CHRISTOPHER  
; APPLICANT: MCKENZIE, GRAHAME JAMES  
; APPLICANT: TUGAL, TAMARA  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS  
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS  
; FILE REFERENCE: 674525-2019  
; CURRENT APPLICATION NUMBER: US/11/078,735  
; CURRENT FILING DATE: 2005-03-10  
; PRIOR APPLICATION NUMBER: PCT/GB03/03908  
; PRIOR FILING DATE: 2003-09-09  
; PRIOR APPLICATION NUMBER: PCT/GB03/03285  
; PRIOR FILING DATE: 2003-08-01  
; PRIOR APPLICATION NUMBER: PCT/GB03/01525  
; PRIOR FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: GB 0300234.2  
; PRIOR FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: PCT/GB02/05137  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: PCT/GB02/05133  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: GB 0220912.0  
; PRIOR FILING DATE: 2002-09-10  
; PRIOR APPLICATION NUMBER: GB 0220913.8  
; PRIOR FILING DATE: 2002-09-10  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 14  
; LENGTH: 63  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-11-078-735-14

Query Match	16.3%;	Score 46;	DB 7;	Length 63;
Best Local Similarity	30.4%;	Pred. No. 11;		
Matches 7; Conservative	5;	Mismatches 11;	Indels	

Qy 19 HACIPQQLRCSSTNPPLTCQRYC 41  
| : : : | : : :  
Db 12 HLEQLQVRCDENYYSATCNKFC 34

```

RESULT 70
US-11-078-735-15
; Sequence 15, Application US/11078735
; Publication No. US20050261477A1
; GENERAL INFORMATION:
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAM JAMES
; APPLICANT: TUGAL, TAMARA
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
; TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
; FILE REFERENCE: 674525-2019
; CURRENT APPLICATION NUMBER: US/11/078,735
; PRIOR FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: PCT/GB03/03908
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: PCT/GB03/03285
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: PCT/GB03/01525
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: GB 0300234.2
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: PCT/GB02/05137
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0220912.0
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 15
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-078-735-15

```

Query Match	16.3%	Score 46;	DB 7;	Length 63;
Best Local Similarity	30.4%	Pred. No. 11;		
Matches	7;	Conservative	5;	Mismatches 11;
				Indels 0;
				Gaps 0;

Qy 19 HACIPQLRCSNTPPLTCQRYC 41  
| : : : | : : :  
Db 12 HLELQIRVRCDENYYSATCNKFC 34

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RESULT 71
US-10-131-826A-296
; Sequence 296, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Andrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven

```



```
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 296
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-296

Query Match 16.3%; Score 46; DB 6; Length 353;
Best Local Similarity 27.3%; Pred. No. 52;
Matches 12; Conservative 7; Mismatches 19; Indels 6; Gaps 3;

QY 6 GGCNQNEVFDLLHACIPQCLRCSSNTPPLTCQRYC---NASVT 46
| | | | | | | | | | | | | | | | | | | | | |
DB 215 GCEVGWVLDE--GACVDVD-ECAABPPPCSAAQFCNANGSYT 255
| | | | | | | | | | | | | | | | | | | | | |

RESULT 72
US-10-763-712A-21
; Sequence 21, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; TITLE OF INVENTION: Production
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Trichomonas vaginalis
US-10-763-712A-21
```

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Query Match 16.3%; Score 46; DB 6; Length 449;
Best Local Similarity 36.6%; Pred. No. 64;
Matches 15; Conservative 1; Mismatches 9; Indels 16; Gaps 3;

QY 14 FDSLHACIPQCLRCSSNTPPLTCQRYC---NASVTNSVK 50
| | | | | | | | | | | | | | | | | | | | | |
DB 24 FD--MHKCINQ-----ACVRACKNVAGOSVLKSVK 52
| | | | | | | | | | | | | | | | | | | | | |

RESULT 73
US-10-763-712A-104
; Sequence 104, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; TITLE OF INVENTION: Production
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Trichomonas vaginalis
US-10-763-712A-104

Query Match 16.3%; Score 46; DB 6; Length 449;
Best Local Similarity 36.6%; Pred. No. 64;
Matches 15; Conservative 1; Mismatches 9; Indels 16; Gaps 3;

QY 14 FDSLHACIPQCLRCSSNTPPLTCQRYC---NASVTNSVK 50
| | | | | | | | | | | | | | | | | | | | | |
DB 24 FD--MHKCINQ-----ACVRACKNVAGOSVLKSVK 52
| | | | | | | | | | | | | | | | | | | | | |

RESULT 74
US-10-641-678-54
; Sequence 54, Application US/10641678
; Publication No. US20050277172A1
; GENERAL INFORMATION:
; APPLICANT: Day, Anthony, G.
; APPLICANT: Goedegebuur, Frits
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Neefe, Paulien
; APPLICANT: Sandgren, Mats
; APPLICANT: Shaw, Andrew
; APPLICANT: Stahlberg, Jerry
; TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1
; TITLE OF INVENTION: Cellulases
; FILE REFERENCE: GC772-3
; CURRENT APPLICATION NUMBER: US/10/641,678
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/458,853
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/458,696
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/456,368
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US 60/404,063
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSEQ for Windows Version 4.0
```



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; SEQ ID NO 54
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Fusarium oxysporum
US-10-641-678-54

Query Match      16.3%; Score 46; DB 6; Length 514;
Best Local Similarity 41.0%; Pred. No. 73;
Matches 16; Conservative 3; Mismatches 16; Indels 4; Gaps 2;

QY      16 SLIHACIPQQLRCSSNT---PPLTCQRYCNCASVTNSVKG 51
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      9 SALIAARAQAQVCSLNTETKPAITWSK-CTSSGCSDVKG 46

RESULT 75
US-11-109-157A-18
; Sequence 18, Application US/11109157A
; Publication No. US20050277175A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: TRUNCATED ADAMTS MOLECULES
; FILE REFERENCE: 01997.030500.
; CURRENT APPLICATION NUMBER: US/11/109,157A
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: 60/562,685
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 938
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-109-157A-18

Query Match      16.3%; Score 46; DB 7; Length 938;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      28 CSSNTPPLTCQRYCNA 43
      |||  |||  |||  |||  |||
DB      630 CSAKTKPVTPEKICNA 645

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Search completed: December 21, 2005, 16:30:55  
Job time : 11.4 secs



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OM protein - protein search, using sw model

Run on: December 21, 2005, 16:11:05 ; Search time 132.6 Seconds  
(without alignments)  
160.704 Million cell updates/sec

Title: US-10-077-137-1\_COPY\_1\_51

Perfect score: 283

Sequence: 1 MLQMAQCQSQNEIFDSLLHA.....TPPLTCQRYCNASVINSVKG 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA Main:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	283	100.0	184	4	US-10-077-438-1
2	283	100.0	184	4	US-10-077-438-7
3	283	100.0	184	4	US-10-077-137-1
4	283	100.0	184	4	US-10-077-137-7
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6	283	100.0	184	4	US-10-151-882-47
7	283	100.0	184	4	US-10-115-192-8
8	283	100.0	184	4	US-10-008-063-7
9	283	100.0	184	4	US-10-152-363A-27
10	283	100.0	184	4	US-10-216-074-11
11	283	100.0	184	4	US-10-087-080-39
12	283	100.0	184	4	US-10-742-634-9
13	283	100.0	184	5	US-10-626-914-6
14	283	100.0	184	5	US-10-485-489-6
15	283	100.0	184	5	US-10-861-049-27
16	283	100.0	184	5	US-10-989-826-46
17	283	100.0	184	6	US-11-021-874-27
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19	269	95.1	51	3	US-09-854-864-6
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21	269	95.1	181	3	US-09-854-864-5
22	269	95.1	181	3	US-09-855-158-5
23	269	95.1	283	3	US-09-854-864-9
24	269	95.1	283	3	US-09-855-158-9
25	263	92.9	207	4	US-10-077-438-3
26	263	92.9	207	4	US-10-077-137-3
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28	249	88.0	249	28	US-09-855-158-21
29	201	71.0	34	3	US-09-854-864-7
30	201	71.0	34	3	US-09-855-158-7
31	201	71.0	81	3	US-09-854-864-13
32	201	71.0	81	3	US-09-855-158-13
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35	181	64.0	185	3	US-10-216-074-17
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37	181	64.0	281	3	US-09-855-158-10
38	158	55.8	42	4	US-10-145-206-197
39	104	36.7	117	3	US-09-854-864-12
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Sequence 43, Appl  
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Sequence 4, Appl



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104	64.5	22.8	418	3	US-10-162-435-21	Sequence 21, Appl	177	58	20.5	162	3	US-09-798-789-10	Sequence 10, Appl
105	64.5	22.8	418	5	US-10-860-779-21	Sequence 21, Appl	178	58	20.5	162	4	US-10-218-102-420	Sequence 420, App
106	64.5	22.8	581	4	US-10-104-047-2804	Sequence 2804, Ap	179	58	20.5	271	5	US-10-846-374B-10	Sequence 10, Appl
107	64.5	22.8	735	3	US-09-898-570-10	Sequence 10, Appl	180	58	20.5	940	4	US-10-369-493-13158	Sequence 13158, A
108	64.5	22.8	735	3	US-09-839-446-10	Sequence 10, Appl	181	58	20.5	1131	4	US-10-437-963-140780	Sequence 140780,
109	64.5	22.8	845	3	US-09-898-570-12	Sequence 12, Appl	182	58	20.5	1816	4	US-10-299-058-2	Sequence 2, Appli
110	64.5	22.8	845	3	US-09-839-446-12	Sequence 12, Appl	183	58	20.5	1816	4	US-10-299-058-4	Sequence 4, Appli
111	64.5	22.8	880	4	US-10-104-047-2834	Sequence 2834, Ap	184	58	20.5	1816	4	US-10-372-683-4	Sequence 4, Appli
112	64.5	22.8	897	4	US-10-239-663-35	Sequence 35, Appl	185	58	20.5	1823	4	US-10-363-616-457	Sequence 457, App
113	64.5	22.8	897	4	US-10-470-390A-12	Sequence 12, Appl	186	57.5	20.3	46	4	US-10-767-701-60022	Sequence 60022, A
114	64.5	22.8	897	5	US-10-450-763-36668	Sequence 36668, A	187	57.5	20.3	76	4	US-10-029-386-31899	Sequence 31899, A
115	64.5	22.8	914	4	US-10-406-073-6	Sequence 6, Appli	188	57.5	20.3	142	4	US-10-618-797-2	Sequence 2, Appli
116	64.5	22.8	939	4	US-10-480-172-22	Sequence 22, Appl	189	57.5	20.3	798	4	US-10-078-929-192	Sequence 192, Appl
117	64.5	22.8	974	3	US-09-898-570-14	Sequence 14, Appl	190	57.5	20.3	1679	6	US-11-097-143-8286	Sequence 8286, Ap
118	64.5	22.8	974	3	US-09-839-446-14	Sequence 14, Appl	191	57.5	20.3	1679	6	US-11-097-143-8298	Sequence 8298, Ap
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120	64.5	22.8	993	4	US-10-406-073-8	Sequence 8, Appli	193	57.5	20.3	1997	4	US-10-296-734-816	Sequence 816, App
121	64.5	22.8	993	4	US-10-406-073-15	Sequence 15, Appl	194	57.5	20.3	2957	5	US-10-450-763-52573	Sequence 52573, A
122	64.5	22.8	993	4	US-10-480-172-21	Sequence 21, Appl	195	57.5	20.3	2957	5	US-10-296-734-810	Sequence 810, App
123	64.5	22.8	1006	3	US-09-930-512-18	Sequence 18, Appl	196	57	20.1	292	5	US-10-846-374B-18	Sequence 18, Appl
124	64.5	22.8	1009	3	US-09-898-570-16	Sequence 16, Appl	197	57	20.1	658	4	US-10-380-438-1	Sequence 1, Appli
125	64.5	22.8	1009	3	US-09-839-446-16	Sequence 16, Appl	198	57	20.1	658	4	US-10-773-302-11	Sequence 11, Appl
126	64.5	22.8	1009	4	US-10-480-172-20	Sequence 20, Appl	199	57	20.1	770	4	US-10-399-456-15	Sequence 15, Appl
127	64	22.6	175	5	US-10-861-049-49	Sequence 49, Appl	200	57	20.1	824	4	US-10-094-749-2573	Sequence 2573, Ap
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131	63	22.3	175	4	US-10-008-063-13	Sequence 13, Appl	204	56.5	20.0	2820	4	US-10-263-929-194	Sequence 194, App
132	63	22.3	175	4	US-10-380-703-9	Sequence 9, Appli	205	56.5	20.0	2820	6	US-11-097-143-16680	Sequence 16680, A
133	63	22.3	175	4	US-10-469-420-1	Sequence 1, Appli	206	56	19.8	37	4	US-10-424-599-253740	Sequence 253740,
134	63	22.3	175	5	US-10-485-489-18	Sequence 18, Appl	207	56	19.8	74	3	US-09-910-082A-226	Sequence 226, App
135	63	22.3	175	5	US-10-861-049-35	Sequence 35, Appl	208	56	19.8	74	4	US-10-765-926-226	Sequence 226, App
136	63	22.3	175	6	US-11-021-874-35	Sequence 35, Appl	209	56	19.8	86	4	US-10-767-701-34266	Sequence 34266, A
137	63	22.3	314	5	US-10-861-049-1	Sequence 1, Appli	210	56	19.8	126	5	US-10-450-763-31916	Sequence 31916, A
138	63	22.3	314	6	US-11-021-874-1	Sequence 1, Appli	211	56	19.8	251	4	US-10-437-963-176580	Sequence 176580,
139	63	22.3	1887	5	US-10-473-451-10	Sequence 10, Appl	212	56	19.8	260	4	US-10-437-963-186621	Sequence 186621,
140	62.5	22.1	985	4	US-10-108-260A-2874	Sequence 2874, Ap	213	56	19.8	268	5	US-10-739-930-10099	Sequence 10099, A
141	62.5	22.1	999	4	US-10-369-493-5671	Sequence 5671, Ap	214	56	19.8	337	4	US-10-270-333-96	Sequence 96, Appl
142	62.5	22.1	999	4	US-10-369-493-5672	Sequence 5672, Ap	215	56	19.8	337	6	US-11-097-143-17679	Sequence 17679, A
143	62	21.9	95	3	US-10-424-599-251720	Sequence 251720	216	56	19.8	760	4	US-10-231-778-224	Sequence 224, App
144	61.5	21.7	99	3	US-09-950-933A-82	Sequence 82, Appl	217	56	19.8	760	6	US-11-097-143-14073	Sequence 14073, A
145	61.5	21.7	353	6	US-11-097-143-41457	Sequence 41457, A	218	56	19.8	2824	4	US-10-369-493-5166	Sequence 5166, Ap
146	61.5	21.7	798	6	US-11-097-143-26277	Sequence 26277, A	219	56	19.8	3597	4	US-10-037-417-2	Sequence 2, Appli
147	61	21.6	246	5	US-10-626-914-14	Sequence 14, Appl	220	56	19.8	3600	4	US-10-037-417-2	Sequence 2, Appli
148	61	21.6	246	5	US-10-861-049-53	Sequence 53, Appl	221	55.5	19.6	225	6	US-11-097-143-41325	Sequence 41325, A
149	61	21.6	246	5	US-11-021-874-53	Sequence 53, Appl	222	55.5	19.6	308	4	US-10-425-115-249202	Sequence 249202,
150	61	21.6	247	5	US-10-485-489-14	Sequence 14, Appl	223	55.5	19.6	339	4	US-10-205-219-54	Sequence 54, Appl
151	60.5	21.4	1574	3	US-09-825-751A-77	Sequence 77, Appl	224	55.5	19.6	350	6	US-11-097-143-32697	Sequence 32697, A
152	60.5	21.4	1574	3	US-10-851-438-77	Sequence 77, Appl	225	55.5	19.6	508	5	US-10-450-763-52572	Sequence 52572, A
153	60.5	21.4	3034	3	US-09-737-149-25	Sequence 25, Appl	226	55.5	19.6	976	4	US-10-276-774-1565	Sequence 1565, Ap
154	60.5	21.4	3034	3	US-09-737-149-30	Sequence 30, Appl	227	55.5	19.6	1149	4	US-10-655-799-30	Sequence 30, Appl
155	60.5	21.4	3034	4	US-10-131-409-30	Sequence 70, Appl	228	55.5	19.6	2052	4	US-10-437-963-137285	Sequence 137285,
156	60.5	21.4	3034	4	US-10-139-854-70	Sequence 70, Appl	229	55.5	19.6	3690	4	US-10-112-944-347	Sequence 347, App
157	60.5	21.4	3034	4	US-10-120-801-52	Sequence 52, Appl	230	55.5	19.6	3696	4	US-10-312-088-31	Sequence 31, Appl
158	60.5	21.4	3034	4	US-10-150-813-70	Sequence 70, Appl	231	55.5	19.6	3696	5	US-10-687-268-31	Sequence 31, Appl
159	60.5	21.4	3034	4	US-10-150-811-70	Sequence 70, Appl	232	55.5	19.6	3705	4	US-10-312-088-30	Sequence 30, Appl
160	60.5	21.4	3034	4	US-10-701-283-25	Sequence 25, Appl	233	55.5	19.6	3705	3	US-09-922-217-1116	Sequence 30, Appl
161	60.5	21.4	3034	4	US-10-701-283-30	Sequence 30, Appl	234	55.5	19.6	5405	3	US-09-922-217-1116	Sequence 1116, Ap
162	60	21.2	426	4	US-10-473-576-14	Sequence 14, Appl	235	55.5	19.6	5405	4	US-10-025-380-1116	Sequence 1116, Ap
163	60	21.2	955	4	US-10-094-749-2632	Sequence 2632, Ap	236	55.5	19.6	5405	5	US-10-723-860-1647	Sequence 1647, Ap
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166	59	20.8	38	3	US-09-779-050A-46	Sequence 46, Appl	239	55	19.4	117	6	US-11-097-143-16290	Sequence 16290, A
167	59	20.8	71	6	US-11-021-874-150	Sequence 150, App	240	55	19.4	284	4	US-10-425-115-231589	Sequence 231589,
168	59	20.8	71	6	US-11-021-874-151	Sequence 151, App	241	55	19.4	331	4	US-10-425-115-256366	Sequence 256366,
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279 54.5 19.3 419 3 US-09-852-209A-12 Sequence 12, Appl  
280 54.5 19.3 419 3 US-09-935-726-2 Sequence 2, Appli  
281 54.5 19.3 419 3 US-09-935-726-18 Sequence 18, Appl  
282 54.5 19.3 419 3 US-09-375-248-4 Sequence 4, Appli  
283 54.5 19.3 419 3 US-09-921-143-2 Sequence 2, Appli  
284 54.5 19.3 419 3 US-09-765-534B-21 Sequence 21, Appl  
285 54.5 19.3 419 4 US-10-127-551-2 Sequence 2, Appli  
286 54.5 19.3 419 4 US-10-044-622-3 Sequence 3, Appli  
287 54.5 19.3 419 4 US-10-084-488-2 Sequence 2, Appli  
288 54.5 19.3 419 4 US-10-084-488-18 Sequence 18, Appl  
289 54.5 19.3 419 4 US-10-131-600-12 Sequence 12, Appl  
290 54.5 19.3 419 4 US-10-201-386-8 Sequence 8, Appli  
291 54.5 19.3 419 4 US-10-201-386-58 Sequence 58, Appl  
292 54.5 19.3 419 4 US-10-262-538-24 Sequence 24, Appl  
293 54.5 19.3 419 4 US-10-346-802-3 Sequence 3, Appli  
294 54.5 19.3 419 4 US-10-120-398-2 Sequence 2, Appli  
295 54.5 19.3 419 4 US-10-120-398-18 Sequence 18, Appl  
296 54.5 19.3 419 4 US-10-120-414-2 Sequence 2, Appli  
297 54.5 19.3 419 4 US-10-120-414-18 Sequence 18, Appl  
298 54.5 19.3 419 4 US-10-120-377-2 Sequence 2, Appli  
299 54.5 19.3 419 4 US-10-120-377-18 Sequence 18, Appl  
300 54.5 19.3 419 4 US-10-081-126-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-10-077-438-1  
; Sequence 1, Application US/10077438  
; Publication No. US20020165156A1  
; GENERAL INFORMATION:  
; APPLICANT: MacKay, Fabienne  
; APPLICANT: Browning, Jeffrey  
; APPLICANT: Ambrose, Christine  
; APPLICANT: Tschoopp, Jurg  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Thompson, Jeffrey  
; APPLICANT: Biogen, Inc.  
; APPLICANT: Apotech R&D S.A.  
; TITLE OF INVENTION: Baff Receptor (BCMA), An

; TITLE OF INVENTION: Immunoregulatory Agent  
; FILE REFERENCE: A080PCT  
; CURRENT APPLICATION NUMBER: US/10/077,438  
; CURRENT FILING DATE: 2002-02-18  
; PRIOR APPLICATION NUMBER: 60/149,378  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/181,684  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: 60/183,536  
; PRIOR FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-10-077-438-1

Query Match 100.0%; Score 283; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCQSQNEYFDSLHACIPQCQLRCSNTPTPLTCQRYCNASVTNSVKG 51  
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Db 1 MLQAGQCQSQNEYFDSLHACIPQCQLRCSNTPTPLTCQRYCNASVTNSVKG 51

RESULT 2  
US-10-077-438-7  
; Sequence 7, Application US/10077438  
; Publication No. US20020165156A1  
; GENERAL INFORMATION:  
; APPLICANT: MacKay, Fabienne  
; APPLICANT: Browning, Jeffrey  
; APPLICANT: Ambrose, Christine  
; APPLICANT: Tschoopp, Jurg  
; APPLICANT: Schneider, Pascal  
; APPLICANT: Thompson, Jeffrey  
; APPLICANT: Biogen, Inc.  
; APPLICANT: Apotech R&D S.A.  
; TITLE OF INVENTION: Baff Receptor (BCMA), An  
; FILE REFERENCE: A080PCT  
; CURRENT APPLICATION NUMBER: US/10/077,438  
; CURRENT FILING DATE: 2002-02-18  
; PRIOR APPLICATION NUMBER: 60/149,378  
; PRIOR FILING DATE: 1999-08-17  
; PRIOR APPLICATION NUMBER: 60/181,684  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: 60/183,536  
; PRIOR FILING DATE: 2000-02-18  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-10-077-438-7

Query Match 100.0%; Score 283; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCQSQNEYFDSLHACIPQCQLRCSNTPTPLTCQRYCNASVTNSVKG 51  
|||||  
Db 1 MLQAGQCQSQNEYFDSLHACIPQCQLRCSNTPTPLTCQRYCNASVTNSVKG 51

RESULT 3  
US-10-077-137-1  
; Sequence 1, Application US/10077137  
; Publication No. US20020172674A1  
; GENERAL INFORMATION:







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; CURRENT APPLICATION NUMBER: US/10/115,192
; CURRENT FILING DATE: 2002-04-02
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-02-11
; PRIOR FILING DATE: 2000-02-11
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 184
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8

Query Match      100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTTCORYCNASVTNSVKG 51
Db 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTTCORYCNASVTNSVKG 51

RESULT 8
US-10-008-063-7
; Sequence 7, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-7

Query Match      100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTTCORYCNASVTNSVKG 51
Db 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTTCORYCNASVTNSVKG 51

RESULT 9
US-10-152-363A-27
; Sequence 27, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TACI-immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-152-363A-27

Query Match      100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTTCORYCNASVTNSVKG 51
Db 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTTCORYCNASVTNSVKG 51

RESULT 10
US-10-216-074-11
; Sequence 11, Application US/10216074
; Publication No. US20030148445A1
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/10/216,074
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-074-11

Query Match      100.0%; Score 283; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTTCORYCNASVTNSVKG 51
Db 1 MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTTCORYCNASVTNSVKG 51

RESULT 11
US-10-087-080-39
; Sequence 39, Application US/10087080
; Publication No. US20030235820A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Markowitz, Sanford David
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: No. US20030235820A1e1 Methods of Diagnosis of Metastatic Colorect
; TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
; FILE REFERENCE: 018501-0008400S
; CURRENT APPLICATION NUMBER: US/10/087,080
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/272,206
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/281,149
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/284,555
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:  
; OTHER INFORMATION: tumor necrosis factor receptor superfamily, member  
; OTHER INFORMATION: 17 (TNFRSF17)  
US-10-087-080-39

Query Match 100.0%; Score 283; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51  
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51

RESULT 12  
US-10-742-634-9  
; Sequence 9, Application US/10742634  
; Publication No. US20040208824A1  
; GENERAL INFORMATION:  
; APPLICANT: Parmelee, David  
; APPLICANT: Yeh, Ren-Hwa  
; APPLICANT: Galperina, Olga  
; APPLICANT: Hilbert, David  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Neutrokin-alpha Conjugate, Neutrokin-alpha Complex, and Uses Thereof  
; FILE REFERENCE: 1488.1810002  
; CURRENT APPLICATION NUMBER: US/10/742,634  
; PRIOR FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: US 60/435,262  
; PRIOR FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: US 60/467,198  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-742-634-9

Query Match 100.0%; Score 283; DB 4; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51  
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51

RESULT 13  
US-10-626-914-6  
; Sequence 6, Application US/10625914  
; Publication No. US20050043516A1  
; GENERAL INFORMATION:  
; Patent Docket Preview  
; APPLICANT: CHUNTHARAPAI, ANAN  
; APPLICANT: GREWAL, IQBAL  
; APPLICANT: KIM, KYUNG JIN  
; APPLICANT: YAN, MINHONG  
; TITLE OF INVENTION: TACI Antibodies and Uses Thereof  
; FILE REFERENCE: P1942R1  
; CURRENT APPLICATION NUMBER: US/10/626,914  
; PRIOR FILING DATE: 2003-07-25  
; PRIOR APPLICATION NUMBER: US 60/398,530  
; PRIOR FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 6  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-626-914-6

Query Match 100.0%; Score 283; DB 5; Length 184;

Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51  
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51

RESULT 14  
US-10-485-489-6  
; Sequence 6, Application US/10485489  
; Publication No. US20050070689A1  
; GENERAL INFORMATION:  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Grewal, Iqbal  
; APPLICANT: Ridgway, John  
; APPLICANT: Yan, Minhong  
; TITLE OF INVENTION: TACIS and BR3 Polypeptides and Uses Thereof  
; FILE REFERENCE: 11669.175USWO  
; CURRENT APPLICATION NUMBER: US/10/485,489  
; CURRENT FILING DATE: 2004-01-30  
; PRIOR APPLICATION NUMBER: PCT/US02/23487  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US 60/310,114  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/377,171  
; PRIOR FILING DATE: 2002-04-30  
; NUMBER OF SEQ ID NOS: 19  
; SEQ ID NO 6  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-489-6

Query Match 100.0%; Score 283; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51  
Db 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51

RESULT 15  
US-10-861-049-27  
; Sequence 27, Application US/10861049  
; Publication No. US20050095243A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew Chan  
; APPLICANT: Qian Gong  
; APPLICANT: Flavius Martin  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040RIUS  
; CURRENT APPLICATION NUMBER: US/10/861,049  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 27  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-861-049-27

Query Match 100.0%; Score 283; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQAGQCSQNEYFDSLHACIPQCLRCSSNTPPLTCQRYCNASVTSVKG 51



Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKG 51

RESULT 16  
US-10-989-826-46  
; Sequence 46, Application US/10989826  
; Publication No. US20050218650A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Crowley, Craig  
; APPLICANT: De Sauvage, Frederic J.  
; APPLICANT: Eaton, Daniel L.  
; APPLICANT: Ebens, Allen  
; APPLICANT: Polson, Andrew  
; APPLICANT: Smith, Victoria  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Tumor of  
; TITLE OF INVENTION: Hematopoietic Origin  
; FILE REFERENCE: P5105R1US  
; CURRENT APPLICATION NUMBER: US/10/989,826  
; CURRENT FILING DATE: 2004-11-16  
; PRIOR APPLICATION NUMBER: US 60/520,842  
; PRIOR FILING DATE: 2003-11-17  
; PRIOR APPLICATION NUMBER: US 60/532,426  
; PRIOR FILING DATE: 2003-12-24  
; NUMBER OF SEQ ID NOS: 75  
; SEQ ID NO 46  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-989-826-46

Query Match 100.0%; Score 283; DB 5; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKG 51  
Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKG 51

RESULT 17  
US-11-021-874-27  
; Sequence 27, Application US/11021874  
; Publication No. US20050163775A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew Chan  
; APPLICANT: Qian Gong  
; APPLICANT: Flavius Martin  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040R1P1  
; CURRENT APPLICATION NUMBER: US/11/021,874  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 10/861,049  
; PRIOR FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 27  
; LENGTH: 184  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-874-27

Query Match 100.0%; Score 283; DB 6; Length 184;  
Best Local Similarity 100.0%; Pred. No. 2.3e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKG 51

Db 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKG 51

RESULT 18  
US-10-115-192-12  
; Sequence 12, Application US/10115192  
; Publication No. US20030082175A1  
; GENERAL INFORMATION:  
; APPLICANT: Apotech R & D S.A.  
; APPLICANT: Biogen, Inc.  
; TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof  
; FILE REFERENCE: A083PCT  
; CURRENT APPLICATION NUMBER: US/10/115,192  
; CURRENT FILING DATE: 2002-04-02  
; PRIOR APPLICATION NUMBER: 60/215688  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/181807  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: 60/157933  
; PRIOR FILING DATE: 1999-10-06  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 302  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-115-192-12

Query Match 100.0%; Score 283; DB 4; Length 302;  
Best Local Similarity 100.0%; Pred. No. 3.7e-25;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKG 51  
Db 24 MLQWAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKG 74

RESULT 19  
US-09-854-864-6  
; Sequence 6, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: BLYS/AGP-3, AND TACI  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-6

Query Match 95.1%; Score 269; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2.9e-24;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKG 51  
Db 1 MAGCQSQNEYFDSLHACIPQLRCSSNTPLTCQRYCNASVTSVKG 48

RESULT 20  
US-09-855-158-6



; Sequence 6, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL  
; TITLE OF INVENTION: 3, AND TACI  
; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-158-6

Query Match 95.1%; Score 269; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 2,9e-24;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51  
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DB 1 MAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 48

## RESULT 21

US-09-854-864-5  
; Sequence 5, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-5

Query Match 95.1%; Score 269; DB 3; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1e-23;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51  
|||||  
DB 1 MAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 48

## RESULT 22

US-09-855-158-5  
; Sequence 5, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL  
; TITLE OF INVENTION: 3, AND TACI

; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-158-5

Query Match 95.1%; Score 269; DB 3; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1e-23;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51  
|||||  
DB 1 MAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 48

## RESULT 23

US-09-854-864-9  
; Sequence 9, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 283  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-9

Query Match 95.1%; Score 269; DB 3; Length 283;  
Best Local Similarity 100.0%; Pred. No. 1.6e-23;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 51  
|||||  
DB 1 MAGCQSQNEYFDSLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKG 48

## RESULT 24

US-09-855-158-9  
; Sequence 9, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: 3, AND TACI  
; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12



```
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-9

Query Match      95.1%; Score 269; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.6e-23;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  4  MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
      |||||||
Db  1  MAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 48

RESULT 25
US-10-077-438-3
; Sequence 3, Application US/10077438
; Publication No. US20020165156A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,438
; CURRENT FILING DATE: 2002-02-18
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 60/183,536
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 207
; TYPE: PRT
; ORGANISM: homo sapien
US-10-077-438-3

Query Match      92.9%; Score 263; DB 4; Length 207;
Best Local Similarity 71.8%; Pred. No. 5.8e-23;
Matches 51; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

Qy  1  MLQWAGQCSQNEYFDSL-----LHACIPQCLRCSSNTPLTCQRY 40
      |||||||
Db  39  MLQWAGQCSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
      |||||||
Qy  41  CNASVTNSVKG 51
      |||||||
Db  99  CNASVTNSVKG 109

RESULT 26
US-10-077-137-3
; Sequence 3, Application US/10077137
; Publication No. US20020172674A1
; GENERAL INFORMATION:
; APPLICANT: MacKay, Fabienne
; APPLICANT: Browning, Jeffrey
; APPLICANT: Ambrose, Christine
; APPLICANT: Tschopp, Jurg
; APPLICANT: Schneider, Pascal
; APPLICANT: Thompson, Jeffrey
; APPLICANT: Biogen, Inc.
; TITLE OF INVENTION: Baff Receptor (BCMA), An
; TITLE OF INVENTION: Immunoregulatory Agent
; FILE REFERENCE: A080PCT
; CURRENT APPLICATION NUMBER: US/10/077,137
; CURRENT FILING DATE: 2001-02-15
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149,378
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/181,684
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 60/183,536
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match      88.0%; Score 249; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 7.4e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  8  CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
      |||||||
Db  1  CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 44

RESULT 27
US-09-854-864-21
; Sequence 21, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-21

Query Match      88.0%; Score 249; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 7.4e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  8  CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
      |||||||
Db  1  CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 44

RESULT 28
US-09-855-158-21
; Sequence 21, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
```



```
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-21

Query Match      88.0%; Score 249; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 7.4e-22;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 51
        |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYCNASVTNSVKG 44

RESULT 29
US-09-854-864-7
; Sequence 7, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-7

Query Match      71.0%; Score 201; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
        |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

RESULT 30
US-09-855-158-7
; Sequence 7, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
```

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; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-7

Query Match      71.0%; Score 201; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
        |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

RESULT 31
US-09-854-864-13
; Sequence 13, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13

Query Match      71.0%; Score 201; DB 3; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.7e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 41
        |||||||
DB      1 CSQNEYFDSLHACIPQCLRCSSNTPLTCQRYC 34

RESULT 32
US-09-855-158-13
; Sequence 13, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
```



; TYPE: PRT  
; ORGANISM: Consensus  
US-09-855-158-13

Query Match 71.0%; Score 201; DB 3; Length 81;  
Best Local Similarity 100.0%; Pred. No. 4.7e-16;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYC 41  
Db 1 CSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYC 34

## RESULT 33

US-09-854-864-11  
; Sequence 11, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Murine  
US-09-854-864-11

Query Match 64.0%; Score 181; DB 3; Length 185;  
Best Local Similarity 70.8%; Pred. No. 2.4e-13;  
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 4 MAGQCSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYCNASVTNSVKG 51  
Db 1 MAQCQFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46

## RESULT 34

US-09-855-158-11  
; Sequence 11, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI  
; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-03-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Murine  
US-09-855-158-11

Query Match 64.0%; Score 181; DB 3; Length 185;  
Best Local Similarity 70.8%; Pred. No. 2.4e-13;  
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 4 MAGQCSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYCNASVTNSVKG 51  
Db 1 MAQCQFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46

## RESULT 35

US-10-216-074-17  
; Sequence 17, Application US/10216074  
; Publication No. US20030148445A1  
; GENERAL INFORMATION:  
; APPLICANT: Shu, Hong-Bing  
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND  
; FILE REFERENCE: 2879-72  
; CURRENT APPLICATION NUMBER: US/10/216,074  
; CURRENT FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US/09/565,423  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: UNKNOWN  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/132,892  
; PRIOR FILING DATE: 1999-05-06  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-216-074-17

Query Match 64.0%; Score 181; DB 4; Length 185;  
Best Local Similarity 70.8%; Pred. No. 2.4e-13;  
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 4 MAGQCSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYCNASVTNSVKG 51  
Db 1 MAQCQFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46

## RESULT 36

US-09-854-864-10  
; Sequence 10, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-854-864-10

Query Match 64.0%; Score 181; DB 3; Length 281;  
Best Local Similarity 70.8%; Pred. No. 3.6e-13;  
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;

Qy 4 MAGQCSQNEYFDSLHACIPCOLRCSSTNPPLTCQRYCNASVTNSVKG 51  
Db 1 MAQCQFHSEYFDSLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46



```

; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-854-864-12

Query Match          36.7%; Score 104; DB 3; Length 117;
Best Local Similarity 69.8%; Pred. No. 0.00018;
Matches 30; Conservative 1; Mismatches 2; Indels 10; Gaps 6;

Qy      9  SONEYFDSLHLHACIPCOLRCSSNTPPLTCORYCNASVTSVKG 51
      : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2  AQCEYFDSLHLHAC-PC-LRCS----PPTCQ-YC--SVT-SVKG 34

RESULT 40
US-09-855-158-12
; Sequence 12, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70,
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 117
; TYPE: PRT
; ORGANISM: human-murine Consensus
US-09-855-158-12

Query Match          36.7%; Score 104; DB 3; Length 117;
Best Local Similarity 69.8%; Pred. No. 0.00018;
Matches 30; Conservative 1; Mismatches 2; Indels 10; Gaps 6;

Qy      9  SONEYFDSLHLHACIPCOLRCSSNTPPLTCORYCNASVTSVKG 51
      : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2  AQCEYFDSLHLHAC-PC-LRCS----PPTCQ-YC--SVT-SVKG 34

RESULT 41
US-10-087-192-1647
; Sequence 1647, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02

```



```
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1647
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-1647

Query Match      25.3%; Score 71.5; DB 4; Length 249;
Best Local Similarity 35.3%; Pred. No. 2.6;
Matches 12; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

Qy      8 CSQNEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
Db      6 CPKQYWDSEKSKVSCALTCQSKS-ORTCTDFC 38

RESULT 42
US-10-180-903-2
; Sequence 2, Application US/10180903
; Publication No. US20030093824A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: SPC6 SERINE PROTEASE GENE DISRUPTIONS,
; FILE REFERENCE: R-720
; CURRENT APPLICATION NUMBER: US/10/180,903
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/300,978
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/324,820
; PRIOR FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1548
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-180-903-2

Query Match      24.9%; Score 70.5; DB 4; Length 1548;
Best Local Similarity 34.7%; Pred. No. 21;
Matches 17; Conservative 5; Mismatches 22; Indels 5; Gaps 1;

Qy      7 QCSQNEYFDSLHACIPQLRCSSNTPP-----LTCQRYCNASVTNSVK 50
Db      1151 ECAAVEYWDGSHRCQPCCHKXCSRCGSPSEDOQVTCPRETFLLNTTCVK 1199

RESULT 43
US-10-028-248A-75
; Sequence 75, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malyankar, Uriel
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangolli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glenda
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernev, Velizar
; APPLICANT: Si, Jingsheng

Query Match      24.6%; Score 69.5; DB 4; Length 5374;
Best Local Similarity 36.8%; Pred. No. 93;
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;

Qy      7 QCSQNEYFDSLHACIP-CQLRCSSNTP--PLTCQRYC 41
Db      3297 QCPTNSQFTDCLPSCVPCSNRCVTPSPVPSRCREGC 3334

RESULT 44
US-10-107-782-75
; Sequence 75, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Casman, Stacie
; APPLICANT: Colman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangolli, Esha,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malyankar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shimkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Taupier, Raymond, Jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zerhusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10/107,782
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
```



; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256,619  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/262,959  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/272,408  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/285,189  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/308,039  
; PRIOR FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: 60/311,266  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/279,344  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: CuraseqList version 0.1  
; SEQ ID NO 75  
; LENGTH: 5374  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-107-782-75

Query Match 24.6%; Score 69.5; DB 4; Length 5374;  
Best Local Similarity 36.8%; Pred. No. 93;  
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;  
  
QY 7 QCSQNEYFDSLHACIP-CQLRCSNTP--PLTCQRYC 41  
Db 3297 QCPNSQFTDCLPSCVPCSNRCVTSVPSSCREGC 3334

RESULT 45  
US-10-028-248A-74  
; Sequence 74, Application US/10028248A  
; Publication No. US20030235882A1  
; GENERAL INFORMATION:  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Vernet, Corine  
; APPLICANT: Casman, Stacie  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Miller, Charles  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Li, Li  
; APPLICANT: Taupier Jr, Raymond J  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Zernhusen, Bryan  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Colman, Steven  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Si, Jingsheng  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Stone, David  
; APPLICANT: Sciore, Paul  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Rothenberg, Mark  
; TITLE OF INVENTION: NO. US20030235882A1el Nucleic Acids and Polypeptides and Methods  
; FILE REFERENCE: 21402-222  
; CURRENT APPLICATION NUMBER: US/10/028,248A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256619  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/252959  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/272408  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/285189

; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/308039  
; PRIOR FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: 60/311266  
; PRIOR FILING DATE: 2001-08-09  
; NUMBER OF SEQ ID NOS: 211  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 74  
; LENGTH: 5376  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-028-248A-74

Query Match 24.6%; Score 69.5; DB 4; Length 5376;  
Best Local Similarity 36.8%; Pred. No. 93;  
Matches 14; Conservative 5; Mismatches 16; Indels 3; Gaps 2;  
  
QY 7 QCSQNEYFDSLHACIP-CQLRCSNTP--PLTCQRYC 41  
Db 3299 QCPNSQFTDCLPSCVPCSNRCVTSVPSSCREGC 3336

RESULT 46  
US-10-107-782-74  
; Sequence 74, Application US/10107782  
; Publication No. US20040018970A1  
; GENERAL INFORMATION:  
; APPLICANT: Boldog, Ferenc  
; APPLICANT: Casman, Stacie  
; APPLICANT: Colman, Steve  
; APPLICANT: Edinger, Shlomit  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Li, Li  
; APPLICANT: Liu, Xiaohong  
; APPLICANT: Malyankar, Uriel  
; APPLICANT: Miller, Charles  
; APPLICANT: Millet, Isabelle  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Rothenberg, Mark  
; APPLICANT: Sciore, Paul  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Si, Jingsheng  
; APPLICANT: Smithson, Glennda  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Stone, David  
; APPLICANT: Taupier, Raymond, Jr.  
; APPLICANT: Tchernev, Velizar,  
; APPLICANT: Vernet, Corine  
; APPLICANT: Zernhusen, Brian  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF  
; FILE REFERENCE: 21402-222CIP  
; CURRENT APPLICATION NUMBER: US/10/107,782  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 10/028,248  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/256,619  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/262,959  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/272,408  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 60/285,189  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/308,039  
; PRIOR FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: 60/311,266  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/279,344  
; PRIOR FILING DATE: 2001-03-28  
; NUMBER OF SEQ ID NOS: 215  
; SOFTWARE: CuraseqList version 0.1



; SEQ ID NO 74  
; LENGTH: 5376  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-107-782-74

Query Match 24.6%; Score 69.5; DB 4; Length 5376;  
Best Local Similarity 36.8%; Pred. No. 93; Mismatches 16; Indels 3; Gaps 2;  
Matches 14; Conservative 5

QY 7 QCSQNEYFDSLLHACIP-COLRCSSNTP--PLTCORYC 41  
DB 3299 QCTNSQFTDCLSCVPCSNRCVTSPPSSCREGC 3336

RESULT 47  
US-10-152-363A-62  
; Sequence 62, Application US/10152363A  
; Publication No. US20030103986A1  
; GENERAL INFORMATION:  
; APPLICANT: Rixon, Mark W.  
; APPLICANT: Gross, Jane A.  
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins  
; FILE REFERENCE: 01-20  
; CURRENT APPLICATION NUMBER: US/10/152,363A  
; CURRENT FILING DATE: 2002-05-20  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 62  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion protein.  
US-10-152-363A-62

Query Match 24.2%; Score 68.5; DB 4; Length 332;  
Best Local Similarity 27.9%; Pred. No. 7.8;  
Matches 12; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

QY 1 MLQWAGCQSQNEYFDSLLHACIPCOLRCSSNTPPLTCORYCNA 43  
DB 17 VLSAMRSCPEQYWDPLLTGTCMSCKTICNHQS-ORTCAAFCS 58

RESULT 48  
US-09-779-050A-45  
; Sequence 45, Application US/09779050A  
; Patent No. US20020160416A1  
; GENERAL INFORMATION:  
; APPLICANT: BOYLE, WILLIAM  
; APPLICANT: HSU, HAILING  
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY  
; FILE REFERENCE: A-570B  
; CURRENT APPLICATION NUMBER: US/09/779,050A  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/181,800  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 45  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-779-050A-45

Query Match 23.9%; Score 67.5; DB 3; Length 37;  
Best Local Similarity 30.6%; Pred. No. 1.2;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCORYCNA 43

DB 2 CPEEQYWDPLLTGTCMSCKTICNHQS-ORTCAAFCS 36

RESULT 49  
US-09-854-864-20  
; Sequence 20, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 59  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-20

Query Match 23.9%; Score 67.5; DB 3; Length 59;  
Best Local Similarity 30.6%; Pred. No. 1.8;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCORYCNA 43  
DB 1 CPEEQYWDPLLTGTCMSCKTICNHQS-ORTCAAFCS 35

RESULT 50  
US-09-855-158-20  
; Sequence 20, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLY  
; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 59  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-158-20

Query Match 23.9%; Score 67.5; DB 3; Length 59;  
Best Local Similarity 30.6%; Pred. No. 1.8;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCORYCNA 43  
DB 1 CPEEQYWDPLLTGTCMSCKTICNHQS-ORTCAAFCS 35

RESULT 51  
US-09-854-864-15  
; Sequence 15, Application US/09854864



```
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-15
```

```
Query Match      23.9%; Score 67.5; DB 3; Length 166;
Best Local Similarity 30.6%; Pred. No. 5.1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
```

```
QY      8 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYCNA 43
| : : | : | : | : | : | : | : | : | : | : | : | :
DB      34 CPEQYWDPLLGTCMCKTICNHQS-QRTCAAFCS 68
```

## RESULT 52

```
US-09-855-158-15
; Sequence 15, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLYS/AGP-3, AND TACI
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-855-158-15
```

```
Query Match      23.9%; Score 67.5; DB 3; Length 166;
Best Local Similarity 30.6%; Pred. No. 5.1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
```

```
QY      8 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYCNA 43
| : : | : | : | : | : | : | : | : | : | : | : | :
DB      34 CPEQYWDPLLGTCMCKTICNHQS-QRTCAAFCS 68
```

## RESULT 53

```
US-10-293-816-6
; Sequence 6, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; FILE REFERENCE: 44158/254623
```

```
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-816-6
```

```
Query Match      23.9%; Score 67.5; DB 4; Length 166;
Best Local Similarity 30.6%; Pred. No. 5.1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
```

```
QY      8 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYCNA 43
| : : | : | : | : | : | : | : | : | : | : | : | :
DB      34 CPEQYWDPLLGTCMCKTICNHQS-QRTCAAFCS 68
```

## RESULT 54

```
US-11-079-418-6
; Sequence 6, Application US/11079418
; Publication No. US20050183148A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/11/079,418
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-079-418-6
```

```
Query Match      23.9%; Score 67.5; DB 6; Length 166;
Best Local Similarity 30.6%; Pred. No. 5.1;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;
```

```
QY      8 CSONEYFDSLHACIPQCLRCSSNTPPLTCQRYCNA 43
| : : | : | : | : | : | : | : | : | : | : | : | :
DB      34 CPEQYWDPLLGTCMCKTICNHQS-QRTCAAFCS 68
```

## RESULT 55

```
US-10-684-149-18
; Sequence 18, Application US/10684149
; Publication No. US20050009149A1
; GENERAL INFORMATION:
; APPLICANT: West, James W.
; APPLICANT: Brandt, Cameron S.
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: Production of Homotrimeric Fusion
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: 02-17
```



[illegible]



```

; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-874-36

```

Query Match 23.9%; Score 67.5; DB 6; Length 265;  
Best Local Similarity 30.6%; Pred. No. 8.1;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

Qy	8	CSQNEYFDSILHACIPQQLRCSSNPPLTCQRYCNA	43
		: :   :   :   :   :   :   :   :   :	
Db	34	CPEQYWDPLGLGTGMSCKTICNHOS-ORTCAAFCS	68

```

RESULT 60
US-09-779-050A-43
? Sequence 43, Application US/09779050A
? Patent No. US2002160416A1
? GENERAL INFORMATION:
?
? APPLICANT: BOYLE, WILLIAM
? APPLICANT: HSU, HAILING
?
? TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
?
? FILE REFERENCE: A-570B
?
? CURRENT APPLICATION NUMBER: US/09/779,050A
? CURRENT FILING DATE: 2001-02-12
?
? PRIOR APPLICATION NUMBER: 60/181,800
? PRIOR FILING DATE: 2000-02-11
?
? NUMBER OF SEQ ID NOS: 52
? SOFTWARE: PatentIn version 3.0
?
? SEQ ID NO 43
?
? LENGTH: 291
?
? TYPE: PRT
?
? ORGANISM: Homo sapiens
US-09-779-050A-43

```

Query Match 23.9%; Score 67.5; DB 3; Length 291;  
Best Local Similarity 30.6%; Pred. No. 8.9;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

**Qy** 8 CSQNEYFDLSLLHACIPQLRCSSTPPLTLCQRYSNA 43  
| : | : | | | : | : | : | : | : | :  
**pB** 34 CPPEOYWDPLLTGTCMSCKTICNHOS-ORTCAAFCRS 68

```

RESULT 61
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PE253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 09/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22

```

```
; LENGTH: 293
;
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22
```

Query Match 23.9%; Score 67.5; DB 3; Length 293;  
Best Local Similarity 30.6%; Pred. No. 9;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

Qy	8	CSQNEYFDSLHACIPQCLRCSSNTPLTCORYCNA	43
		: : :     : : :   : :   : :   : :	
Dd	34	CPEQYWDPLGLTQMSCKTTCNHQS-QRTCAAFCS	68

RESULT 62  
US-09-854-864-14  
; Sequence 14, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCES: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-854-864-14

Query Match 23.9%; Score 67.5; DB 3; Length 293;  
Best Local Similarity 30.6%; Pred. No. 9;  
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

Qy 8 CSQNEYFDSLHACIPQLRCSNSTPLTCORYCNA 43  
| : : | | | : : : | : : | : :  
Db 34 CPESQYWDPLGLTNCMSKCTICNHQS-QRTCAAFCS 68

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RESULT 63
US-09-855-158-14
; Sequence 14, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS
; TITLE OF INVENTION: '3, AND TAC1
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-14

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Query Match	23.9%	Score 67.5;	DB 3;	Length 293;
Best Local Similarity	30.6%	Pred. No. 9;		



	Matches	11;	Conservative	9;	Mismatches	15;	Indels	1;	Gaps	1;
Qy	8	CSQNEYFSL	LHACIPQL	RCSSTNP	PLTCQRYCNA	43				
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Db	34	CPREQYWD	PLLTGTCM	SKTICNHQS	-ORTCAAFCS	68				

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RESULT 64
US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor Trl17
; FILE REFERENCE: PF524P1
; CURRENT APPLICATION NUMBER: US/09/961,376
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-376-2

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Query Match	23.9%	Score 67.5	DB 3	Length 293
Best Local Similarity	30.6%	Pred. No. 9		
Matches 11	Conservative	9	Mismatches 15	Indels 1
Gaps	1			

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RESULT 65
US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, WILLIAM
; APPLICANT: HSU, WILLIAM
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

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	Query Match	23.9%	Score 67.5	DB 3	Length 293
	Best Local Similarity	30.6%	Prod. No. 9		
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	Gaps				1
QY		8	CSQNEYFSLSLHACIPCOLRCSSNTPLTTCORYCNA	43	
ph		14	CPRECYWPIILGTGMSCKTICNHOS-ORTCAAFCS	68	

RESULT 66

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US-09-302-863--2
; Sequence 2, Application US/09302863
; Publication No. US2003002223A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wanwan S.
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-302-863--2
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      Best Local Similarity 30.6%; Pred. No. 9;
      Matches 11; Conservative 9; Mismatches 15; Indels 1.

Qy      8 CSQNEYFDLSLLHACIFCQLRCSSNTPLPTCRQYCN A 43
Db      34 CPREOYDPLILGTCMSCKTICNHOS-QRTCAAFCS 68

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RESULT 67
US-09-855-564-2
; Sequence 2, Application US/09855564
; Publication No. US20030165986A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wanwan S.
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/855,564
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/302,863
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-855-564-2

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	Query Match	23.9%	Score 67.5;	DB 3;	Length 293;
	Best Local Similarity	30.6%;	Pred. No. 9;		
	Matches 11; Conservative	9;	Mismatches 15;	Indels 1;	Gaps 1;
QY	8 CSQNEYFDSLHACIPCOLRCSSNTPLTTCQYCNA	43			
	: .   :               :				
DP	34 CPBROYWDPILGLTGMSCKTTICNHOS-ORTCAAFCS	68			
	: .   :               :				

RESULT 68  
US-10-087-192-1650  
; Sequence 1650, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02



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; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1650
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-1650

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY   8 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNA 43
    |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db    34 CPEEQYWDPLLGTCSCKTICNHQS-QRTCAAFCRS 68

RESULT 69
US-10-084-971-2
; Sequence 2, Application US/10084971
; Publication No. US20020187526A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neurokine-alpha Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PF524PCT
; CURRENT APPLICATION NUMBER: US/10/084,971
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/533,822
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-971-2

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY   8 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNA 43
    |:|:|:|:|:|:|:|:|:|:|:~
Db    34 CPEEQYWDPLLGTCSCKTICNHQS-QRTCAAFCRS 68

RESULT 70
US-10-068-725-4
; Sequence 4, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindevogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
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; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-4

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY   8 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNA 43
    |:|:~
Db    34 CPEEQYWDPLLGTCSCKTICNHQS-QRTCAAFCRS 68

RESULT 71
US-10-151-882-46
; Sequence 46, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-46

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Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY   8 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNA 43
    |:|:~
Db    34 CPEEQYWDPLLGTCSCKTICNHQS-QRTCAAFCRS 68

RESULT 72
US-10-293-816-2
; Sequence 2, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-2

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY   8 CSQNEYFDSLHACIPQLRCSSNTPPLTCORYCNA 43
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Db    34 CPEEQYWDPLLGTCSCKTICNHQS-QRTCAAFCRS 68

RESULT 73

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US-10-008-063-8
; Sequence 8, Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
; APPLICANT: Gross, Jane A.
; APPLICANT: Xu, Wenfeng
; APPLICANT: Henne, Randal M.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
; FILE REFERENCE: 00-103
; CURRENT APPLICATION NUMBER: US/10/008,063
; CURRENT FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 46
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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-008-063-8

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQLRCSSNTPLTCORYCNA 43
Db      34 CPBEQYWDPLLTGTCMSCKTICNHQS-ORTCAAFCRS 68

RESULT 74
US-10-152-363A-2
; Sequence 2, Application US/10152363A
; Publication No. US20030103986A1
; GENERAL INFORMATION:
; APPLICANT: Rixon, Mark W.
; APPLICANT: Gross, Jane A.
; TITLE OF INVENTION: TAC1-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/293,343
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-2

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQLRCSSNTPLTCORYCNA 43
Db      34 CPBEQYWDPLLTGTCMSCKTICNHQS-ORTCAAFCRS 68

RESULT 75
US-10-268-951-22
; Sequence 22, Application US/10268951
; Publication No. US20030166864A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P2
; CURRENT APPLICATION NUMBER: US/10/268,951
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 10/082,260
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: 09/879,919
; PRIOR FILING DATE: 2001-06-14
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; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/328,401
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/293,812
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-951-22

Query Match      23.9%; Score 67.5; DB 4; Length 293;
Best Local Similarity 30.6%; Pred. No. 9;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSQNEYFDSLHACIPQLRCSSNTPLTCORYCNA 43
Db      34 CPBEQYWDPLLTGTCMSCKTICNHQS-ORTCAAFCRS 68

Search completed: December 21, 2005, 16:30:36
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103	53.5	18.9	77	1	US-08-634-641-40	Sequence 40, Appl	176	53	18.7	167	1	US-08-050-319B-2	Sequence 2, Appl
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106	53.5	18.9	77	2	US-09-249-472-4	Sequence 4, Appl	179	53	18.7	167	1	US-08-465-982-57	Sequence 57, Appl
107	53.5	18.9	77	2	US-09-249-472-40	Sequence 40, Appl	180	53	18.7	197	2	US-08-828-683A-21	Sequence 21, Appl
108	53.5	18.9	77	2	US-09-249-451-4	Sequence 40, Appl	181	53	18.7	199	1	US-08-050-319B-48	Sequence 48, Appl
109	53.5	18.9	77	2	US-09-249-451-40	Sequence 40, Appl	182	53	18.7	199	1	US-08-465-982-48	Sequence 48, Appl
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111	53.5	18.9	77	2	US-08-809-455-40	Sequence 40, Appl	184	53	18.7	256	2	US-08-804-166-2	Sequence 2, Appl
112	53.5	18.9	77	2	US-09-249-461-4	Sequence 4, Appl	185	53	18.7	256	2	US-08-910-991-2	Sequence 2, Appl
113	53.5	18.9	77	2	US-09-249-461-40	Sequence 40, Appl	186	53	18.7	256	2	US-09-756-186-2	Sequence 2, Appl
114	53.5	18.9	77	2	US-09-249-448-4	Sequence 4, Appl	187	53	18.7	280	2	US-08-974-022-46	Sequence 46, Appl
115	53.5	18.9	77	2	US-09-249-448-40	Sequence 40, Appl	188	53	18.7	280	2	US-08-795-445A-46	Sequence 46, Appl
116	53.5	18.9	77	2	US-09-249-473-4	Sequence 4, Appl	189	53	18.7	280	2	US-08-795-447A-46	Sequence 46, Appl
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120	53.5	18.9	81	1	US-08-465-380-7	Sequence 7, Appl	193	53	18.7	280	2	US-08-577-788C-46	Sequence 46, Appl
121	53.5	18.9	81	1	US-08-480-478-36	Sequence 36, Appl	194	53	18.7	307	2	US-08-804-166-4	Sequence 4, Appl
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125	53.5	18.9	81	1	US-08-326-110A-36	Sequence 36, Appl	198	53	18.7	320	2	US-09-183-861-55	Sequence 55, Appl
126	53.5	18.9	81	1	US-08-634-641-7	Sequence 7, Appl	199	53	18.7	320	2	US-09-022-765-22	Sequence 22, Appl
127	53.5	18.9	81	2	US-09-249-471-7	Sequence 7, Appl	200	53	18.7	320	2	US-09-022-765-55	Sequence 55, Appl
128	53.5	18.9	81	2	US-09-249-472-7	Sequence 7, Appl	201	53	18.7	320	2	US-09-551-974A-22	Sequence 22, Appl
129	53.5	18.9	81	2	US-09-249-451-7	Sequence 7, Appl	202	53	18.7	320	2	US-09-551-974A-55	Sequence 55, Appl
130	53.5	18.9	81	2	US-08-809-455-7	Sequence 7, Appl	203	53	18.7	320	2	US-09-565-501A-22	Sequence 22, Appl
131	53.5	18.9	81	2	US-09-249-461-7	Sequence 7, Appl	204	53	18.7	320	2	US-09-565-501A-55	Sequence 55, Appl
132	53.5	18.9	81	2	US-09-249-448-7	Sequence 7, Appl	205	53	18.7	320	2	US-09-639-206A-22	Sequence 22, Appl
133	53.5	18.9	81	2	US-09-249-448-7	Sequence 7, Appl	206	53	18.7	320	2	US-09-639-206A-55	Sequence 55, Appl
134	53.5	18.9	81	2	US-09-498-556-7	Sequence 7, Appl	207	53	18.7	320	2	US-09-874-923-22	Sequence 22, Appl
135	53.5	18.9	84	2	US-09-950-933A-54	Sequence 54, Appl	208	53	18.7	320	2	US-09-874-923-55	Sequence 55, Appl
136	53.5	18.9	100	1	US-08-465-380-20	Sequence 20, Appl	209	53	18.7	320	2	US-08-798-841-22	Sequence 22, Appl
137	53.5	18.9	100	1	US-08-480-478-48	Sequence 48, Appl	210	53	18.7	336	2	US-08-804-166-8	Sequence 8, Appl
138	53.5	18.9	100	1	US-08-486-399-20	Sequence 20, Appl	211	53	18.7	336	2	US-08-910-991-8	Sequence 8, Appl
139	53.5	18.9	100	1	US-08-486-399-20	Sequence 20, Appl	212	53	18.7	336	2	US-09-756-186-8	Sequence 8, Appl
140	53.5	18.9	100	1	US-08-461-965-20	Sequence 20, Appl	213	53	18.7	426	2	US-08-747-562-37	Sequence 37, Appl
141	53.5	18.9	100	1	US-08-326-110A-48	Sequence 48, Appl	214	53	18.7	453	2	US-09-086-483A-5	Sequence 5, Appl
142	53.5	18.9	100	1	US-08-634-641-20	Sequence 20, Appl	215	53	18.7	453	2	US-09-580-212-5	Sequence 5, Appl
143	53.5	18.9	100	2	US-09-249-471-20	Sequence 20, Appl	216	53	18.7	453	2	US-09-769-402-5	Sequence 5, Appl
144	53.5	18.9	100	2	US-09-249-472-20	Sequence 20, Appl	217	53	18.7	455	1	US-08-050-319B-25	Sequence 25, Appl
145	53.5	18.9	100	2	US-09-249-451-20	Sequence 20, Appl	218	53	18.7	455	1	US-08-321-668-2	Sequence 2, Appl
146	53.5	18.9	100	2	US-08-809-455-20	Sequence 20, Appl	219	53	18.7	455	1	US-08-837-941-2	Sequence 2, Appl
147	53.5	18.9	100	2	US-09-249-461-20	Sequence 20, Appl	220	53	18.7	455	1	US-08-126-016-2	Sequence 2, Appl
148	53.5	18.9	100	2	US-09-249-448-20	Sequence 20, Appl	221	53	18.7	455	1	US-08-465-982-25	Sequence 25, Appl
149	53.5	18.9	100	2	US-09-249-473-20	Sequence 20, Appl	222	53	18.7	455	2	US-08-815-469-5	Sequence 5, Appl
150	53.5	18.9	100	2	US-09-498-556-20	Sequence 20, Appl	223	53	18.7	455	2	US-09-006-353A-3	Sequence 3, Appl
151	53.5	18.9	140	2	US-09-252-991A-25894	Sequence 25894, A	224	53	18.7	455	2	US-09-527-236A-5	Sequence 5, Appl
152	53.5	18.9	192	1	US-08-086-428B-81	Sequence 81, Appl	225	53	18.7	455	2	US-08-054-970-2	Sequence 2, Appl
153	53.5	18.9	192	1	US-08-468-570-81	Sequence 81, Appl	226	53	18.7	455	2	US-09-565-918-4	Sequence 4, Appl
154	53.5	18.9	192	1	US-08-290-665A-81	Sequence 81, Appl	227	53	18.7	455	2	US-09-573-986-3	Sequence 3, Appl
155	53.5	18.9	192	2	US-08-466-601A-81	Sequence 81, Appl	228	53	18.7	455	2	US-09-027-287-3	Sequence 3, Appl
156	53.5	18.9	192	4	PCT-US95-10398-81	Sequence 81, Appl	229	53	18.7	455	2	US-09-252-656B-3	Sequence 3, Appl
157	53.5	18.9	381	2	US-09-257-580-2	Sequence 2, Appl	230	53	18.7	455	2	US-08-406-824A-4	Sequence 4, Appl
158	53	18.7	93	2	US-09-640-211A-975	Sequence 975, App	231	53	18.7	455	2	US-09-523-323-3	Sequence 3, Appl
159	53	18.7	103	2	US-09-950-933A-52	Sequence 52, Appl	232	53	18.7	455	2	US-09-756-854-5	Sequence 5, Appl
160	53	18.7	108	2	US-09-950-933A-61	Sequence 61, Appl	233	53	18.7	455	2	US-09-557-908-5	Sequence 5, Appl
161	53	18.7	139	2	US-08-706-945D-129	Sequence 129, App	234	53	18.7	455	2	US-09-874-138-3	Sequence 3, Appl
162	53	18.7	153	1	US-08-050-319B-52	Sequence 52, Appl	235	53	18.7	455	2	US-09-333-966-5	Sequence 5, Appl
163	53	18.7	153	1	US-08-465-982-52	Sequence 52, Appl	236	53	18.7	455	2	US-09-565-009B-3	Sequence 3, Appl
164	53	18.7	153	1	US-08-219-237B-4	Sequence 4, Appl	237	53	18.7	455	2	US-10-175-903-4	Sequence 4, Appl
165	53	18.7	153	2	US-08-477-347-12	Sequence 12, Appl	238	53	18.7	455	2	US-10-041-574-5	Sequence 5, Appl
166	53	18.7	153	2	US-08-476-862-3	Sequence 3, Appl	239	53	18.7	455	2	US-09-095-094-5	Sequence 5, Appl
167	53	18.7	133	2	US-08-468-560C-4	Sequence 4, Appl	240	53	18.7	455	2	US-09-314-889-5	Sequence 5, Appl
168	53	18.7	153	2	US-09-800-909-3	Sequence 3, Appl	241	53	18.7	458	2	US-09-949-016-7946	Sequence 7946, App
169	53	18.7	153	2	US-09-800-908-12	Sequence 12, Appl	242	53	18.7	709	2	US-09-874-923-121	Sequence 121, App
170	53	18.7	153	2	US-09-884-987-4	Sequence 4, Appl	243	53	18.7	909	2	US-09-013-895A-4	Sequence 4, Appl
171	53	18.7	154	2	US-08-828-683A-12	Sequence 12, Appl	244	53	18.7	909	2	US-09-448-868-4	Sequence 4, Appl
172	53	18.7	154	2	US-09-523-323-53	Sequence 53, Appl	245	53	18.7	909	2	US-10-226-296-4	Sequence 4, Appl
173	53	18.7	157	1	US-08-050-319B-50	Sequence 50, Appl	246	53	18.7	3033	1	US-07-925-695-9	Sequence 9, Appl



Sequence 535, App  
Sequence 497, App  
Sequence 2, Appl  
Sequence 47, Appl  
Sequence 4, Appl  
Sequence 151, App  
Sequence 65, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 18, Appl  
Sequence 24, Appl  
Sequence 26, Appl  
Sequence 28, Appl  
Sequence 208, App  
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Sequence 61, Appl  
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Sequence 26, Appl  
Sequence 24, Appl  
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Sequence 14, Appl  
Sequence 12, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 302, App  
Sequence 6, Appl  
Sequence 40, Appl  
Sequence 48, Appl

ALIGNMENTS

RESULT 1  
US-09-565-423-11  
; Sequence 11, Application US/09565423  
; Patent No. 6475987  
; GENERAL INFORMATION:  
; APPLICANT: SHU, Hong-Bing  
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 2879-72  
; CURRENT APPLICATION NUMBER: US/09/565,423  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: UNKNOWN  
; PRIOR FILING DATE: 2000-05-01  
; PRIOR APPLICATION NUMBER: 60/132,892

Query Match 100.0%; Score 283; DB 2; Length 184;  
Best Local Similarity 100.0%; Pred. No. 4e-26; Indels 0; Gaps 0;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Query 1 MLQMGQCQSQNEFYFDSLHACIPQCQLRCSSTPPLTCQRYCNASVTNSVKG 51  
Db 1 MLQMGQCQSQNEFYFDSLHACIPQCQLRCSSTPPLTCQRYCNASVTNSVKG 51

RESULT 2  
US-09-949-016-11115  
; Sequence 11115, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11115  
; LENGTH: 192  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11115

Query Match 100.0%; Score 283; DB 2; Length 192;  
Best Local Similarity 100.0%; Pred. No. 4.2e-26; Indels 0; Gaps 0;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Query 1 MLQMGQCQSQNEFYFDSLHACIPQCQLRCSSTPPLTCQRYCNASVTNSVKG 51  
Db 9 MLQMGQCQSQNEFYFDSLHACIPQCQLRCSSTPPLTCQRYCNASVTNSVKG 59

RESULT 3  
US-09-854-864-6  
; Sequence 6, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 51  
; TYPE: PRT



; ORGANISM: Homo sapiens  
US-09-854-864-6

Query Match 95.1%; Score 269; DB 2; Length 51;  
Best Local Similarity 100.0%; Pred. No. 4.7e-25;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 51  
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DB 1 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 48  
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## RESULT 4

US-09-854-864-5  
; Sequence 5, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: BLYS/AGP-3, AND TACI  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; SOFTWARE: PatentIn version 3.1  
; NUMBER OF SEQ ID NOS: 31  
; SEQ ID NO 5  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-5

Query Match 95.1%; Score 269; DB 2; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1.8e-24;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 51  
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DB 1 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 48  
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## RESULT 5

US-09-854-864-9  
; Sequence 9, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: BLYS/AGP-3, AND TACI  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 283  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-9

Query Match 95.1%; Score 269; DB 2; Length 283;  
Best Local Similarity 100.0%; Pred. No. 2.9e-24;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 51  
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DB 1 MAGQCSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 48  
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## RESULT 6

US-09-854-864-21  
; Sequence 21, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: BLYS/AGP-3, AND TACI  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; SOFTWARE: PatentIn version 3.1  
; NUMBER OF SEQ ID NOS: 31  
; SEQ ID NO 21  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-21

Query Match 88.0%; Score 249; DB 2; Length 58;  
Best Local Similarity 100.0%; Pred. No. 1.3e-22;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 51  
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DB 1 CSQNEYFDSLHACIPCOLRCSSTPPLTCORYCNASVTNSVKG 44  
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## RESULT 7

US-09-854-864-7  
; Sequence 7, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: BLYS/AGP-3, AND TACI  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 34  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-7

Query Match 71.0%; Score 201; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.7e-17;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CSQNEYFDSLHACIPCOLRCSSTPPLTCORYC 41  
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DB 1 CSQNEYFDSLHACIPCOLRCSSTPPLTCORYC 34  
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## RESULT 8

US-09-854-864-13



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; Sequence 13, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Consensus
US-09-854-864-13
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Best Local Similarity 100.0%; Pred. No. 9.2e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 8 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 41
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DB 1 CSONEYFDSLHACIPQLRCSSNTPPLTCQRYC 34
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RESULT 9
US-09-565-423-17
; Sequence 17, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-565-423-17
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Query Match 64.0%; Score 181; DB 2; Length 185;
Best Local Similarity 70.8%; Pred. No. 5.2e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
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DB 1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSVTSSVKG 46
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RESULT 10
US-09-854-864-11
; Sequence 11, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
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; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
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; SEQ ID NO 11
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11
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Query Match 64.0%; Score 181; DB 2; Length 185;
Best Local Similarity 70.8%; Pred. No. 5.2e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
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RESULT 11
US-09-854-864-10
; Sequence 10, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10
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Query Match 64.0%; Score 181; DB 2; Length 281;
Best Local Similarity 70.8%; Pred. No. 8.2e-14;
Matches 34; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
```

```
QY 4 MAGQCSQNEYFDSLHACIPQLRCSSNTPPLTCQRYCNASVTNSVKG 51
| | | | | | | | | | | | | | | | | | | | | |
DB 1 MAQQCFHSEYFDSLHACKPCHLRCSN--PPATCQPCDPSVTSSVKG 46
```

```
RESULT 12
US-09-854-864-12
; Sequence 12, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
```







```

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-290-333-6

Query Match      23.9%; Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPCOLRCSNTPTLTQORYCNA 43
DB      34 CPEEQYWDPLLGTCMSCKTICNHQS-ORTCAAFCS 68

RESULT 16
US-09-782-857A-6
; Sequence 6, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857A-6

Query Match      23.9%; Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

```

```

QY      8 CSONEYFDSLHACIPCOLRCSNTPTLTQORYCNA 43
DB      34 CPEEQYWDPLLGTCMSCKTICNHQS-ORTCAAFCS 68

RESULT 17
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-15

Query Match      23.9%; Score 67.5; DB 2; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.4;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY      8 CSONEYFDSLHACIPCOLRCSNTPTLTQORYCNA 43
DB      34 CPEEQYWDPLLGTCMSCKTICNHQS-ORTCAAFCS 68

RESULT 18
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800

```



```

; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-810-572A-2

Query Match 23.9%; Score 67.5; DB 1; Length 293;
Best Local Similarity 30.6%; Pred. No. 2.6;
Matches 11; Conservative 9; Mismatches 15; Indels 1; Gaps 1;

QY 8 CSQNEYVDSLLHACIPQLRCSNTPPLTCQRYCNA 43
| : | : | : | : | : | : | : | : | :
DB 34 CPBEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCS 68

RESULT 19
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bran, Richard J.
; INVENTOR: Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
;
US-09-290-333-2

Query Match 23.9%; Score 67.5; DB 2; Length 293;

```











```
RESULT 30
US-09-252-991A-18110
; Sequence 18110, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18110
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18110

Query Match      20.8%; Score 59; DB 2; Length 556;
Best Local Similarity 40.0%; Pred. No. 51;
Matches 14; Conservative 6; Mismatches 11; Indels 4; Gaps 2;

Qy      20 ACIPQLRCSSNTPLTCQ---RYCNASVTNSVKG 51
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      503 ACPSSARRSASSPTTACSWPRCCSAR-SSSVSG 536

RESULT 31
US-09-270-767-41037
; Sequence 41037, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41037
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41037

Query Match      20.7%; Score 58.5; DB 2; Length 670;
Best Local Similarity 42.9%; Pred. No. 72;
Matches 15; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

Qy      6 GQCQNEFYDSLHACIPQLRCSSNTPLTCQRY 40
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      455 GRCFKNRQLSHLRYCKKCTI-CSSNI--LRCTRY 486

RESULT 32
US-09-270-767-56253
; Sequence 56253, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56253
```

```
; LENGTH: 670
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56253

Query Match      20.7%; Score 58.5; DB 2; Length 670;
Best Local Similarity 42.9%; Pred. No. 72;
Matches 15; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

Qy      6 GQCQNEFYDSLHACIPQLRCSSNTPLTCQRY 40
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      455 GRCFKNRQLSHLRYCKKCTI-CSSNI--LRCTRY 486

RESULT 33
US-09-561-818A-4
; Sequence 4, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561.818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1792
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-4

Query Match      20.5%; Score 58; DB 2; Length 1792;
Best Local Similarity 21.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 13; Mismatches 20; Indels 16; Gaps 2;

Qy      5 AGQCQNEFYDSLHACIPQ-----LRCSNTPLTCQRYCNASVTNSV 49
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      40 AERKNAG-PPHTLSGECVPCDCNGNSNECLDGSYCVHCORNTTGEHCEKCLDGYIGDSI 98

Qy      50 KG 51
      :|
Db      99 RG 100

RESULT 34
US-09-561-818A-8
; Sequence 8, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tryggvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99,274-D
; CURRENT APPLICATION NUMBER: US/09/561.818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1800
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-818A-8

Query Match      20.5%; Score 58; DB 2; Length 1800;
Best Local Similarity 21.0%; Pred. No. 2.4e+02;
Matches 13; Conservative 13; Mismatches 20; Indels 16; Gaps 2;

Qy      5 AGQCQNEFYDSLHACIPQ-----LRCSNTPLTCQRYCNASVTNSV 49
      |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
```







Query Match 20.1%; Score 57; DB 2; Length 201;  
Best Local Similarity 31.1%; Pred. No. 30;  
Matches 14; Conservative 4; Mismatches 13; Indels 14; Gaps 3;

Qy 7 QCSQNEVFDLLHAC--IPQLRC-----SSNTPLTLCQRYCN 42  
Db 33 KQENSSF-----ACPKNCSLECSGYQDMSNGCPTCECRNYCN 72

## RESULT 40

US-09-589-892B-11

; Sequence 11, Application US/09589892B

; Patent No. 6689583

; GENERAL INFORMATION:

; APPLICANT: Jenuwein, Thomas

; APPLICANT: Laible, Gotz

; APPLICANT: O'Carroll, Donal

; APPLICANT: Eisenhaber, Frank

; APPLICANT: Rea, Stephen

; TITLE OF INVENTION: Chromatin-Regulator Genes

; FILE REFERENCE: 0652.1670001

; CURRENT APPLICATION NUMBER: US/09/589,892B

; CURRENT FILING DATE: 2000-06-09

; PRIOR APPLICATION NUMBER: US 08/945,988

; PRIOR FILING DATE: 1997-11-10

; PRIOR APPLICATION NUMBER: PCT/EP96/01818

; PRIOR FILING DATE: 1996-05-02

; PRIOR APPLICATION NUMBER: DE 195 16 776.7

; PRIOR FILING DATE: 1995-05-10

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11

; LENGTH: 760

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-589-892B-11

Query Match 20.1%; Score 57; DB 2; Length 760;  
Best Local Similarity 26.7%; Pred. No. 1.2e+02;  
Matches 12; Conservative 8; Mismatches 23; Indels 2; Gaps 1;

Qy 2 LQAGQCSQNEVFDLL--HACICQLRCSSNTPLTLCQRYCNAS 44  
Db 521 IQLKSSSNHVNVTYTRCDHPGCDMNCSCIQTQNFCEKFCNCS 565

## RESULT 41

US-08-276-967-2

; Sequence 2, Application US/08276967

; Patent No. 5851817

; GENERAL INFORMATION:

; APPLICANT: Hardy, Daniel M.

; APPLICANT: Garbers, David L.

; TITLE OF INVENTION: Spectes-Specific Egg-Binding Proteins of

; TITLE OF INVENTION: Sperm

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White &amp; Durkee

; STREET: P. O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/276,967

; FILING DATE: Submitted Herewith

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: UTSD:418\KIT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 713-787-1400  
; TELEFAX: 713-789-2679  
; TELEX: 79-0924

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2476 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-276-967-2

Query Match 19.8%; Score 56; DB 1; Length 2476;  
Best Local Similarity 31.6%; Pred. No. 5.7e+02;  
Matches 12; Conservative 8; Mismatches 14; Indels 4; Gaps 2;

Qy 8 CSQNEVFDLLHACIP-CQ---LRCSNTPPLTLCQRYC 41  
Db 1851 CSAHSVYTCVPSCLPSCQDPEGQCTGAGAPSTCEGEC 1888

## RESULT 42

US-10-037-417-6

; Sequence 6, Application US/10037417

; Patent No. 6903201

; GENERAL INFORMATION:

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Alsobrook II, John P

; APPLICANT: Tchernev, Velizar T

; APPLICANT: Liu, Xiaohong

; APPLICANT: Spytek, Kimberly A

; APPLICANT: Patturajan, Meera

; APPLICANT: Grosse, William M

; APPLICANT: Lepley, Denise M

; APPLICANT: Burgess, Catherine E

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Li, Li

; APPLICANT: Gorman, Linda

; APPLICANT: Edinger, Shomit R

; APPLICANT: Sciore, Paul

; APPLICANT: Ellerman, Karen

; APPLICANT: Malyankar, Uriel M

; APPLICANT: Rothenberg, Mark

; APPLICANT: Stone, David J

; APPLICANT: Boldog, Ferenc L

; APPLICANT: Guo, Xiaojia

; APPLICANT: Shenoy, Suresh G

; APPLICANT: Anderson, David W

; APPLICANT: Padigaru, Muralidhara

; APPLICANT: Taupier Jr, Raymond J

; APPLICANT: Miller, Charles E

; APPLICANT: Eisen, Andrew J

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-235

; CURRENT APPLICATION NUMBER: US/10/037,417

; CURRENT FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: 60/260,018

; PRIOR FILING DATE: 2001-01-05

; PRIOR APPLICATION NUMBER: 60/260,360

; PRIOR FILING DATE: 2001-01-08

; PRIOR APPLICATION NUMBER: 60/272,411

; PRIOR FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 60/272,817

; PRIOR FILING DATE: 2001-03-02

; PRIOR APPLICATION NUMBER: 60/291,186

; PRIOR FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: 60/303,231

; PRIOR FILING DATE: 2001-07-05







```
;
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,388
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0230-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5405 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-718-388-9

Query Match 19.4%; Score 55.5; DB 2; Length 5405;
Best Local Similarity 33.3%; Pred. No. 1.5e+03;
Matches 12; Conservative 6; Mismatches 13; Indels 5; Gaps 2;

QY 7 QCSQNEYFDSLHACIPCOLRCSSNTPPLTCORYC 41
Db 2732 ECPQSHYE----LCADTCSLGCALSAPLQCPDGC 2763

RESULT 46
US-09-270-767-56958
; Sequence 56958, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56958
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56958

Query Match 19.4%; Score 55; DB 2; Length 142;
Best Local Similarity 29.2%; Pred. No. 36;
Matches 14; Conservative 8; Mismatches 20; Indels 6; Gaps 2;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCOR--YCNASVTNSV 49
Db 29 VATYCTGDDYDLSGLCYCVSRQVA----TPVAGCNRCQYATSTFFNAV 72

RESULT 47
US-09-270-767-41714
; Sequence 41714, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41714
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-41714

Query Match 19.4%; Score 55; DB 2; Length 392;
Best Local Similarity 29.2%; Pred. No. 1.1e+02;
Matches 14; Conservative 8; Mismatches 20; Indels 6; Gaps 2;

QY 4 MAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTCOR--YCNASVTNSV 49
Db 279 VATYCTGDDYDLSGLCYCVSRQVA----TPVAGCNRCQYATSTFFNAV 322

RESULT 48
US-09-902-540-11984
; Sequence 11984, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11984
; LENGTH: 991
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11984

Query Match 19.4%; Score 55; DB 2; Length 991;
Best Local Similarity 26.8%; Pred. No. 2.8e+02;
Matches 15; Conservative 9; Mismatches 24; Indels 8; Gaps 2;

QY 3 QMAGQCSQNEYFDSLHACIPCOLRCSSNTPPLTC-----QRYCNASVTNSVKG 51
Db 453 QVVSACAEDPE-DTALRGCVPRVRAIINTPTGCSIQAPLPDAVNAVGVPLTLTG 507

RESULT 49
US-09-561-818A-12
; Sequence 12, Application US/09561818A
; Patent No. 6638907
; GENERAL INFORMATION:
; APPLICANT: Kortessmaa, Jarrko
; APPLICANT: Tytgqvason, Karl
; TITLE OF INVENTION: Laminin 8 and Methods For Its Use
; FILE REFERENCE: 99/274-D
; CURRENT APPLICATION NUMBER: US/09/561,818A
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1792
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-561-818A-12

Query Match 19.4%; Score 55; DB 2; Length 1792;
Best Local Similarity 22.6%; Pred. No. 5.3e+02;
Matches 14; Conservative 10; Mismatches 22; Indels 16; Gaps 2;

QY 5 AGQCSQNEYFDSLHACIPQ-----LRCSNTPPLTCORYCNASVTNSV 49
Db 40 AERCDAG-FFRTLSGECAPDCDNGNSHECLDGSFCLHCQRTTGEHCCKLDGYIGDSI 98
QY 50 KG 51
Db 99 RG 100
```



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/999,811
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-999-811-4

Query Match 19.3%; Score 54.5; DB 1; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLRCSSNTP--PLTCQRYCNAS 44
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

RESULT 53
US-08-824-996-2
Sequence 2, Application US/08824996B
Patent No. 5935820
GENERAL INFORMATION:
APPLICANT: Hu, Jing-Shan
APPLICANT: Rosen, Craig A.
APPLICANT: Cao, Liang
TITLE OF INVENTION: Polynucleotides Encoding Vascular Endothelial Growth
FILE REFERENCE: PF112D1
CURRENT APPLICATION NUMBER: US/08/824,996B
CURRENT FILING DATE: 1997-03-27
EARLIER APPLICATION NUMBER: 08/207,550
EARLIER FILING DATE: 1994-03-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
US-08-824-996-2

Query Match 19.3%; Score 54.5; DB 1; Length 350;
Best Local Similarity 35.0%; Pred. No. 1.1e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
STREET: 1100 NEW YORK AVENUE
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/999,811
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/207,550
FILING DATE: 8-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,968
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MARKOWICZ, KAREN R.
REGISTRATION NUMBER: 36,351
REFERENCE/DOCKET NUMBER: 1488.1000004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2600
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-999-811-4

Query Match 19.4%; Score 55; DB 2; Length 1816;
Best Local Similarity 22.8%; Pred. No. 5.4e+02;
Matches 14; Conservative 10; Mismatches 22; Indels 16; Gaps 2;

QY 5 AGCQNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNASVNSV 49
DB 64 AERCDAG-FPRTLSGECAPDCNGNSHECLDGSFCLHQRNTTGEHCKECLDGVIGDSI 122

QY 50 KG 51
DB 123 RG 124

RESULT 51
US-09-270-767-32231
Sequence 32231, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32231
LENGTH: 145
TYPE: PRT
ORGANISM: Drosophila melanogaster
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-32231

Query Match 19.3%; Score 54.5; DB 2; Length 145;
Best Local Similarity 27.8%; Pred. No. 42;
Matches 15; Conservative 3; Mismatches 23; Indels 13; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQ-----LRCSNTPPLTCQRYCNASVNS 48
DB 12 QCHRRTHGTGRPHVCTVCQGFARSYKLOQHMRIHSGRPFYKC-TYCEKSFQTS 64

RESULT 52
US-08-999-811-4
Sequence 4, Application US/08999811
Patent No. 5932540
GENERAL INFORMATION:
APPLICANT: HU JING-SHAN
APPLICANT: ROSEN, CRAIG A.
APPLICANT: CAO, LIANG
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
NUMBER OF SEQUENCES: 15

```



QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

RESULT 54  
US-09-042-105-4  
; Sequence 4, Application US/09042105  
; Patent No. 6040157  
; GENERAL INFORMATION:  
; APPLICANT: HU, JING-SHAN  
; APPLICANT: ROSEN, CRAIG A.  
; APPLICANT: CAO, LIANG  
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
; STREET: 1100 NEW YORK AVENUE  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/042.105  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/207,550  
; FILING DATE: 8-MAR-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/465,968  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: TO BE ASSIGNED  
; FILING DATE: 24-DEC-1997  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERIC K. STEFFE  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1000003/EKS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2600  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 350 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-042-105-4

Query Match 19.3%; Score 54.5; DB 2; Length 350;  
Best Local Similarity 35.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

RESULT 55  
US-08-510-133A-33  
; Sequence 33, Application US/08510133A  
; Patent No. 6221839  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari

; Joukov, Vladomir  
; TITLE OF INVENTION: Receptor Ligand  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/510.133A  
; FILING DATE: 01-Aug-1995  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153  
; REFERENCE/DOCKET NUMBER: 28113/32863  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 350 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-08-510-133A-33

Query Match 19.3%; Score 54.5; DB 2; Length 350;  
Best Local Similarity 35.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
Db 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKACECTES 296

RESULT 56  
US-08-585-895-33  
; Sequence 33, Application US/08585895  
; Patent No. 6245530  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Joukov, Vladomir  
; TITLE OF INVENTION: Receptor Ligand  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/585,895  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153



REFERENCE/DOCKET NUMBER: 28113/33072  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-585-895-33

Query Match 19.3%; Score 54.5; DB 2; Length 350;  
Best Local Similarity 35.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLRCSSNTP--PLTCQRYCNAS 44  
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 296

RESULT 57  
US-10-084-488-4  
Sequence 4, Application US/10084488  
Patent No. 6734285  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/084,488  
FILING DATE: 28-Feb-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/623,725  
FILING DATE: 07-Sep-2000  
APPLICATION NUMBER: US 09/042,105  
FILING DATE: 13-MAR-1998  
APPLICATION NUMBER: US 09/107,997  
FILING DATE: 30-JUN-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: MICHELE M. WALES  
REGISTRATION NUMBER: 43,975  
REFERENCE/DOCKET NUMBER: PF112PCT3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301)309-8504  
TELEFAX: (301)309-8439

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-084-488-4  
Query Match 19.3%; Score 54.5; DB 2; Length 350;  
Best Local Similarity 35.0%; Pred. No. 1.1e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLRCSSNTP--PLTCQRYCNAS 44  
DB 258 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 296

RESULT 58  
US-08-999-811-2  
Sequence 2, Application US/08999811  
Patent No. 5932540  
GENERAL INFORMATION:  
APPLICANT: HU, JING-SHAN  
APPLICANT: ROSEN, CRAIG A.  
APPLICANT: CAO, LIANG  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 NEW YORK AVENUE  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/999,811  
FILING DATE: HERewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/207,550  
FILING DATE: 8-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: MARKOWICZ, KAREN R.  
REGISTRATION NUMBER: 36,351  
REFERENCE/DOCKET NUMBER: 1488.1000004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 419 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-999-811-2

Query Match 19.3%; Score 54.5; DB 1; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQLRCSSNTP--PLTCQRYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 59  
US-09-042-105-2  
Sequence 2, Application US/09042105  
Patent No. 6040157  
GENERAL INFORMATION:  
APPLICANT: HU, JING-SHAN  
APPLICANT: ROSEN, CRAIG A.  
APPLICANT: CAO, LIANG  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX



STREET: 1100 NEW YORK AVENUE  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042.105  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/207,550  
FILING DATE: 8-MAR-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,968  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
APPLICATION NUMBER: TO BE ASSIGNED  
FILING DATE: 24-DEC-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: ERIC K. STEFFE  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 419 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-042-105-2

Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QCSQNEFYDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
Db 327 QCGANREFDENTCCVC-CRRTCPRNQPLNPGKACECTES 365

RESULT 60  
US-09-042-105-18  
Sequence 18, Application US/09042105  
Patent No. 6040157  
GENERAL INFORMATION:  
APPLICANT: HU, JING-SHAN  
APPLICANT: ROSEN, CRAIG A.  
APPLICANT: CAO, LIANG  
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 NEW YORK AVENUE  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/042.105  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/207,550  
FILING DATE: 8-MAR-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/465,968  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
APPLICATION NUMBER: TO BE ASSIGNED  
FILING DATE: 24-DEC-1997  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: ERIC K. STEFFE  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1000003/EKS  
TELEPHONE: (202)371-2600  
TELEFAX: (202)371-2540  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 419 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-042-105-18

Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QCSQNEFYDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
Db 327 QCGANREFDENTCCVC-CRRTCPRNQPLNPGKACECTES 365

RESULT 61  
US-08-795-430-8  
Sequence 8, Application US/08795430  
Patent No. 6130071  
GENERAL INFORMATION:  
APPLICANT: Altalo, Kari  
APPLICANT: Joukov, Vladimir  
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Garstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,430  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FI96/00427  
FILING DATE: 01-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/671,573  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:



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; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; PRIOR APPLICATION DATA: 08/510,133
; FILING DATE: 01-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/33691
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-430-8

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDLSLHACIPQLRCSNTP--PLTCQRYCNAS 44
||| ||| :|: ||| ||| |||
Db 327 QCGANREFDNTCCQV-CKRTCPRNQPLNPGKCACTES 365

RESULT 62
US-08-510-133A-35
; Sequence 35, Application US/08510133A
; Patent No. 6221839
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; Joukov, Vladimir
; TITLE OF INVENTION: Receptor Ligand
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,133A
; FILING DATE: 01-AUG-1995
; CLASSIFICATION: <UNKNOWN>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/32863
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid

Query Match      19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDLSLHACIPQLRCSNTP--PLTCQRYCNAS 44
||| ||| :|: ||| ||| |||
Db 327 QCGANREFDNTCCQV-CKRTCPRNQPLNPGKCACTES 365

RESULT 63
US-09-355-700-8
; Sequence 8, Application US/093555700
; Patent No. 6361946
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; Helsinki University Licensing
; Alitalo, Kari (U.S. only)
; Joukov, Vladimir (U.S. only)
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/355,700
; FILING DATE: 05-NO. 6361946-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/795,430
; FILING DATE: 05-FEB-1997
; APPLICATION NUMBER: PCT/FI96/00427
; FILING DATE: 01-AUG-1996
; APPLICATION NUMBER: 08/671,573
; FILING DATE: 28-JUN-1996
; APPLICATION NUMBER: 08/601,132
; FILING DATE: 14-FEB-1996
; APPLICATION NUMBER: 08/585,895
; FILING DATE: 12-JAN-1996
; APPLICATION NUMBER: 08/510,133
; FILING DATE: 01-AUG-1995
; APPLICATION NUMBER: 08/340,011
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28967/34140
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
; US-09-355-700-8
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Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQQLRCSSNTP--PLTCORYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 64  
US-09-355-700-58  
; Sequence 58, Application US/09355700  
; Patent No. 6361946  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research  
; Helsinki University Licensing  
; Alitalo, Kari (U.S. only)  
; Joukov, Vladimir (U.S. only)  
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/355,700  
; FILING DATE: 05-NOV-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/795,430  
; FILING DATE: 05-FEB-1997  
; APPLICATION NUMBER: PCT/FI96/00427  
; FILING DATE: 01-AUG-1996  
; APPLICATION NUMBER: 08/671,573  
; FILING DATE: 28-JUN-1996  
; APPLICATION NUMBER: 08/601,132  
; FILING DATE: 14-FEB-1996  
; APPLICATION NUMBER: 08/585,895  
; FILING DATE: 12-JAN-1996  
; APPLICATION NUMBER: 08/510,133  
; FILING DATE: 01-AUG-1995  
; APPLICATION NUMBER: 08/340,011  
; FILING DATE: 14-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153  
; REFERENCE/DOCKET NUMBER: 28967/34140  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 419 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: other  
; LOCATION: 156  
; OTHER INFORMATION: /note= "codon 156 can be anything other  
; than cysteine, or can be nothing"

; SEQUENCE DESCRIPTION: SEQ ID NO: 58:  
US-09-355-700-58  
Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQQLRCSSNTP--PLTCORYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 65  
US-08-601-132-33  
; Sequence 33, Application US/08601132  
; Patent No. 6403088  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Joukov, Vladimir  
; TITLE OF INVENTION: Receptor Ligand  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/601,132  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153  
; REFERENCE/DOCKET NUMBER: 28113/33118  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 419 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-601-132-33  
Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQQLRCSSNTP--PLTCORYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 66  
US-08-706-054A-3  
; Sequence 3, Application US/08706054A  
; Patent No. 6451764  
; GENERAL INFORMATION:  
; APPLICANT: Lee, James  
; TITLE OF INVENTION: VEGF-Related Protein  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.



STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/706,054A  
FILING DATE: 30-Aug-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/003491  
FILING DATE: 08-Sep-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: P-40,378  
REFERENCE/DOCKET NUMBER: P0963R1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 419 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-08-706-054A-3

Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 67  
US-09-313-299-3  
Sequence 3, Application US/09313299B  
Patent No. 6576608  
GENERAL INFORMATION:  
APPLICANT: Lee, James  
TITLE OF INVENTION: VEGF-RELATED PROTEIN  
FILE REFERENCE: P0963R1D1  
CURRENT APPLICATION NUMBER: US/09/313,299B  
EARLIER FILING DATE: 1999-05-17  
EARLIER APPLICATION NUMBER: US 08/706,054  
EARLIER FILING DATE: 1996-08-30  
EARLIER APPLICATION NUMBER: US 60/003,491  
EARLIER FILING DATE: 1995-09-08  
NUMBER OF SEQ ID NOS: 12  
SEQ ID NO 3  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Human  
FEATURE:  
NAME/KEY: Human  
LOCATION: 1-419  
OTHER INFORMATION: Sequence source: VRP  
Patent No. 6576608  
US-09-313-299-3

Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365  
RESULT 68  
US-08-465-968-2  
Sequence 2, Application US/08465968E  
Patent No. 6608182  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Vascular Endothelial Growth Factor 2  
FILE REFERENCE: PF112P1  
CURRENT APPLICATION NUMBER: US/08/465,968E  
CURRENT FILING DATE: 1995-06-06  
EARLIER APPLICATION NUMBER: 08/207,550  
EARLIER FILING DATE: 1994-03-08  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-08-465-968-2

Query Match 19.3%; Score 54.5; DB 2; Length 419;  
Best Local Similarity 35.0%; Pred. No. 1.3e+02;  
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

QY 7 QCSQNEYFDSLHACIPQCLRCSSNTP--PLTCQRYCNAS 44  
DB 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 69  
US-08-671-573B-33  
Sequence 33, Application US/08671573B  
Patent No. 6645933  
GENERAL INFORMATION:  
APPLICANT: Alitalo, Kari  
APPLICANT: Joukov, Vladimir  
TITLE OF INVENTION: Receptor Ligand  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/671,573B  
FILING DATE: 28-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/601,132  
FILING DATE: 14-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/585,895  
FILING DATE: 12-JAN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/510,133  
FILING DATE: 01-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Gass, David A.  
REGISTRATION NUMBER: 38,153  
REFERENCE/DOCKET NUMBER: 28967/33348  
TELECOMMUNICATION INFORMATION:



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; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-671-573B-33

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QCSQNEYFDSLHACIPQLRCSNTP--PLTCQRYCNAS 44
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 70
US-09-438-046-14
; Sequence 14, Application US/09438046
; Patent No. 6706687
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: AASE, Karin
; APPLICANT: LEE, Xuri
; APPLICANT: PONTN, Annica
; APPLICANT: UUTELA, Marko
; APPLICANT: ALITALO, Kari
; APPLICANT: OESTMAN, Arne
; APPLICANT: HELDIN, Carl-Henrik
; TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING
; FILE REFERENCE: Ulf Eriksson et al 1064-44833
; CURRENT APPLICATION NUMBER: US/09/438,046
; CURRENT FILING DATE: 1999-11-10
; EARLIER APPLICATION NUMBER: 60/107,852
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 60/113,997
; EARLIER FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: 60/150,604
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: 60/157,108
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 60/157,756
; EARLIER FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-438-046-14

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QCSQNEYFDSLHACIPQLRCSNTP--PLTCQRYCNAS 44
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 71
US-09-631-092B-33
; Sequence 33, Application US/09631092B
; Patent No. 6730658
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: RECEPTOR LIGAND VEGF-C
; FILE REFERENCE: 28967/33348A
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; CURRENT APPLICATION NUMBER: US/09/631,092B
; CURRENT FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 08/671,573
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/601,132
; PRIOR FILING DATE: 1996-02-14
; PRIOR APPLICATION NUMBER: 08/585,895
; PRIOR FILING DATE: 1996-01-12
; PRIOR APPLICATION NUMBER: 08/510,133
; PRIOR FILING DATE: 1995-08-01
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 33
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-631-092B-33

Query Match 19.3%; Score 54.5; DB 2; Length 419;
Best Local Similarity 35.0%; Pred. No. 1.3e+02;
Matches 14; Conservative 2; Mismatches 21; Indels 3; Gaps 2;

Qy 7 QCSQNEYFDSLHACIPQLRCSNTP--PLTCQRYCNAS 44
Db 327 QCGANREFDENTCQCV-CKRTCPRNQPLNPGKCACTES 365

RESULT 72
US-10-084-488-2
; Sequence 2, Application US/10084488
; Patent No. 6734285
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/084,488
; FILING DATE: 28-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/623,725
; FILING DATE: 07-Sep-2000
; APPLICATION NUMBER: US 09/042,105
; FILING DATE: 13-MAR-1998
; APPLICATION NUMBER: US 09/107,997
; FILING DATE: 30-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: MICHELE M. WALES
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF112PCT3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301)309-8504
; TELEFAX: (301)309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-084-488-2
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